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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	08
	Maximum Match	1000

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	2402	100.0	2402	6	AX365149	AX365149 Sequence
2	2334	97.2	2952	6	BD178872	BD178872 NR10 split
3	2334	97.2	5271	6	BD178871	BD178871 NR10 split
4	2258.6	94.0	2480	6	AX467333	AX467333 Sequence
5	2225.6	92.7	2238	6	AX467335	AX467335 Sequence
6	2204	91.8	3072	6	BD178873	BD178873 NR10 split
7	2195.8	91.4	2199	9	AF486620	AF486620 Homo sapi
8	2160	88.9	2870	6	BD178874	BD178874 NR10 split
9	2136	88.9	2858	6	BD178875	BD178875 NR10 split
10	2075	86.4	2529	6	AX365193	AX365193 Sequence
11	2016	83.9	4315	6	BD178870	BD178870 NR10 split
12	1972	82.1	2776	6	BD178876	BD178876 NR10 split
13	1947	81.1	2119	6	BD091877	BD091877 Novel hem
14	1945.4	81.0	2913	6	AX365201	AX365201 Sequence
15	1932.8	80.5	2969	6	BD091864	BD091864 Novel hem
16	1592.2	66.3	2196	6	AX365152	AX365152 Sequence
17	1586.8	66.1	2245	6	AX365216	AX365216 Sequence
18	1568.4	65.3	2445	6	AX358838	AX358838 Sequence
19	1568.4	65.3	2445	6	AX362331	AX362331 Sequence
20	1568.4	65.3	2445	6	AX454786	AX454786 Sequence
21	1568.4	65.3	2445	6	AX491264	AX491264 Sequence
22	1481.6	61.7	1761	9	AF106913	AF106913 Homo sapi
23	1415	58.9	1986	6	AX365203	AX365203 Sequence
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30	1133	47.2	2181	6	AX467358	AX467358 Sequence
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34	803	33.4	2728	6	AX365240	AX365240 Sequence
35	763.4	31.8	765	6	AX365157	AX365157 Sequence
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40	503.4	21.0	204250	2	AC022655	AC022655 Homo sapi
41	319	13.3	937	6	BD178879	BD178879 NR10 split
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## ALIGNMENTS

RESULT 1				
AX365149				
LOCUS	AX365149	2402 bp	DNA	Linear
DEFINITION	Sequence 1 from Patent WO0200721.			PAT 15-FEB-2002
ACCESSION	AX365149			
VERSION	AX365149.1	GI:18696908		
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1			
AUTHORS	Speicher C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuljper,J.L. and Maurer,M.F.			
TITLE	Cytokine receptor zcytor17			





Db 1681 ACGGAGACACATAAATTTTCAAGACATGTCATTCAGTGTCTTTGAGATTATCCCTCAAA 1740  
QY 1741 CTCTCTGATTGGTGGAGGCTCTTATTCATTTATCTGACAGATGGCATATGGTCTCA 1800  
Db 1741 CTCTCTGATTGGTGGAGGCTCTTATTCATTTATCTGACAGATGGCATATGGTCTCA 1800  
QY 1801 AAAAACCACAAATTTGACTCATCTGTGTGGCCACCGCTTCCCAACCTGCTGAAGTA 1860  
Db 1801 AAAAACCACAAATTTGACTCATCTGTGTGGCCACCGCTTCCCAACCTGCTGAAGTA 1860  
QY 1861 GTATAGCCACATGGCATGGAGATGATTTCAAGATAAGCTAAACCTGAAGAGTCTATG 1920  
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QY 1921 ACTCTGTGAACACAGAGAGAGATCTTAAACCATTTCCACCCCGAGTGAAGTGG 1980  
Db 1921 ACTCTGTGAACACAGAGAGAGATCTTAAACCATTTCCACCCCGAGTGAAGTGG 1980  
QY 1981 TGATTGACAAAGTTGGTGGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTCAACAGATGAG 2040  
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QY 2401 CA 2402  
Db 2401 CA 2402

RESULT 2  
BD178872 2952 bp DNA linear PAT 16-APR-2003  
LOCUS BD178872  
DEFINITION NR10 splicing variants.  
ACCESSION BD178872.1 GI:30016139  
VERSION BD178872.1 GI:30016139  
KEYWORDS WO 02077230-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2952)  
AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.  
TITLE NR10 splicing variants  
JOURNAL Patent: WO 02077230-A 3 03-OCT-2002;  
CHUGAI PHARMACEUTICAL CO LTD, MASATOSUGU MAEDA, NORIKO YAGUCHI,  
MASAKAZU HASEGAWA  
OS Homo sapiens (human)  
PN WO 02077230-A/3  
PD 03-OCT-2002  
PF 22-MAR-2002 WO 2002JP002769  
PR 26-MAR-2001 JP 01P 087298

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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
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Query Match 97.2%; Score 2334; DB 6; Length 2952;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 69 CTGGGAATGTCATCAGCAACTCAAGTTTTCACACAGGAGTGTCTGTAATGCCG 128  
Db 1 CTGGGAATGTCATCAGCAACTCAAGTTTTCACACAGGAGTGTCTGTAATGCCG 60  
QY 129 CAAACATTCCTCTCCCAAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGCA 188  
Db 61 CAAACATTCCTCTCCCAAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGCA 120  
QY 189 CTGTGATGCTCCCTCAGCTCTGCAATTCAGCTGGGAGCTGCCAGTAAACCTGAG 248  
Db 121 CTGTGATGCTCCCTCAGCTCTGCAATTCAGCTGGGAGCTGCCAGTAAACCTGAG 180  
QY 249 AACATTCCTGTGTCTACTACTATAGGAAAAATTAACCTGACCTGGAGTCAGAGAA 308  
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QY 489 ATTAATCTCATATGACATACCTGAGATTTAGAGAACTAGCGAAACCTGAAACCTAAG 548  
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QY 609 CCTGAGTTGGCGCCTGTTTCATCTGATTTAAATATACACTTCGATTCAGAGAGTCAAC 668  
Db 541 CCTGAGTTGGCGCCTGTTTCATCTGATTTAAATATACACTTCGATTCAGAGAGTCAAC 600  
QY 669 AGTACCACTGGATGAGAGTCACTGCTGTAAGAACCGTAAAGATTAACCAACCTGAC 728  
Db 601 AGTACCACTGGATGAGAGTCACTGCTGTAAGAACCGTAAAGATTAACCAACCTGAC 660  
QY 729 AACCTCAGGGGGCGAGCCTTTTACAGAAATATGCTAGCTGCGCATGGCGGTCAAG 788  
Db 661 AACCTCAGGGGGCGAGCCTTTTACAGAAATATGCTAGCTGCGCATGGCGGTCAAG 720  
QY 789 GAGTCAAAAGTTCTGAGTGAAGTGAAGCAAAAAATGAGAACTGAGAGAAAGCT 848  
Db 721 GAGTCAAAAGTTCTGAGTGAAGTGAAGCAAAAAATGAGAACTGAGAGAAAGCT 780  
QY 849 CCAATGTGCTGGAACCTGTGAGAGTCTGAAACCACTGAGGCGGATGAGAGAGGCA 908  
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Dd		841	GTGGCGTGTTATGTGAAGAAAGCAAGAGAGCCCCAGTCTTAGAGAAAACCTTGGCTAC	900
Oy		969	AACATATNGSTACTATCCAGAAAGCAACACTAACCTCACAGAAACAATATGACACTACTAC	1028
Dd		901	AACATATNGSTACTATCCAGAAAGCAACACTAACCTCACAGAAACAATATGACACTACTAC	960
Oy		1029	CAGACAGCTTGAACATGCACTGTGGAGGGGAGAGCTTTTTGGGTGCTCATGATTTCTTTAAT	1088
Dd		961	CAGACAGCTTGAACATGCACTGTGGAGGGGAGAGCTTTTTGGGTGCTCATGATTTCTTTAAT	1020
Oy		1089	TCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTT	1148
Dd		1021	TCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTT	1080
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Dd		1081	CAGTGCATTTGAGTGCATGCAAGCCCTGGCTGCTGAGCAACGCTAATGTGTAACTGGCAA	1140
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Oy		1269	CCCACACCCCTTCTCTGGGAATCTGTGCTCAGGCCACGACGTGACGATCCAGCAAGAT	1328
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Dd		1261	AAATTAACACCTTCTGTGCTATACACTCTCTGTATACCAATGTTCATGACAAAGTT	1320
Oy		1389	GGCGAGCCATATTCATCTCAGGCTTATGACCAGAAAGGCGTTCCATCAGAGAGTCTGAG	1448
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Oy		1869	ACATGCGCATGAGATGATTTCAAGGATTAAGCTGAAGAAGTCTGATGACTCTGTG	1928
Dd		1801	ACATGCGCATGAGATGATTTCAAGGATTAAGCTGAAGAAGTCTGATGACTCTGTG	1860
Oy		1929	AACACAGAGACAGATCTTTAAACCAATGTTCCACCCCACTGACAGTTGGTATATGAC	1988
Dd		1861	AACACAGAGACAGATCTTTAAACCAATGTTCCACCCCACTGACAGTTGGTATATGAC	1920

QY	1989	AAATTGGTGGGAACTTTGGGAATCTCTGCAAGAAATTTTCACGATGAAAGCCGAAAGC	2048
Db	1921	AAAGTTGGTGGTGAACCTTTGGGAATCTCTGCAAGAAATTTTCACGATGAAAGCCGAAAGC	1980
QY	2049	GGTCAGCAAAACAATTTAGAGAGGGGAAAAGAAATGGGTATGTGACCTGGCCCTTTCAGGCTT	2108
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QY	2169	AAATGCCAATACCTCTGCTTCGAGATGGCAGAGGGGAGCCGCCGCAAGAGCCAAAGAGAG	2228
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QY	2229	CTTCTCTTTCTGTGTCAAAGTTTGTAGTACCAGATCATCTGTGTGAGGAAGAGAGCCCAAT	2288
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QY	2289	CCATATTTGAAAAATTCAGTGCAGCAGCCAGGGAATTTCTTTGTCTCGAAAAACTTTCACAG	2348
Db	2221	CCATATTTGAAAAATTCAGTGCAGCAGCCAGGGAATTTCTTTGTCTCGAAAAACTTTCACAG	2280
QY	2349	CACACCAAGGAGGAATCTAAATGGAGCATATGATGAGACCTTGGGGGCTCTCA	2402
Db	2281	CACACCAAGGAGGAATCTAAATGGAGCATATGATGAGACCTTGGGGGCTCTCA	2334
RESULT 3			
BD178871			
LOCUS	BD178871	5271 bp	DNA
DEFINITION	NR10 splicing variants.		Linear
ACCESSION	BD178871		
VERSION	BD178871.1	GI:30016138	
KEYWORDS	WO 02077230-A/2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 5271)		
JOURNAL	Maeda, M., Yaguchi, N. and Hasegawa, M.		
	NR10 splicing variants		
	Patent: WO 02077230-A 2 03-OCT-2002;		
	CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,		
	MASAKAZU HASEGAWA		
COMMENT	OS Homo sapiens (human)		
	PN WO 02077230-A/2		
	PD 03-OCT-2002		
	PF 22-MAR-2002 WO 2002JP002769		
	PR MAS-MAR-2001 JP 01P 087298		
	PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC		
	CI2N15/12, C07K14/715, C07K16/28, CI2N1/15, CI2N1/19, CI2N1/21, PC		
	CI2N5/10,		
	PC CI2P21/02, G01N33/15, G01N33/50, G01N33/53		
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	FT CDS (7)..(2298).		
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Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2334; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Db 901 AACATATGCTACTATCCAGAAACCAACACTTAACCTACAGAAAACATGAACTACTATAC 960  
OY 1029 CACAGACTTGAACCTGATCTGGAGAGGAGAGGCTTTTGGGTGTCTATGATTTCTTAAAT 1088  
Db 961 CACAGACTTGAACCTGATCTGGAGAGGAGAGGCTTTTGGGTGTCTATGATTTCTTAAAT 1020  
OY 1089 TCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCACACTATTTCAAGAAAATCATTT 1148  
Db 1021 TCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCACACTATTTCAAGAAAATCATTT 1080  
OY 1149 CAGTGCATTTAGGTCATGACAGGCTGCGTTGTGTGAGAGCAAGCTAGTGTGGAAGTGCCAA 1208  
Db 1081 CAGTGCATTTAGGTCATGACAGGCTGCGTTGTGTGAGAGCAAGCTAGTGTGGAAGTGCCAA 1140

OY 1209 AGCTCTGCTCTAGACGTGAACACTTGGATGATTAAGTGTTCGGATGTGACCTCAGAG 1268  
Db 1141 AGCTCTGCTCTAGACGTGAACACTTGGATGATTAAGTGTTCGGATGTGACCTCAGAG 1200  
OY 1269 CCCACACCCCTTTCCTGGGAATCTGTCTCAGGCCACGAACTGACGATCCAGAGAT 1328  
Db 1201 CCCACACCCCTTTCCTGGGAATCTGTCTCAGGCCACGAACTGACGATCCAGAGAT 1260  
OY 1329 AAATTTAAACCTTTCGTGTCTATTAACATCTCTGTGTATTCATATTTGATGCAAAAGTT 1388  
Db 1261 AAATTTAAACCTTTCGTGTCTATTAACATCTCTGTGTATTCATATTTGATGCAAAAGTT 1320  
OY 1389 GCGGACCATATTCATCCATCCAGGCTTATGCAAAAGAGGCTTCCATCAGAGAGTCCCTGAG 1448  
Db 1321 GCGGACCATATTCATCCATCCAGGCTTATGCAAAAGAGGCTTCCATCAGAGAGTCCCTGAG 1380  
OY 1449 ACCAAGGTGGAAGACATTTGGCGTGAAGACGCTGACGATCAATGGAAGAGATTTCCAG 1508  
Db 1381 ACCAAGGTGGAAGACATTTGGCGTGAAGACGCTGACGATCAATGGAAGAGATTTCCAG 1440  
OY 1509 AGTGAAGAAAGGCTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAAA 1568  
Db 1441 AGTGAAGAAAGGCTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGGAAAA 1500  
OY 1569 GGAATTCCTCAAGACAGTCAATTCACAGCATCTTGACAGTACGAGGCTGAGTCCGAAAAAGA 1628  
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OY 1629 AAGACCTCTTACATTTGTTGACGTATGCGCAGACCAAGTCTGGGGGAACCAAGGGAGCC 1688  
Db 1561 AAGACCTCTTACATTTGTTGACGTATGCGCAGACCAAGTCTGGGGGAACCAAGGGAGCC 1620  
OY 1689 AGCATTAATTTCAAGCATTTGATTCAGTGTCTTTGAGATTAATTCATTAATCTCTG 1748  
Db 1621 AGCATTAATTTCAAGCATTTGATTCAGTGTCTTTGAGATTAATTCATTAATCTCTG 1680  
OY 1749 ATTGGTGGAGCCCTTCTATTCATTAATTCAGTGTGATGATGATGCTCAAAAAACC 1808  
Db 1681 ATTGGTGGAGCCCTTCTATTCATTAATTCAGTGTGATGATGATGATGCTCAAAAAACC 1740  
OY 1809 AACAAATTTGACATCTGTGTGGCCACCCTTCCACACCTGCTGAAGTATGATAGCC 1868  
Db 1741 AACAAATTTGACATCTGTGTGGCCACCCTTCCACACCTGCTGAAGTATGATAGCC 1800  
OY 1869 ACATGCGATGAGATGATTTTCAAGGATTAACCTGAAGAGTCTGATGACTCTGTG 1928  
Db 1801 ACATGCGATGAGATGATTTTCAAGGATTAACCTGAAGAGTCTGATGACTCTGTG 1860  
OY 1929 AACACAGAAACAGGATCTTAAAAACATGTTCCACCCCGAGTACAAAGTTGGATTGAC 1988  
Db 1861 AACACAGAAACAGGATCTTAAAAACATGTTCCACCCCGAGTACAAAGTTGGATTGAC 1920  
OY 1989 AAGTTGCTGTGAACCTTGGGAATGTTCTCAGAAATTTTTCACAGATGAAGCCAGAACG 2048  
Db 1921 AAGTTGCTGTGTGAACCTTGGGAATGTTCTCAGAAATTTTTCACAGATGAAGCCAGAACG 1980  
OY 2049 GGTGAGGAAACAAATTTAGAGGGGAAAGAAATGCGATGTGACCTCCCTTCAAGGCT 2108  
Db 1981 GGTGAGGAAACAAATTTAGAGGGGAAAGAAATGCGATGTGACCTCCCTTCAAGGCT 2040  
OY 2109 GATTGTCCCTGGGGAAAAATTTTGGAGACTCCCAATTTACCTGAGATTTCCGCCAGAG 2168  
Db 2041 GATTGTCCCTGGGGAAAAATTTTGGAGACTCCCAATTTACCTGAGATTTCCGCCAGAG 2100  
OY 2169 AAATCCCAATACCTACCTTCGAGAGATGCAAGAGGGACCCGCCAGAGAGCCAAAGAGACAG 2228  
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OY 2229 CTTCCTTTTCTGTGCAAAAGTTTATGATCAGATCATCTGTGTGAGGAAGAGCCCAAT 2288  
Db 2161 CTTCCTTTTCTGTGCAAAAGTTTATGATCAGATCATCTGTGTGAGGAAGAGCCCAAT 2220

QY	2289	CCATATTTGAAAAAATTCGTACACGACCCGAGGAATTTCTGTGCTGTGAAAAAATTCCAGAG	2348
Db	2221	CCATATTTGAAAAAATTCGTACACGACCCGAGGAATTTCTGTGCTGTGAAAAAATTCCAGAG	2280
OY	2349	CACACCAAGGAGAGAAGTCTAAATGCGACCATAGCATGAGACCCTTCGGGGCCTCA	2402
Db	2281	CACACCAAGGAGAGAAGTCTAAATGCGACCATAGCATGAGACCCTTCGGGGCCTCA	2334
RESULT 4			
LOCUS	AX467333	2480 bp	DNA
DEFINITION	Sequence 3 from Patent W00229060.	linear	PAT 16-JUL-2002
ACCESSION	AX467333		
VERSION	AX467333.1	GI:21900584	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.		
TITLE	Hematopoietic receptors hp1 and hp2		
JOURNAL	Patent: WO 0229060-A 3 11-APR-2002;		
FEATURES	Immunex Corporation (US)		
SOURCE	location/Qualifiers		
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	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	722 a	558 c	600 g
ORIGIN			600 t

Query Match	94.0%	Score 2258.6	DB 6	Length 2480
Best Local Similarity	99.8%	Prod. No. 0		
Matches 2261	Conservative 0	Mismatches 4	Indels 0	Gaps 0
QY	138	CTCTCTCCCCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCGCTGGTGTG	197	
Db	138	CTCTCTCCCCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCGCTGGTGTG	197	
QY	198	CTCCCTCTACTCTGCAGAAATTCAGCCTGGCAGCTCTGGCAGCTTAAGCCTGAGAACATTTCC	257	
Db	198	CTCCCTCTACTCTGCAGAAATTCAGCCTGGCAGCTCTGGCAGCTTAAGCCTGAGAACATTTCC	257	
QY	258	TGTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGGAAAGGAACCAAGT	317	
Db	258	TGTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGGAAAGGAACCAAGT	317	
QY	318	TATACCAAGTACACAGTTAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACA	377	
Db	318	TATACCAAGTACACAGTTAGAGAACTTACGCTTTTGGAGAAAAACATGATAATTGTACA	377	
QY	378	ACCAATAGTCTACAAAGTAAAACTGCTTCGTCCTTTTTCCTCCAGAAATPACG	437	
Db	378	ACCAATAGTCTACAAAGTAAAACTGCTTCGTCCTTTTTCCTCCAGAAATPACG	437	
QY	438	ATCCAGATAATTATACCATTTAGAGTGGAACTTAAATGAGATGCTGTATTAATAATCT	497	
Db	438	ATCCAGATAATTATACCATTTAGAGTGGAACTTAAATGAGATGCTGTATTAATAATCT	497	
QY	498	CATATGACANACTGGAGATTAGAGACATAGCGAAAACTGAACCCACTAAGATTTCCGT	557	
Db	498	CATATGACANACTGGAGATTAGAGACATAGCGAAAACTGAACCCACTAAGATTTCCGT	557	
QY	558	GTGAACACAGTTTGGGCAATCAACGAAATGTTAAATTGAATGATTAAGCCTGAATGG	617	
Db	558	GTGAACACAGTTTGGGCAATCAACGAAATGTTAAATTGAATGATTAAGCCTGAATGG	617	
QY	618	GCAGCTTTTCATCTGATTTAAATTAACAACATTCGATTCAGGACAGTCAACAGTACAGC	677	
Db	618	GCAGCTTTTCATCTGATTTAAATTAACAACATTCGATTCAGGACAGTCAACAGTACAGC	677	

QY	678	1GGATGGAAGTC	AACTGGCTT	AGACCCGTA	AGGATTA	AAAAACCA	AGCTAC	ACCTCAG	737
Db	678	TGGATGGAAGTC	AACTGGCTT	AGACCCGTA	AGGATTA	AAAAACCA	AGCTAC	ACCTCAG	737
QY	728	GGCGTCGACG	CCCTTTAC	AGAAATAT	GTCTACT	CTCGCAT	GTGCGG	GTCAAGAGCAAG	797
Db	728	GGCGTCGACG	CCCTTTAC	AGAAATAT	GTCTACT	CTCGCAT	GTGCGG	GTCAAGAGCAAG	797
QY	798	TTTCTGAGATG	AC	TGAGAGCC	AAAGAAAAA	TGGGAAT	GACT	TGAGGAAGAA	857
Db	798	TTTCTGAGATG	AC	TGAGAGCC	AAAGAAAAA	TGGGAAT	GACT	TGAGGAAGAA	857
QY	858	CTGGAAC	TGTGAGAGT	CCTCTGA	AAACAG	CTGAGG	GGATG	GAAGAGCC	917
Db	858	CTGGAAC	TGTGAGAGT	CCTCTGA	AAACAG	CTGAGG	GGATG	GAAGAGCC	917
QY	918	TTATGGAAGAA	GGCGACAG	AGCCCA	CTCTAG	AGAAAC	ACTTGG	CTACACAT	977
Db	918	TTATGGAAGAA	GGCGACAG	AGCCCA	CTCTAG	AGAAAC	ACTTGG	CTACACAT	977
QY	978	TACTAT	CCAGAAAG	CAACACTA	ACCCTC	ACAGAA	CAATGA	CACTACTA	1037
Db	978	TACTAT	CCAGAAAG	CAACACTA	ACCCTC	ACAGAA	CAATGA	CACTACTA	1037
QY	1038	GAACTG	CATCTG	GAGAGG	CGAGAG	CTTTGG	GTCTAT	GATTTCT	1097
Db	1038	GAACTG	CATCTG	GAGAGG	CGAGAG	CTTTGG	GTCTAT	GATTTCT	1097
QY	1098	AAGTC	CCAG	GGCCAC	CCCTG	AGATTC	CCACTA	TTTCA	1157
Db	1098	AAGTC	CCAG	GGCCAC	CCCTG	AGATTC	CCACTA	TTTCA	1157
QY	1158	GAGTCAT	CAGCAG	CGCTG	CGTTG	CTG	TAGAGAC	CAGCTAG	1217
Db	1158	GAGTCAT	CAGCAG	CGCTG	CGTTG	CTG	TAGAGAC	CAGCTAG	1217
QY	1218	CTAGAC	GCTGA	ACACTT	GGATG	ATG	TGATG	TTCCG	1277
Db	1218	CTAGAC	GCTGA	ACACTT	GGATG	ATG	TGATG	TTCCG	1277
QY	1278	CTTTC	CGTGG	GAATCG	TGTG	CTC	CAGG	CCAGCA	1337
Db	1278	CTTTC	CGTGG	GAATCG	TGTG	CTC	CAGG	CCAGCA	1337
QY	1338	CCCTT	CTG	GGTCT	TAACAT	CTCTG	TGTAT	CAATG	1397
Db	1338	CCCTT	CTG	GGTCT	TAACAT	CTCTG	TGTAT	CAATG	1397
QY	1398	TATTC	CAAT	CCAG	GCTTAT	GCCA	AAAG	AGGCTTC	1457
Db	1398	TATTC	CAAT	CCAG	GCTTAT	GCCA	AAAG	AGGCTTC	1457
QY	1458	GAGAA	CAATGG	CGCTGA	AGAG	CGGTAC	ACAT	TCATG	1517
Db	1458	GAGAA	CAATGG	CGCTGA	AGAG	CGGTAC	ACAT	TCATG	1517
QY	1518	AAGG	TAT	CACTCT	CAAC	ACTTAC	CAAC	ATCTTT	1577
Db	1518	AAGG	TAT	CACTCT	CAAC	ACTTAC	CAAC	ATCTTT	1577
QY	1578	AAGAC	AGTCA	ATTC	CAG	ATCTTG	CA	AGTCC	1637
Db	1578	AAGAC	AGTCA	ATTC	CAG	ATCTTG	CA	AGTCC	1637
QY	1638	TACAT	TGTT	CAG	GTCA	TG	GGCCAG	CAAC	1697
Db	1638	TACAT	TGTT	CAG	GTCA	TG	GGCCAG	CAAC	1697
QY	1698	TTCA	AGCAT	TGTAT	TCT	AGTGT	CTTTG	GAGATT	1757
Db	1698	TTCA	AGCAT	TGTAT	TCT	AGTGT	CTTTG	GAGATT	1757
QY	1758	GGC	CTT	ATAT	TCTAT	TAT	CTT	CAC	1817

Db	1758	GGCCTTCCTTATATTCATTAATTCATACAGTGGCATATATGCTCTCAAAAAAACCCAAATATG	1817		
QY	1818	ACTCATCTGTGTGGCCACACCGTTCCCAACCCCTGCTGAAAGTAGATATAGCCATATG	1877		
Db	1818	ACTCATCTGTGTGGCCACACCGTTCCCAACCCCTGCTGAAAGTAGATATAGCCATATG	1877		
QY	1878	GGAGATATATTTCAAGAGATTAAGCTTAACCTGACAGAGTCTGATCTGTGACACAGAA	1937		
Db	1878	GGAGATATATTTCAAGAGATTAAGCTTAACCTGACAGAGTCTGATCTGTGACACAGAA	1937		
QY	1938	GACAGATATTTAAACCATGTTCACACCCCAAGTACAGATGGATGGACAGTGGTG	1997		
Db	1938	GACAGATATTTAAACCATGTTCACACCCCAAGTACAGATGGATGGACAGTGGTG	1997		
QY	1998	GTGAACCTTTGGGAATGTTCTGCAGAAATTTTCACAGATGAAGCCAGAACGGTCAAGAA	2057		
Db	1998	GTGAACCTTTGGGAATGTTCTGCAGAAATTTTCACAGATGAAGCCAGAACGGTCAAGAA	2057		
QY	2058	AACAATTTAGAGGGGAAAAAGATGGGTATGTGACCTGCCCTTCAGGCTGATGTGCC	2117		
Db	2058	AACAATTTAGAGGGGAAAAAGATGGGTATGTGACCTGCCCTTCAGGCTGATGTGCC	2117		
QY	2118	CTGGGGAAGAGTTTGTGAGAGCTCCCAAGTTTACCTGAGATTTCCGCCAGAAATCCCA	2177		
Db	2118	CTGGGGAAGAGTTTGTGAGAGCTCCCAAGTTTACCTGAGATTTCCGCCAGAAATCCCA	2177		
QY	2178	TACCTACGTTGAGAGATGCCAGAGGGGACCCGCCAGAAAGCCAAAGACACTTCTCTT	2237		
Db	2178	TACCTACGTTGAGAGATGCCAGAGGGGACCCGCCAGAAAGCCAAAGACACTTCTCTT	2237		
QY	2238	TCTGTGCAAGATTATGATACAGATCATCTGTGTGAGAGAGAGCCCAATTCATATTG	2297		
Db	2238	TCTGTGCAAGATTATGATACAGATCATCTGTGTGAGAGAGAGCCCAATTCATATTG	2297		
QY	2298	AAAAATTCAGAGACGACGGGAAATTTCTGTGCTGAAACCTTCCAGACACACCAAG	2357		
Db	2298	AAAAATTCAGAGACGACGGGAAATTTCTGTGCTGAAACCTTCCAGACACACCAAG	2357		
QY	2358	GGAGAGATCTTAATGCGACCATATGACATGAGACCCCTGGGGCTCTCA	2402		
Db	2358	GGAGAGATCTTAATGCGACCATATGACATGAGACCCCTGGGGCTCTCA	2402		
RESULT 5	AX467335	2238 bp	DNA	linear	PAT 16-JUL-2002
LOCUS	AX467335	Sequence 5 from Patent WO0229060.			
DEFINITION	AX467335				
ACCESSION	AX467335.1	GI:21900585			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM		Homo sapiens (human)			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE		Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.			
JOURNAL		Hematopoietin receptors hprt1 and hprt2			
FEATURES		Patent: WO 0229060-A 5 11-APR-2002;			
SOURCE		Immunex Corporation (US)			
ORIGIN		Location/Qualifiers			
BASE COUNT		1. 2238			
ORIGIN		/organism="Homo sapiens"			
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Best Local Similarity	99.8%;	Pred. No. 0;			
Matches 2228;	Conservative	0;	Mismatches	4;	Indels
				0;	Gaps
QY	138	CTCTCTCCCAACGCTTATGTGTTAACCTGGGAGATATGACCTGGGACCTGTGATG	197		

Db	7	CTCTCTCCCGACCTTCATGTGTAACTCGGGGATGATGTGGACCTGGGCACCTGTGGATG	66
QY	198	CTCCCTCAGCTCTGCAAAATTCAGCCCGGAGCTCTGCCAGCTAAGCCTGGAACATTTCC	257
Db	67	CTCCCTTCACCTCTGCAAAATTCAGCCCGGAGCTCTGCCAGCTAAGCCTGGAACATTTCC	126
QY	258	TGTGTCTACTACTATAGAAAAATTTAACTCTGACTTTGGAGCTCCAGAAAAAGAACCACT	317
Db	127	TGTGTCTACTACTATAGAAAAATTTAACTCTGACTTTGGAGCTCCAGAAAAAGAACCACT	186
QY	318	TATACCAGGTACACAGTTTAGAGAACTTCGCTTTGGAGAAAAACATGATTAATTGACA	377
Db	187	TATACCAGGTACACAGTTTAGAGAACTTCGCTTTGGAGAAAAACATGATTAATTGACA	246
QY	378	ACCAATAGTTCTACACAGTGAATAATCGCTGCTGCTCTTTTTCCTTCCAAACATTAACG	437
Db	247	ACCAATAGTTCTACACAGTGAATAATCGCTGCTGCTCTTTTTCCTTCCAAACATTAACG	306
QY	438	ATCCAGATTAATTAACCTTTGAGTGGAGAACTGAAATAATGAGATGGTGAATTAATCT	497
Db	307	ATCCAGATTAATTAACCTTTGAGTGGAGAACTGAAATAATGAGATGGTGAATTAATCT	366
QY	498	CATATGACATCTGGAGATTAGAGAACTTAGGAAACCTGAACCTACCTAAGATTTCCT	557
Db	367	CATATGACATCTGGAGATTAGAGAACTTAGGAAACCTGAACCTACCTAAGATTTCCT	426
QY	558	GTTAAACCAAGTTTGGGCTCAACCAAGATTTCAATTTGAATGAATGAATGAAGCTGAGTTG	617
Db	427	GTTAAACCAAGTTTGGGCTCAACCAAGATTTCAATTTGAATGAATGAATGAAGCTGAGTTG	486
QY	618	GGCGCTGTTTCATCTGATTTAAATAATACACACTTCGATTCAGGACAGTCAACACTACAGC	677
Db	487	GGCGCTGTTTCATCTGATTTAAATAATACACACTTCGATTCAGGACAGTCAACACTACAGC	546
QY	678	TGGATGGAAGTCACTTGGCTTAAGAACCGTAGGATTAATAACCAACGTTCAACCTTACG	737
Db	547	TGGATGGAAGTCACTTGGCTTAAGAACCGTAGGATTAATAACCAACGTTCAACCTTACG	606
QY	738	GGGCTGACAGCTTTTACAGAAATATGTGCATATAGCTCTGCGATGTGCGGTCAAGAGTCAAG	797
Db	607	GGGCTGACAGCTTTTACAGAAATATGTGCATATAGCTCTGCGATGTGCGGTCAAGAGTCAAG	666
QY	798	TTCTGGAAGTGAAGTGAAGCAAGAAAAATGGGAATGACTGAGGAGAGCAAGCTCCATGTGC	857
Db	667	TTCTGGAAGTGAAGTGAAGCAAGAAAAATGGGAATGACTGAGGAGAGCAAGCTCCATGTGC	726
QY	858	CTGGAACCTTGGAGAGTCTTGAACCAAGCTGAGGGCGGATGGAAGAGGCCAGTGCCTTG	917
Db	727	CTGGAACCTTGGAGAGTCTTGAACCAAGCTGAGGGCGGATGGAAGAGGCCAGTGCCTTG	786
QY	918	TTATGGAAGAAGCAAGAGAGAGGCCCGGCTGTGAGAAAAAACCTTTGGCTTCAACATTTGG	977
Db	787	TTATGGAAGAAGCAAGAGAGAGGCCCGGCTGTGAGAAAAAACCTTTGGCTTCAACATTTGG	846
QY	978	TACTATCCAGAAAGCAACTAATCTACAGAAACATGAACACTACTAACCAGCAGCTT	1037
Db	847	TACTATCCAGAAAGCAACTAATCTACAGAAACATGAACACTACTAACCAGCAGCTT	906
QY	1038	GAACTGCACTTGGGAGGCGAGAGCTTTTGGGTCTATGATTTTCTTAATTTCTTTGGG	1097
Db	907	GAACTGCACTTGGGAGGCGAGAGCTTTTGGGTCTATGATTTTCTTAATTTCTTTGGG	966
QY	1098	AAGTCTCCAGTGGGCCACCTGAGAGATTCCAGCAATTCAGAAAAATCATTTCAAGTGAT	1157
Db	967	AAGTCTCCAGTGGGCCACCTGAGAGATTCCAGCAATTCAGAAAAATCATTTCAAGTGAT	1026
QY	1158	GAGGTATATCAGAGCCCTGCTTGTCTGAGGACAGCTAGTGGTGAAGTGGCAAGCTCTGCT	1217
Db	1027	GAGGTATATCAGAGCCCTGCTTGTCTGAGGACAGCTAGTGGTGAAGTGGCAAGCCCTGCT	1086
QY	1218	CTAGACGTGAACACTTGGATGATTAATGATGTTCCGAGATGTGCACTCAGAGCCACCAAC	1277

Db 1087 CTAGACGTGAACACTTGGATGATGTAATGTTCCGGATGTGACTAGAGCCACACACC 1146  
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Oy 1458 GAGAACATTTGGCGTGAAGACGGTCCAGTACATGAGAAAGATTTCCCAAGGTGAGAGA 1517  
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Oy 1518 AAGGGTATCATCTGCACACTACACCACTTTTACCAAGCTGAGAGGTGAAAAGATTCTCC 1577  
Db 1387 AAGGGTATCATCTGCACACTACACCACTTTTACCAAGCTGAGAGGTGAAAAGATTCTCC 1446  
Oy 1578 AAGACAGTCATTCAGAGATCTTGACAGTACGGCTGGAGTCCCTGAAAAGAAAGCTCT 1637  
Db 1447 AAGACAGTCATTCAGAGATCTTGACAGTACGGCTGGAGTCCCTGAAAAGAAAGCTCT 1506  
Oy 1638 TACATTTGTTACAGTATGAGCCAGCACAGTCTGGGGGAGAACAGGGAGCAGCATTAAT 1697  
Db 1507 TACATTTGTTACAGTATGAGCCAGCACAGTCTGGGGGAGAACAGGGAGCAGCATTAAT 1566  
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Db 1567 TTCAAGACATTTGTCATTCAGTGTCTTTGAGATTATCTCATTAATCTCTGTATGTGTGA 1626  
Oy 1758 GGGCTCTTATTCATCATATATCTGACAGTGGCATATGCTCTCAAAAAAACCACAAATG 1817  
Db 1627 GGGCTCTTATTCATCATATATCTGACAGTGGCATATGCTCTCAAAAAAACCACAAATG 1686  
Oy 1818 ACTCATCTGTGTGGCCAGCCAGTCCCAACCTGCTGAAGTAGATAGCCACATGGCAT 1877  
Db 1687 ACTCATCTGTGTGGCCAGCCAGTCCCAACCTGCTGAAGTAGATAGCCACATGGCAT 1746  
Oy 1878 GGAAGATGATTTCAAGGATTAAGCTTAACCTGAAGAGTCTGATGACTGTGAACACAGAA 1937  
Db 1747 GGAAGATGATTTCAAGGATTAAGCTTAACCTGAAGAGTCTGATGACTGTGAACACAGAA 1806  
Oy 1938 GACAGATCTTAAGAAACATGTTCCACCCCGACAGTGAAGTGTGATGAGCAAGTTGGTG 1997  
Db 1807 GACAGATCTTAAGAAACATGTTCCACCCCGACAGTGAAGTGTGATGAGCAAGTTGGTG 1866  
Oy 1998 GTGAACATTTGGGATGTTCTGCAAGAAATTTTCAACAGATGAAGCCAGAACGGTCAGGAA 2057  
Db 1867 GTGAACATTTGGGATGTTCTGCAAGAAATTTTCAACAGATGAAGCCAGAACGGTCAGGAA 1926  
Oy 2058 AACAAATTTAGAGGGGAAAAGATGGTATGTGACCTGCCCCCTTCAGGCTGTATGTCCTC 2117  
Db 1927 AACAAATTTAGAGGGGAAAAGATGGTATGTGACCTGCCCCCTTCAGGCTGTATGTCCTC 1986  
Oy 2118 CTGGGAAAAGATTTTGGAGAGCTCCAGTTTCACTGTGATTTCCGCCCCAGAAAATCCCAA 2177  
Db 1987 CTGGGAAAAGATTTTGGAGAGCTCCAGTTTCACTGTGATTTCCGCCCCAGAAAATCCCAA 2046  
Oy 2178 TACCTAGCTTGAGAGATCCAGAGGGAGCCCGCCAGAAAGCCAAAGACACTTCTCTTT 2237  
Db 2047 TACCTAGCTTGAGAGATCCAGAGGGAGCCCGCCAGAAAGCCAAAGACACTTCTCTTT 2106  
Oy 2238 TCTGCTCAAGATTTAGTACAGATCTGTGTGAGAGAGAGGCCCAAAATCCATATTTG 2297  
Db 2107 TCTGCTCAAGATTTAGTACAGATCTGTGTGAGAGAGAGGCCCAAAATCCATATTTG 2166  
Oy 2298 AAAAATTCAGTACAGCCAGGGAATTTCTGTCTGAAAAAATTTCCAGACACACACAG 2357  
Db 2167 AAAAATTCAGTACAGCCAGGGAATTTCTGTGTGAAAAAATTTCCAGACACACACAG 2226

Oy 2358 GGAGAGTCTAA 2369  
Db 2227 GGAGAGTCTAA 2238  
RESULT 6  
LOCUS BD178873  
DEFINITION NR10 splicing variants.  
ACCESSION BD178873  
VERSION BD178873.1 GI:30016140  
KEYWORDS WO 02077230-A/4.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3072)  
AUTHORS Maeda, M., Yaguchi, N. and Hasegawa, M.  
TITLE NR10 splicing variants  
JOURNAL Patient; WO 02077230-A 4 03-OCT-2002;  
CHUGAI PHARMACEUTICAL CO LTD; MASATSUGU MAEDA, NORIKO YAGUCHI,  
MASAKAZU HASEGAWA  
COMMENT OS Homo sapiens (human)  
PN WO 02077230-A/4  
PD 03-OCT-2002  
PE 22-MAR-2002 WO 2002JP002769  
PR 26-MAR-2001 JP 01P 087298  
PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC  
C12N15/12, C07K14/775, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10,  
PC C12P21/02, G01N33/15, G01N33/50, G01N33/53  
CC NR10 splicing variants  
FH key location/Qualifiers  
FT CDS location/Qualifiers  
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Best Local Similarity 95.1%; Pred. No. 0;  
Matches 2234; Conservative 0; Mismatches 0; Indels 120; Gaps 1;  
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Db 1 CTGGGATGTCATCAGGCAACTCAAGTTTTCACACGAGCATGTCTGTGAATGTCG 60  
Oy 129 CAAAACATTTCTCTCCCGACGCTTCATGTTAACTGGGGAGTGTGACCTGGGCA 188  
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Db	361	AGATTAACGATCCCAAGTAATTAATTAACCATTTGAGTGGTAACCTGAAATGGAATGGTGCTA	420
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OY	549	ATTTCGCGTGGAAACGATTTTGGGATCAAAAGATGATTCAAATTGAATTGATTAAG	608
Db	481	ATTTCGCGTGGAAACGATTTTGGGATCAAAAGATGATTCAAATTGAATTGATTAAG	540
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OY	669	AGTACCAAGCTGGATGAGATGACATCTGCTAAGACCGTAAGGATTAATAAACCAACGTAC	728
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OY	729	AACCTCAAGGGGCGCTGACAGCCTTTTACAGAAATATGTCTACTCTCGCATGTGGGGTCAAG	788
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OY	909	GTCGGGTTGTTATGGAAGAAAGCCAGAGGCCCACTCTAGAGAAACACTTTGGCTAC	968
Db	841	GTCGGGTTGTTATGGAAGAAAGCCAGAGGCCCACTCTAGAGAAACACTTTGGCTAC	900
OY	969	AACATATGATGATCTATCCAGAAAAGCAACATAACCTCCAGAAAACATGAACACTACTAAC	1028
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OY	1029	CAGCAGCTTGAATGCAATCTGGGAGGCGAGAGCTTTTGGGTGTCATGATTTCTTATTAAT	1088
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OY	1089	TCTCTTGGGAAGCTCCAGATGGGCCACCTGAGATTCACGATATTCAGAAAATTCATTT	1148
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Db	1081	CAGTGCATTTGAGTCAATGACAGGCTGCGTTGCTAGAGACCAGACTAGTGGGTAATGGCAAA	1140
OY	1209	AGCTCTGCTTAGACGTGAACACTTTGGATGATTTCCGATGTGGACTCGAG	1268
Db	1141	AGCTCTGCTTAGACGTGAACACTTTGGATGATTTCCGATGTGGACTCGAG	1200
OY	1269	CCCACACACCTTTTCTGGGAATCTGTGCTTAGGCCACGAAGTGGACGATTCAGCAAGAT	1328
Db	1201	CCCACACACCTTTTCTGGGAATCTGTGCTTAGGCCACGAAGTGGACGATTCAGCAAGAT	1260
OY	1329	AAATTAACACCTTTCTGGTGTATTAACATCTCTGTATTCCTAATGTGGCAATGAAGTT	1388
Db	1261	AAATTAACACCTTTCTGGTGTATTAACATCTCTGTATTCCTAATGTGGCAATGAAGTT	1320
OY	1389	GGCAGAGCCATTTTCCATTCACAGGCTTATGCCCCAAGAGCGTTCCATCAGAAAGTCTGAG	1448
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OY	1449	ACCAAGGTGAGAAACATTTGGCGTGAAGACGGTCAAGATCACATGAGAAAGATTTCCCAAG	1508
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OY	1509	AGTAGAGAAAGGATATCATCTGCAACTACACCATCTTTTACCAAGCTGAAAGGTGGAAAA	1568
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QY	1689	AGCATTAATTT <td>CAAGACATTTG<td>CTCAATTCAGTCTCTTT<td>GAGATTTATCTCATTAACCTCTCTG</td><td></td><td>1748</td></td></td>	CAAGACATTTG <td>CTCAATTCAGTCTCTTT<td>GAGATTTATCTCATTAACCTCTCTG</td><td></td><td>1748</td></td>	CTCAATTCAGTCTCTTT <td>GAGATTTATCTCATTAACCTCTCTG</td> <td></td> <td>1748</td>	GAGATTTATCTCATTAACCTCTCTG		1748
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QY	1809	AACAAATTTG <td>ACATCTG<td>TGTTGGCCACCGTTC<td>CCCAACCTGCTGTAACATAGTATAGCC</td><td></td><td>1868</td></td></td>	ACATCTG <td>TGTTGGCCACCGTTC<td>CCCAACCTGCTGTAACATAGTATAGCC</td><td></td><td>1868</td></td>	TGTTGGCCACCGTTC <td>CCCAACCTGCTGTAACATAGTATAGCC</td> <td></td> <td>1868</td>	CCCAACCTGCTGTAACATAGTATAGCC		1868
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Db	1801	ACATGCGATG <td>GAGATGATTTCA</td> <td>-----</td> <td>-----</td> <td></td> <td>1860</td>	GAGATGATTTCA	-----	-----		1860
QY	1892	-----	-----	-----	-----		1891
Db	1861	CTACATGCC <td>AGGTGCTGGGCTAG<td>GGCCCTAGG</td><td>GGATACAAATGACAAAGTCACTGTCCCTGC</td><td></td><td>1920</td></td>	AGGTGCTGGGCTAG <td>GGCCCTAGG</td> <td>GGATACAAATGACAAAGTCACTGTCCCTGC</td> <td></td> <td>1920</td>	GGCCCTAGG	GGATACAAATGACAAAGTCACTGTCCCTGC		1920
QY	1892	-----	-----	-----	-----		1928
Db	1921	CATGAGG <td>CCACTTGTGATTTCTTG<td>GATTAAGTAAACCTG<td>GAAGGATGCTGATGACTCTGTG</td><td></td><td>1980</td></td></td>	CCACTTGTGATTTCTTG <td>GATTAAGTAAACCTG<td>GAAGGATGCTGATGACTCTGTG</td><td></td><td>1980</td></td>	GATTAAGTAAACCTG <td>GAAGGATGCTGATGACTCTGTG</td> <td></td> <td>1980</td>	GAAGGATGCTGATGACTCTGTG		1980
QY	1929	AACACAGAA <td>GCAGAGATCTTAA</td> <td>AAACCATGTTC<td>CAACCCCACTGCAAGTTGGTATTGAC</td><td></td><td>1988</td></td>	GCAGAGATCTTAA	AAACCATGTTC <td>CAACCCCACTGCAAGTTGGTATTGAC</td> <td></td> <td>1988</td>	CAACCCCACTGCAAGTTGGTATTGAC		1988
Db	1981	AACACAGAA <td>GCAGAGATCTTAA</td> <td>AAACCATGTTC<td>CAACCCCACTGCAAGTTGGTATTGAC</td><td></td><td>2040</td></td>	GCAGAGATCTTAA	AAACCATGTTC <td>CAACCCCACTGCAAGTTGGTATTGAC</td> <td></td> <td>2040</td>	CAACCCCACTGCAAGTTGGTATTGAC		2040
QY	1989	AAGTTGGG <td>TGAGTCTTGGG</td> <td>AATGTTCTG<td>CAACAAATTTTTCACAGATGAAAGCCAGAACG</td><td></td><td>2048</td></td>	TGAGTCTTGGG	AATGTTCTG <td>CAACAAATTTTTCACAGATGAAAGCCAGAACG</td> <td></td> <td>2048</td>	CAACAAATTTTTCACAGATGAAAGCCAGAACG		2048
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QY	2109	GATGTGCC <td>CCGGGGGAAAGTTT<td>GAGAGCTCC<td>CACTTTCACCTGAGATTTCCGCCCAGA</td><td></td><td>2168</td></td></td>	CCGGGGGAAAGTTT <td>GAGAGCTCC<td>CACTTTCACCTGAGATTTCCGCCCAGA</td><td></td><td>2168</td></td>	GAGAGCTCC <td>CACTTTCACCTGAGATTTCCGCCCAGA</td> <td></td> <td>2168</td>	CACTTTCACCTGAGATTTCCGCCCAGA		2168
Db	2161	GATGTGCC <td>CCGGGGGAAAGTTT<td>GAGAGCTCC<td>CACTTTCACCTGAGATTTCCGCCCAGA</td><td></td><td>2220</td></td></td>	CCGGGGGAAAGTTT <td>GAGAGCTCC<td>CACTTTCACCTGAGATTTCCGCCCAGA</td><td></td><td>2220</td></td>	GAGAGCTCC <td>CACTTTCACCTGAGATTTCCGCCCAGA</td> <td></td> <td>2220</td>	CACTTTCACCTGAGATTTCCGCCCAGA		2220
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QY	2289	CCATATTT <td>GAAAAATTC<td>AGTACAG<td>CCAGGAATTTCTTG<td>TGTGTGAAAAACTTCCAGAG</td><td>2348</td></td></td></td>	GAAAAATTC <td>AGTACAG<td>CCAGGAATTTCTTG<td>TGTGTGAAAAACTTCCAGAG</td><td>2348</td></td></td>	AGTACAG <td>CCAGGAATTTCTTG<td>TGTGTGAAAAACTTCCAGAG</td><td>2348</td></td>	CCAGGAATTTCTTG <td>TGTGTGAAAAACTTCCAGAG</td> <td>2348</td>	TGTGTGAAAAACTTCCAGAG	2348
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RESULT 7

AF486620

LOCUS

DEFINITION Homo sapiens gpi30-like monocyte receptor mRNA, complete cds.

ACCESSION AF486620

VERSION AF486620.1

KEYWORDS

GI:20563276

2199 bp

mRNA

linear

PRI 14-MAY-2002



SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2199)  
AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de Sauvage, F. J.  
TITLE A novel type I cytokine receptor is expressed on monocytes, signals proliferation, and activates STAT-3 and STAT-5  
JOURNAL J. Biol. Chem. 277 (19), 16831-16836 (2002)  
MEDLINE 21988187  
PUBMED 11877449  
REFERENCE 2 (bases 1 to 2199)  
AUTHORS Ghilardi, N., Li, J., Hongo, J. A., Yi, S., Gurney, A. and de Sauvage, F. J.  
TITLE Direct Submission  
JOURNAL Submitted (21-FEB-2002) Molecular Oncology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA  
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Best Local Similarity 99.9% Pred. No. 0;  
Matches 2197; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 VERSION BDI18874.1 GI:30016141  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 2870)  
 AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.  
 TITLE NR10 splicing variants  
 JOURNAL Patent: WO 02077230-A 5 03-OCT-2002;  
 CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,  
 MASAKAZU HASEGAWA  
 COMMENT OS Homo sapiens (human)  
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 PD 03-OCT-2002

PF 22-MAR-2002 WO 2002JP002769  
 PR 26-MAR-2001 JP 01P 087298  
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 PC C12P21/02, G01N33/15, G01N33/50, G01N33/53  
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 Matches 2252; Conservative 0; Mismatches 0; Indels 82; Gaps 1;  
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 QY 129 CAAAACATTTCTCTCCCGCAGCTTCATGCTTAACCTGGGGAGATGTGGACCTGGGCA 188  
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 Db 61 CAAAACATTTCTCTCCCGCAGCTTCATGCTTAACCTGGGGAGATGTGGACCTGGGCA 120  
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QY	1449	ACCAAGGTGAGAAACATTGGCGCTGAAGACGGTCACAGATCACATGTGAAGAGATTTCCAAAG	1508
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Qy	2349	CACACCAGGGGAGAGCTAATTAATGGACATAGATGAGACCCGCGGGCCCTCA	2402
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RESULT	9
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LOCUS	BD178875
DEFINITION	NRI0 splicing variants.
ACCESSION	BD178875
VERSION	BD178875.1 GI:30016142
KEYWORDS	WO 02077230-A/6.
SOURCE	Homo sapiens (human)
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 2858)
AUTHORS	Maeda,M., Yaguchi,N. and Hasegawa,M.
TITLE	NRI0 SPLICING VARIANTS
JOURNAL	Patent: WO 02077230-A 6 03-OCT-2002; CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MAEDA,NORIKO YAGUCHI, MASAKAZU HASEGAWA
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QY 1989 AAGTTGTGTGTAAGTGTGGGAATGTTCTGCAAGAAATTTTCAAGATGAGAACCAAGAG 2048  
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QY 2229 CTTCCTTTTCTGTGCAAAAGTTTATACAGATCATCTGTGTGAGGAAGAGCCCAAT 2288  
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QY	2289	CCATATTTGAAAAATTCAGTCAGCAGCCAGGGAATTTCTTGTCGTGAAAAAATCTTCAGAG	23468
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QY	2349	CACACCAAGGAGGAGCTAAATGGCACCATTAGCATGTGAGACCCGCGGCGCTCA	2402
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DEFINITION	Sequence 45 from Patent WO0200721.	Linear	PAT 15-FEB-2002
ACCESSION	AX365193		
VERSION	AX365193.1	GI:18696949	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuljper, J.L.		
TITLE	Cytokine receptor zcytor17		
JOURNAL	Patent: WO 0200721-A 45 03-JAN-2002;		
FEATURES	Zymogenetics, Inc. (US)		
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	CVADQLVKNWQSSALDVNTWMIEMFDPVDEPPTLSVESVSQATNMTIQDRLKPE		
	GIINNYTPEMLDKGEPEYSIQAVAKKEGVPSEPTKYNIGKVTITIMKEIPKSEK		
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	NFTLSFEVFEIILITSLIGGGLILILITLVAYGILKRNKRLTHLCMPYVPAESSIA		
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BASE COUNT	764 a	530 c	576 g 659 t
ORIGIN			
Query Match	86.4%;	Score 2075;	DB 6; Length 2529;
Best Local Similarity	100.0%;	Pred. No. 0;	
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QY	70	TGGGAATGTGATACGACGACACGCAAGTTTTCACACAGGCGCATGTGCTGTGAATGTCCG	129
Db	61	TGGGAATGTGATACGACGACCACTCAAGTTTTCACACAGGCGCATGTGCTGTGAATGTCCG	120
QY	130	AAACATTTCTCTCCACAGCCTTCATGTGTTAACTGGGAGATGTGGACCTGGGAC	189
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QY	190	TGTGATGTCTCCCTCACTCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCCTGAGA	249
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QY	230	ACATTTCCTGTCTACTACTATAGAGAAAATTTAACTGCACCTTGGAGTCCAGAAAGC	309
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QY	310	AAACACAGTTATCCCAAGTACACAGTTAAGAGAACTTACGCTTTTGGAAAAACATGTATA	369
Db	301	AAACACAGTTATCCCAAGTACACAGTTAAGAGAACTTACGCTTTTGGAAAAACATGTATA	360
QY	370	ATTGTACAACCAATAGTTCTACAACTGAAAATCGTGCTTCTTTTTCCTTCCAA	429
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QY	430	GAATACAGATCCCAATATATTACCATTTGAGGTGGAAAGCTGAATGGAGATGGTGTAA	489
Db	421	GAATACAGATCCCAATATATTACCATTTGAGGTGGAAAGCTGAATGGAGATGGTGTAA	480
QY	490	TTTAAATCTCATATGACATACCTGGAGATTAGAGAACATAGCGAAAACTGACACCCTTAAGA	549
Db	481	TTTAAATCTCATATGACATACCTGGAGATTAGAGAACATAGCGAAAACTGACACCCTTAAGA	540
QY	550	TTTTTCCGTGTGAACACAGTTTTTGGGCATCAAAACGATATTCGAAATTAATGGATAAGC	609
Db	541	TTTTTCCGTGTGAACACAGTTTTTGGGCATCAAAACGATATTCGAAATTAATGGATAAGC	600
QY	610	CTGAATTTGGCGCTTTTCATCTGATTTTAAAAATACACATTCGATTCAGACAGTCAACA	669
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QY	670	GTACACAGCTGCATGGAGAGTCAACTTCCGCTAAGAACCGTAAGATTAACCAACCACTTACA	729
Db	661	GTACACAGCTGCATGGAGAGTCAACTTCCGCTAAGAACCGTAAGATTAACCAACCACTTACA	720
QY	730	ACCTCAGGGGCTGTGAGGCTTTTACAGAAATGTGATAGGCTGTGGATGTGCGGCTCAAG	789
Db	721	ACCTCAGGGGCTGTGAGGCTTTTACAGAAATGTGATAGGCTGTGGATGTGCGGCTCAAG	780
QY	790	AGTCAAAAGTTCTGAGTACTGTGAGCCCAAGAAAAATGGGATGACTGAGAGACAAGCTC	849
Db	781	AGTCAAAAGTTCTGAGTACTGTGAGCCCAAGAAAAATGGGATGACTGAGAGACAAGCTC	840
QY	850	CATGTGGCGCTGGAACATGTGTGAGAGTCGTAAGAACGAGTGGAGGCGATGGAGAAAGCCAG	909
Db	841	CATGTGGCGCTGGAACATGTGTGAGAGTCGTAAGAACGAGTGGAGGCGATGGAGAAAGCCAG	900
QY	910	TGCGGTTGTTATGGAAGAAAGCAGAGAGGCCCACTGCTGAGAAAACTTGGCTTACA	969
Db	901	TGCGGTTGTTATGGAAGAAAGCAGAGAGGCCCACTGCTGAGAAAACTTGGCTTACA	960
QY	970	ACATATGCTACTATCCAGAAAGCACTAACCTTACACGAAAAACATGAACTACTAACCC	1029
Db	961	ACATATGCTACTATCCAGAAAGCACTAACCTTACACGAAAAACATGAACTACTAACCC	1020
QY	1030	AGCAGCTTGAACATGCATCTGGGAGCGCAGACCTTTTGGGTGCTATGATTTCTTATAATT	1089
Db	1021	AGCAGCTTGAACATGCATCTGGGAGCGCAGACCTTTTGGGTGCTATGATTTCTTATAATT	1080
QY	1090	CTCTTTGGGAAGTCTCAGTGGCCACCTTGAGAGATTCCAGTATTCAGAAAAATCATTTTC	1149
Db	1081	CTCTTTGGGAAGTCTCAGTGGCCACCTTGAGAGATTCCAGTATTCAGAAAAATCATTTTC	1140
QY	1150	AGTGATTTAGAGTCAATGCAAGCGCTGCGTGTGAGAGACCACTAGTGTGTAAGTGGCAAA	1209
Db	1141	AGTGATTTAGAGTCAATGCAAGCGCTGCGTGTGAGAGACCACTAGTGTGTAAGTGGCAAA	1200
QY	1210	GCTTGCCTCTAGACCTGAAACCTTGGATGTGATGGTTTCCGGATTTGGACTCAGAGC	1269
Db	1201	GCTTGCCTCTAGACCTGAAACCTTGGATGTGATGGTTTCCGGATTTGGACTCAGAGC	1260
QY	1270	CCACACACCTTCTCTGGGAATCTGTGTCTCAGGCCACGAACTGGACATCCAGCAAGATA	1329
Db	1261	CCACACACCTTCTCTGGGAATCTGTGTCTCAGGCCACGAACTGGACATCCAGCAAGATA	1320
QY	1330	AATTAAACCTTCTCTGGGTCTATAACATCTCTGCTATCCAAATGTGATGACAAAAGTGT	1389

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1510 GTGAGAGAAAGGATATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTGAGAAAG 1569  
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1870 CATGCGATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGACTCTGTA 1929  
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RESULT 11  
BD178870  
LOCUS BD178870 4315 bp DNA linear PAT 16-Apr-2003  
DEFINITION NR10 splicing variants.  
ACCESSION BD178870  
VERSION BD178870.1 GI:30016137  
KEYWORDS WO 02077230-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 4315)  
REFERENCE  
AUTHORS Mameda,M., Yaguchi,N. and Hasegawa,M.  
TITLE NR10 splicing variants  
JOURNAL Patent: WO 02077230-A 1 03-OCT-2002;  
CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MAEDA,NORIKO YAGUCHI,  
MASAKAZU HASEGAWA  
OS Homo sapiens (human)  
PN WO 02077230-A/1  
PD 03-OCT-2002  
PF 22-MAR-2002 WO 2002JP002769

PR 26-MAR-2001 JP 01P 087298  
PI MASATSUGU MAEDA,NORIKO YAGUCHI,MASAKAZU HASEGAWA PC  
C12N15/12,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10  
PC C12P21/02,G01N33/15,G01N33/50,G01N33/53  
CC NR10 splicing variants  
FH Key Location/Qualifiers  
FT CDS (7)..(2049).  
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BASE COUNT 1187 a 1008 c 1061 g 1059 t  
ORIGIN  
Query Match 83.98; Score 2016; DB 6; Length 4315;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2016; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 69 CTGGGATGTGCAATCAGCAACCTCAATTTTTCACACGCGCATGCTGTGAATGCC 128  
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QY 129 CAAACATTTCTCTCCCAAGCTTCAATGTTAACTGGGAGATGATGACCTGGCA 188  
DB 61 CAAACATTTCTCTCTCCCAAGCTTCAATGTTAACTGGGAGATGATGACCTGGCA 120  
QY 189 CTGTGATGCTCCCTCAGTCTGCAAAATGACCTGCGACCTGCGACCTAG 248  
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QY 489 ATTAAATCTATATGACATAGTGAAGATTAAGAGAACTAGAGAACTGAACCTAAG 548  
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D	841	GTGGCGTTGTTATGGAGAGCAAGAGAGAGCCCCAGTCTTAGAGAAAAACCTTGGCTAC	900
O	969	AACATATGTTCTATCCAGAAAAGCAACACTAACCTCACAAGAAACAATACACTACTAAC	1028
O	1029	CAGCAGCTTGAACCTCATCTGGAGAGCCGAGAGCTTTGGTGTCTATGATTTCTATAT	1088
D	961	CAGCAGCTTGAACCTCATCTGGAGAGCCGAGAGCTTTGGTGTCTATGATTTCTATAT	1020
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D	1021	TCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCACGCTATTCAGAAAAATCATTT	1080
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D	1081	CAGTGCATTTGAGGTATCATCAGAGCCCTGCTTGTCTGAGACCAGCTATGTGTAAAGTCCAA	1140
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D	1261	AAATTTAAACCTTTCTGTGCTATTAACACTCTCTGTATCCAATGTTCCATGACAAAGTT	1320
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D	1321	GGCGAGCCATTTCCATCCATCCAGGCTTATCCCAAGAAAGCCGTTCCATCGAAGGTCCTGAG	1380
O	1449	ACCAAGGTGAGAACATTTGGCGGTGAAGAGGTCACAGATCAGATGGAAAGAGATTTCCCAAG	1508
D	1381	ACCAAGGTGAGAACATTTGGCGGTGAAGAGGTCACAGATCAGATGGAAAGAGATTTCCCAAG	1440
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D	1441	AGTAGAGAAAGGATATCATCTGCACACTACACCATTTTCCAAAGCTGAAGGTGGAAAA	1500
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D	1501	GGATTTCCTCAAGACAGTCAATTTCCAGCACTCTTGAGTACGGCCCTGGAGTCCCTCAAGCA	1560
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D	1561	AAGACCTTTCATTTGTTACAGTATGGCCACGACACAGTGTGGGGGAACCAAGCGGACCC	1620
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D	1621	AGCATTAATTTCAAGACACTTGTCACTTCAAGTCTTTTGAATTAATCTCATTAATCTTCTGT	1680
O	1749	ATTGTGTGAGGCTTCTTATTCATCTCATTAATCTTCAAGTGTGGGATATGGCTCTCAAAAAACC	1808
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D	1741	AACAAATTTGACATCTCTGTGTGGCCCAACCTTCCCAACCTGTGCGTGAAGTATGATGCC	1800
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D	1801	ACATGGCATGAGATGATTTCCAAAGATTAAGCTAAACCTGAAGGAGTCTGATGACTCTGTG	1860
O	1929	AACACAGAGACAGGATCTTAAACCATGTTCCACCCCACTGACCAAGTGGTGAATTCAC	1988

Db	1861	NACACAGAAACGACGATCTTAAACCAATGTTCCACCACCAGACGACAAAGTTGGTGA	192
Qy	1989	AAGTTGGTGGAACCTTTGGGAATGTTCTGCAGAAGAAATTTTTCACAGATGCAACGAGAACG	2046
Db	1921	AAGTTGGTGGAACCTTTGGGAATGTTCTGCAGAAGAAATTTTTCACAGATGCAACGAGAACG	1980
Qy	2049	GTCAGGAAACCAATTTAGAGGGGAGAAAAGAAATGGG	2084
Db	1981	GTCAGGAAACCAATTTAGAGGGGAGAAAAGAAATGGG	2016
RESULT 12			
LOCUS	BD178876	2776 bp	linear
DEFINITION	NR10 splicing variants.		
ACCESSION	BD178876		
VERSION	BD178876.1	GI:30016143	
KEYWORDS	WO 02077230-A/7.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	1 (bases 1 to 2776)		
TITLE	Maeda,M., Yaguchi,N. and Hasegawa,M.		
JOURNAL	NR10 splicing variants		
	Patent: WO 02077230-A 7 03-OCT-2002;		
	CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MAEDA,NORIKO YAGUCHI,		
	MASAKAZU HASEGAWA		
COMMENT	OS Homo sapiens (human)		
	PN WO 02077230-A/7		
	PD 03-OCT-2002 WO 2002JP002769		
	PF 22-MAR-2002 JP 01P 087298		
	PR 26-MAR-2001 JP 01P 087298		
	PI MASATSUGU MAEDA,NORIKO YAGUCHI,MASAKAZU HASEGAWA PC		
	C12N5/12,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC		
	C12N5/10		
	PC C12P21/02,G01N33/15,G01N33/50,G01N33/53		
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Db	1	CTGGAAATGTCATCAGGCACTCAAGTTTTCACACAGGCATGCTGGAATGTCG	60
Qy	129	CAAAACATTTCTCTCCACAGCTTCATGTTTAACTGGGAGATGTGGACCTGGGCA	188
Db	61	CAAAACATTTCTCTCCACAGCTTCATGTTTAACTGGGAGATGTGGACCTGGGCA	120
Qy	189	CTGTGATGTCCTCCCTCAGCTGTGCAAAATTCAGCTGGCAGCTTGGCAGCTAG	248
Db	121	CTGTGATGTCCTCCCTCAGCTGTGCAAAATTCAGCTGGCAGCTTGGCAGCTAG	180
Qy	249	AACATTTCTGTGCTACTACTATAGGAAAAATTTAACCTGCCTGGAGTCCAGGAAG	308
Db	181	AACATTTCTGTGCTACTACTATAGGAAAAATTTAACCTGCCTGGAGTCCAGGAAG	240
Qy	309	GAACCGATTATACCACTACAGATTAGAGAACTTACGCTTTTGGAGAAAAACATGAT	368
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## RESULT 13

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DEFINITION Novel hemopoietin receptor protein, NR10.  
ACCESSION BD091877  
VERSION BD091877.1 GI:22637488  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;







OY	1878	GGAGATATTTCAGAGGTAAGCTAAACCTGAGAGACTGTGATGACTCTGTGTAACACAGAA	1937
Db	1757	GGAAATATTATTCAGAGGTAAGCTAAACCTGAGAGACTGTGATGACTCTGTGTAACACAGAA	1816
OY	1938	GACAGGATCTTAAACCATGTTCCACCCAGAGGACAAAGTGGTGAATTGACAAAGTTGGG	1997
Db	1817	GACAGGATCTTAAACCATGTTCCACCCAGAGGACAAAGTGGTGAATTGACAAAGTTGGG	1876
OY	1998	GTGAAGTTTGGGAATGTTTCGCAAGAAATTTTTCACAGATGAAGCCGGAAGGTCAGGAA	2057
Db	1877	GTGAAGTTTGGGAATGTTTCGCAAGAAATTTTTCACAGATGAAGCCGGAAGGTCAGGAA	1936
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ACCESSION	AX365201		PAT 15-FEB-2002
VERSION	AX365201.1	GI:18696955	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kujiper, J.L. and Maurer, M.F.		
TITLE	Cytokine receptor zcyfor17		
JOURNAL	Patent: WO 0200721-A 53 03-JAN-2002; ZymoGenetics, Inc. (US)		
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Db	863	CATATGACATACAGGAGATTAGAGAACATAGGAAACATGAAACCACTTAAGTTTCCGT	922
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Db	983	GCGCCTGTTTCATCTGATTTAAATACACACTTCGATTGAGACAGTCAACAGTACAGC	1042
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Db	1043	TGGATGGAATCAACTTCGCTTAAGAACCTGTAAGGATTAATAACCAACGTAACCTCAGC	1102
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Db	1103	GCGCTGAGCCTTTTACAGAAATATGTCATAGCTCTGCATGTGCGGTCAAGAGTCGAAG	1162
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Db	1163	TTCTGAGTACCTGAGAGCCCAAGAAAAATGGGAATGACTGAGAGAAAGCTTCATGTGC	1222
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OY	978	TACTATCCAGAAAGCAACACTAATCTACAGAAACATGAAACACTAATACCAAGCAGCTT	1037
Db	1343	TACTATCCAGAAAGCAACACTAATCTACAGAAACATGAAACACTAATACCAAGCAGCTT	1402
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QY	1458	GAGAACATTGGCGTGAAGACGGTCACGATCAACATGAGAAAGATTCCCAAGAGTAGAGA	1517
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Db	1943	AAGACATCAATTCCAGCATCTTGGAGTAGCGGCCGTGGATCCCTTAACAGAAAGACCTCT	2002
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Db	2003	TACATTTGTCACAGTCATGCGCCAGCACACAGTCTGGGGGAGAACCAAGGACACATTAAT	2062
QY	1698	TTCAAGCATTTGTCATTTAGTGTCTTTGAGATTATCTCATAACTTCTGATTGGTGGGA	1755
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BD091864			
LOCUS	BD091864	2969 bp	DNA linear
DEFINITION	Novel hemopoietin receptor protein, NR10.		
ACCESSION	BD091864		
VERSION	BD091864.1	GI:22637475	
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ORGANISM	Homo sapiens (human)		
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TITLE	PN WO 0075314-A/1		
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	PR 02-JUN-1999 JP 99P 155797, 30-JUL-1999 JP 99P 217797 PT		
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Dd	829	ATCCAGATTAATTATACCATGAGGTGAAGCTCAAAATGGAGATGGTGTATTAATAATCT	888				
OY	498	CATATGACATCTGAGATTTAGAGAACATVAGCAAACCTGAACCCAGCTAAGATTTCCTG	557				
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Dd	1009	GCGCCTGTTTATCGATTTTAAATTTACACATCTTGATTCAGAGACAGTCAACAGTAGCACG	1068				
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Db 2101 TCAGGCGCTGATTTGCCCTGGGGAAGATTTTGAAGAGCTCCAGTTTACCTGAGATTC 2160
QY 2161 CGGCCAGAAATCCCATACCTACGTGCGAGGATGCGAGAGGGAGCCGCCCAAGACCA 2220
    |||||||
Db 2161 CGGCCAGAAATCCCATACCTACGTGCGAGGATGCGAGAGGGAGCCGCCCAAGACCA 2220
QY 2221 AAGAGAGCTTCTCTTTTCTGTCAAAGTTAGTACAGATCATCTGTGAGAGAGAG 2280
    |||||||
Db 2221 AAGAGAGCTTCTCTTTTCTGTCAAAGTTAGTACAGATCATCTGTGAGAGAGAG 2280
QY 2281 CCCCAATTCATATTTAAAAAATTCAGTACAGCCAGGGAATTTCTGTCTGAAAAAC 2340
    |||||||
Db 2281 CCCCAATTCATATTTAAAAAATTCAGTACAGCCAGGGAATTTCTGTCTGAAAAAC 2340
QY 2341 TTCAGAGCACACCAAGGAGAGTCTAAATGCGACATAGCATGA 2386
    |||||||
Db 2341 TTCAGAGCACACCAAGGAGAGTCTAAATGCGACATAGCATGA 2386

RESULT 2
AB083365
ID AB083365 standard; cDNA; 2952 BP.
XX
AC AB083365;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:5.
XX
KW NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 7..2301
FT CDS /*tag= a
FT /product= "NR10.4"
XX
XX MO200277230-1.
```

```
PD 03-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-JP02769.
XX
XX 26-MAR-2001; 2001JP-0087298.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
XX WPI; 2003-018925/01.
XX
XX P-PDB; ABP54365.
XX
XX NR10 splicing variants of haematopoietin receptor proteins and encoded
PT genes; applicable in searching haematopoietic factors and developing
PT remedies for immunological and haematopoietic diseases
XX
XX Claim 1; Fig 7-9; 250bp; Japanese.
XX
XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate
CC in in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence encodes the human NR10.4 protein
CC from the present invention.
XX
XX Sequence 2952 BP; 821 A; 688 C; 727 G; 716 T; 0 other;
S0
Query Match 97.2%; Score 2334; DB 25; Length 2952;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 69 CTGGGAATGTGCATCAGGCAACCTCAAGTTTTCACACGCGCATGTCTGTGAATGCC 128
    |||||||
Db 1 CTGGGAATGTGCATCAGGCAACCTCAAGTTTTCACACGCGCATGTCTGTGAATGCC 60
    |||||||
QY 129 CAAACATTTCTCTCTCCCGACGCTTCAATGTGTTAACCTGGGAGATGTGACCTGGGCA 188
    |||||||
Db 61 CAAACATTTCTCTCTCCCGACGCTTCAATGTGTTAACCTGGGAGATGTGACCTGGGCA 120
    |||||||
QY 189 CTGTGATGTGCTCCCTACACTGTGCAAAATTCAGCTGCGAGCTGCCAGTAACTGAG 248
    |||||||
Db 189 CTGTGATGTGCTCCCTACACTGTGCAAAATTCAGCTGCGAGCTGCCAGTAACTGAG 248
    |||||||
QY 121 CTGTGATGTGCTCCCTACACTGTGCAAAATTCAGCTGCGAGCTGCCAGTAACTGAG 180
    |||||||
Db 121 CTGTGATGTGCTCCCTACACTGTGCAAAATTCAGCTGCGAGCTGCCAGTAACTGAG 180
    |||||||
QY 249 AACATTTCTGTGTCTACTACTATAGAAAAAATTTAACTGTGCACTTGGAGTCCAGAAAG 308
    |||||||
Db 249 AACATTTCTGTGTCTACTACTATAGAAAAAATTTAACTGTGCACTTGGAGTCCAGAAAG 308
    |||||||
QY 181 AACATTTCTGTGTCTACTACTATAGAAAAAATTTAACTGTGCACTTGGAGTCCAGAAAG 240
    |||||||
Db 181 AACATTTCTGTGTCTACTACTATAGAAAAAATTTAACTGTGCACTTGGAGTCCAGAAAG 240
    |||||||
QY 309 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAACATGAT 368
    |||||||
Db 309 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAACATGAT 368
    |||||||
QY 241 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAACATGAT 300
    |||||||
Db 241 GAAACCACTTATACCCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAACATGAT 300
    |||||||
QY 369 AATGTACACCAATAGTGTCTACAGAGTAAAGTGTGCTGCTCTTTTTCCTTCCA 428
    |||||||
Db 301 AATGTACACCAATAGTGTCTACAGAGTAAAGTGTGCTGCTCTTTTTCCTTCCA 360
    |||||||
QY 429 AGAATTAACGATCCAGATAATTAATACATTGAGTGAAGCTGAAATGAGATGCTGTA 488
    |||||||
Db 361 AGAATTAACGATCCAGATAATTAATACATTGAGTGAAGCTGAAATGAGATGCTGTA 420
    |||||||
QY 489 ATTAAATCTCATATGACATACTGAGAGATAGAGAACTAGGAAACTGAACCTTAAG 548
    |||||||
Db 421 ATTAAATCTCATATGACATACTGAGAGATAGAGAACTAGGAAACTGAACCTTAAG 480
    |||||||
QY 549 ATTTCGCTGTGAACACAGTTTGGGATCAACAGATGATTCAAATTTGAATGATTAAG 608
    |||||||
Db 481 ATTTCGCTGTGAACACAGTTTGGGATCAACAGATGATTCAAATTTGAATGATTAAG 540
    |||||||
QY 609 CCTGAGTTGGCGCTGTTTCACTGATTTAAATATACACACTTCGATTGAGAGAGTCAAC 668
    |||||||
```

Db 541 CCTGAGTGTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAAC 600  
 QY AGTACACAGCTGGATGGAAGTCACTGCTAGAAACGCTAAGGATTAATAACCAACGCTAC 728  
 Db 669 |||||||  
 Db 601 AGTACACAGCTGGATGGAAGTCACTGCTAGAAACGCTAAGGATTAATAACCAACGCTAC 660  
 QY 729 AACCTCAGGGGGCTGACAGCTTTTACAAATATGTCATAGCTGTCGATGTGCGGTCAAG 788  
 Db 661 AACCTCAGGGGGCTGACAGCTTTTACAAATATGTCATAGCTGTCGATGTGCGGTCAAG 720  
 QY 789 GAGTCAAAAGTCTGAGAGTGAAGTGAAGCCCAAGAAAAATGGAAATGACTGAGAGAAAGCT 848  
 Db 721 GAGTCAAAAGTCTGAGAGTGAAGTGAAGCCCAAGAAAAATGGAAATGACTGAGAGAAAGCT 780  
 QY 849 CCATGTGGCCCTGGAACCTGTGAGAGTCTGAAACACAGCTGAGCGGATGAGAAAGGCCA 908  
 Db 781 CCATGTGGCCCTGGAACCTGTGAGAGTCTGAAACACAGCTGAGCGGATGAGAAAGGCCA 840  
 QY 909 GTGCGGTTGTTATGGAAGAGGCAAGAGAGCCCAAGTCTGAGAAAAACACTTGGCTAC 968  
 Db 841 GTGCGGTTGTTATGGAAGAGGCAAGAGAGCCCAAGTCTGAGAAAAACACTTGGCTAC 900  
 QY 969 AACATATGCTACTATCCAGAAAGCAACACTAATCTCAGAGAAACATGATGACACTACTAC 1028  
 Db 901 AACATATGCTACTATCCAGAAAGCAACACTAATCTCAGAGAAACATGATGACACTACTAC 960  
 QY 1029 CAGCAGCTTGAACCTGCTGGAGGCGAGAGCTTTTGGGTGCTCATGATTTCTTATAT 1088  
 Db 961 CAGCAGCTTGAACCTGCTGGAGGCGAGAGCTTTTGGGTGCTCATGATTTCTTATAT 1020  
 QY 1089 TCTCTTGGGAAGTCTCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTT 1148  
 Db 1021 TCTCTTGGGAAGTCTCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTT 1080  
 QY 1149 CAGTGCANTGAGTATCAGCAGGCTGCTGCTGAGAGCAGCTAAGTGTGTAATGTCGCA 1208  
 Db 1081 CAGTGCANTGAGTATCAGCAGGCTGCTGCTGAGAGCAGCTAAGTGTGTAATGTCGCA 1140  
 QY 1209 AGCTGCTGTAGACGTGAACACTTGGATGATTAATGTTCCGATGTGAGTCTCAGAG 1268  
 Db 1141 AGCTGCTGTAGACGTGAACACTTGGATGATTAATGTTCCGATGTGAGTCTCAGAG 1200  
 QY 1269 CCCACACCCCTTCTCTGGGAATCTGTGCTCAGGCCACAGAACTGAGACATCCAGAAAT 1328  
 Db 1201 CCCACACCCCTTCTCTGGGAATCTGTGCTCAGGCCACAGAACTGAGACATCCAGAAAT 1260  
 QY 1329 AAATTAACCTTCTGGTGTATACATCTCTGTATCCATGTTGCATGACAAAGTT 1388  
 Db 1261 AAATTAACCTTCTGGTGTATACATCTCTGTATCCATGTTGCATGACAAAGTT 1320  
 QY 1389 GCGAGGCCATATTCATCCAGGCTTATGCCAAAGAGCGTTCCATCAGAAAGTCTGAG 1448  
 Db 1321 GCGAGGCCATATTCATCCAGGCTTATGCCAAAGAGCGTTCCATCAGAAAGTCTGAG 1380  
 QY 1449 ACCAAGTGGGAACATTTGGCGTGAAGAGCTCAGATCACATGAGAAAGAGATTCACAG 1508  
 Db 1381 ACCAAGTGGGAACATTTGGCGTGAAGAGCTCAGATCACATGAGAAAGAGATTCACAG 1440  
 QY 1509 AGTGAAGAAAGGCTATCATCTGCACTACACATCTTTTACCAAGCTGAAAGGTGGAAGA 1568  
 Db 1441 AGTGAAGAAAGGCTATCATCTGCACTACACATCTTTTACCAAGCTGAAAGGTGGAAGA 1500  
 QY 1569 GGATTTCTCAAGACAGTCAATTCAGCATCTTGCAGTACGGCTGAGATCCCTGAAACGA 1628  
 Db 1501 GGATTTCTCAAGACAGTCAATTCAGCATCTTGCAGTACGGCTGAGATCCCTGAAACGA 1560  
 QY 1629 AAGACCTTTACATTTGTCAGGTATGCGCAGACACAGTGTGGGGGAACCAACGGGACC 1688  
 Db 1561 AAGACCTTTACATTTGTCAGGTATGCGCAGACACAGTGTGGGGGAACCAACGGGACC 1620  
 QY 1689 AGCATTAATTTCAAGACATGTCTCATAGTGTCTTTAGANTATTCCTATTAATCTTCTG 1748  
 Db 1621 AGCATTAATTTCAAGACATGTCTCATAGTGTCTTTAGANTATTCCTATTAATCTTCTG 1680

QY 1749 ATTGCTGAGGCGCTTCTTATTTCTCATTTATCCGACAGTGGGATATGGTCTCAAAAAACCC 1808  
 Db 1661 ATTGCTGAGGCGCTTCTTATTTCTCATTTATCTTGACAGTGGGATATGGTCTCAAAAAACCC 1740  
 QY 1809 AACAAATGACTCATCTGTGTGGCCACCGTTCACCAACCCGTGGAAGTATATAGCC 1868  
 Db 1741 AACAAATGACTCATCTGTGTGGCCACCGTTCACCAACCCGTGGAAGTATATAGCC 1800  
 QY 1869 ACATGGCATGAGATGATTTCAAGATATAGCTAAACCTGAAAGAGTCTGATGACTCTGTG 1928  
 Db 1801 ACATGGCATGAGATGATTTCAAGATATAGCTAAACCTGAAAGAGTCTGATGACTCTGTG 1860  
 QY 1929 AACACAGAAAGACAGATCTTAAACCATAGTTCACACCCCACTGACAAATGTTGATGAC 1988  
 Db 1861 AACACAGAAAGACAGATCTTAAACCATAGTTCACACCCCACTGACAAATGTTGATGAC 1920  
 QY 1989 AAGTTGCTGTGAACCTTTGGGAATGTCTGCAAGAAATTTTTCACAGATGAAGCAGAACG 2048  
 Db 1921 AAGTTGCTGTGAACCTTTGGGAATGTCTGCAAGAAATTTTTCACAGATGAAGCAGAACG 1980  
 QY 2049 GGTGAGGAAACATTTTAGAGGGGAAAGAAATGGTATGTGACTGCTCCCTTACAGGCT 2108  
 Db 1981 GGTGAGGAAACATTTTAGAGGGGAAAGAAATGGTATGTGACTGCTCCCTTACAGGCT 2040  
 QY 2109 GATTGTCCTCCCTGGGGGAAAGTTTGGAGAGCTCCAGTTTACCTGAGATTCGCGCCAGA 2168  
 Db 2041 GATTGTCCTCCCTGGGGGAAAGTTTGGAGAGCTCCAGTTTACCTGAGATTCGCGCCAGA 2100  
 QY 2169 AAATCCCAATACCTACGTTTCAGAGATGCCAGAGGGGAGCCCGCCAGAAAGCCAAAGAGAG 2228  
 Db 2101 AAATCCCAATACCTACGTTTCAGAGATGCCAGAGGGGAGCCCGCCAGAAAGCCAAAGAGAG 2160  
 QY 2229 CTTCCTTTTCTGGTCAAAAGTTTATGATACAGATATCTGTGTGAGAAAGAGCCCAAT 2288  
 Db 2161 CTTCCTTTTCTGGTCAAAAGTTTATGATACAGATATCTGTGTGAGAAAGAGCCCAAT 2220  
 QY 2289 CCATATTTGAAAAATTCAGTACAGCAGCAGGAAATTTCTGTGTGAAAAACTTCAGAG 2348  
 Db 2221 CCATATTTGAAAAATTCAGTACAGCAGCAGGAAATTTCTGTGTGAAAAACTTCAGAG 2280  
 QY 2349 CACACCAAGGAGAGTCTAAATCCAGCATATGACATGAGAGCCCTGGGGGCTCA 2402  
 Db 2281 CACACCAAGGAGAGTCTAAATCCAGCATATGACATGAGAGCCCTGGGGGCTCA 2334

RESULT 3  
 AB083364  
 ID AB083364 standard; cDNA: 5271 BP.  
 XX  
 AC AB083364;  
 XX  
 DT 20-JAN-2003 (first entry)  
 XX  
 DE Human NR10.4 splicing variant encoding cDNA seq ID NO:3.  
 XX  
 KW NR10: splicing variant; haematopoietic receptor; immunomodulator;  
 KW haematopoietic factor; immunological disease;  
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 7..2301  
 FT /\*tag= a  
 FT /product= "NR10.4"  
 XX  
 PN MO200277230-A1.  
 XX  
 PD 03-Oct-2002.  
 XX  
 PF 22-MAR-2002; 2002WO-JP02769.  
 XX



PR 26-MAR-2001; 2001JP-0087298.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Maeda M, Yaguchi N, Hasegawa M.  
XX  
DR WPI; 2003-018925/01.  
XX  
P-PSDB; ABP54364.  
XX  
NR10 splicing variants of haematopoietin receptor proteins and encoded  
PT genes, applicable in searching haematopoietic factors and developing  
PT remedies for immunological and haematopoietic diseases  
XX  
XX Claim 1; Fig 4-5; 250pp; Japanese.  
XX  
XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (I). (I) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors. The haematopoietin receptor genes participate  
CC in in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence encodes the human NR10.4 protein  
CC from the present invention.  
XX  
XX Sequence 5271 BP; 1312 A; 1302 C; 1318 G; 1339 T; 0 other;  
SQ  
Query Match 97.2%; Score 2334; DB 25; Length 5271;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
69 CTGGGAATGTGCATCAGCACTCAAGTTTTCACACGCGCATGTCTGTGATGTCCG 128  
1 CTGGGAATGTGCATCAGCACTCAAGTTTTCACACGCGCATGTCTGTGATGTCCG 60  
129 CAAACATTTCTCTCTCCCGACCTTCATGTGTTAACTGGGGATGATGTGACCTGGCA 188  
61 CAAACATTTCTCTCTCCCGACCTTCATGTGTTAACTGGGGATGATGTGACCTGGCA 120  
189 CTGTGATGTCTCCCGTCTGCTGCAATTCAGCTGTGACCTGTGCGACGTAACCTGAG 248  
121 CTGTGATGTCTCCCGTCTGCTGCAATTCAGCTGTGACCTGTGCGACGTAACCTGAG 180  
249 AACATTTCTGTGTCTACTACTATAGGAAAAATTTAACTGCACTGTGAGTCCAGAAAG 308  
181 AACATTTCTGTGTCTACTACTATAGGAAAAATTTAACTGCACTGTGAGTCCAGAAAG 240  
309 GAAACCGATTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGAT 368  
241 GAAACCGATTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGAT 300  
369 AATTGTCAACCAATAGTTCTACAAAGTGAATGCTGCTGCTGCTTTTCTTCTCCA 428  
301 AATTGTCAACCAATAGTTCTACAAAGTGAATGCTGCTGCTGCTTTTCTTCTCCA 360  
429 AGAATAACGATCCCGATTAATATACATTGAGGTGAGAGCTGAAATGAGATGTGTA 488  
361 AGAATAACGATCCCGATTAATATACATTGAGGTGAGAGCTGAAATGAGATGTGTA 420  
489 AATTAATCTCATATGATATGATAGATGAGATGAGAACTAGCGAAACCTGAAACCTGAA 548  
421 AATTAATCTCATATGATATGATAGATGAGATGAGAACTAGCGAAACCTGAAACCTGAA 480  
549 AATTTCGCTGGAACCCAGTTTGGGATCAAAAGATGATCAATTAATGATGATTAAG 608  
481 AATTTCGCTGGAACCCAGTTTGGGATCAAAAGATGATCAATTAATGATGATTAAG 540  
609 CTTGAGTTGGCGCTGTTTCATCTGATTTAAATATACACACTTCGATTCAGACAGTCAAC 668  
541 CTTGAGTTGGCGCTGTTTCATCTGATTTAAATATACACACTTCGATTCAGACAGTCAAC 600  
669 AGTACCACTGTGATGAGATCACTTGGCTTAAGAACCTGAAGATTAATAAACCAACGTAC 728  
|||||

601 AGTACCACTGTGATGAGATCACTTGGCTTAAGAACCTGAAGATTAATAAACCAACGTAC 660  
729 AACCTACAGGAGGCTGCAGCCCTTTACAGAAATATGTACATGCTGCGATGGCGTAAAG 788  
661 AACCTACAGGAGGCTGCAGCCCTTTACAGAAATATGTACATGCTGCGATGGCGTAAAG 720  
789 GAGTCAAAAGTTCTGAGATGACTGAGGACCAAGAAAAATGGGAATGACTGAGGAAGAACT 848  
721 GAGTCAAAAGTTCTGAGATGACTGAGGACCAAGAAAAATGGGAATGACTGAGGAAGAACT 780  
849 CCAATGTGCGCTGGAAGTGTGAGAGTCTCTGAACACAGCTGAGGCGGATGGAAGAGCCA 908  
781 CCAATGTGCGCTGGAAGTGTGAGAGTCTCTGAACACAGCTGAGGCGGATGGAAGAGCCA 840  
909 GTGCGGTTGTTATGGAAGAAAGCAAGAGGAGACCCCTGATCTGAGAAACCTTGCGTAC 968  
841 GTGCGGTTGTTATGGAAGAAAGCAAGAGGAGACCCCTGATCTGAGAAACCTTGCGTAC 900  
969 AACATATGATATCTATCCAGAAAGCAAGCACTAACCTCAGAGAAACATGAACACTACTAAC 1028  
901 AACATATGATATCTATCCAGAAAGCAAGCACTAACCTCAGAGAAACATGAACACTACTAAC 960  
1029 CAGCAGCTTGACATGCACTGTGGAGGCGAGAGCTTTTGGGTGTTATGATTTCTTATAT 1088  
961 CAGCAGCTTGACATGCACTGTGGAGGCGAGAGCTTTTGGGTGTTATGATTTCTTATAT 1020  
1089 TCTCTTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGATCTATCAAGAAATATCATTT 1148  
1021 TCTCTTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGATCTATCAAGAAATATCATTT 1080  
1149 CAGTGCATTTGAGTGCATGACAGGCTGCTGCTGAGAGACCAAGTATGTTGTAAGTGGCAA 1208  
1081 CAGTGCATTTGAGTGCATGACAGGCTGCTGCTGAGAGACCAAGTATGTTGTAAGTGGCAA 1140  
1209 AGCTCTGCTCTAGACGTGAACACTTGGATGATTAATGTTTCCGATATGAGACTCAGAG 1268  
1141 AGCTCTGCTCTAGACGTGAACACTTGGATGATTAATGTTTCCGATATGAGACTCAGAG 1200  
1269 CCCGACCAACCTTCTCTGGGAATCTGTCTCAGGCGCAGAACTGAGATGCACCAAGAT 1328  
1201 CCCGACCAACCTTCTCTGGGAATCTGTCTCAGGCGCAGAACTGAGATGCACCAAGAT 1260  
1329 AAATTAACCTTCTCTGCTATATACATCTCTGTATCCAAATGTTGATGATGACAAAGTT 1388  
1261 AAATTAACCTTCTCTGCTATATACATCTCTGTATCCAAATGTTGATGATGACAAAGTT 1320  
1389 GCGCAGCCATATTCATCTCAGGCTTATGCCAAGAGCGCTTCCATATGAAAGTCTGAG 1448  
1321 GCGCAGCCATATTCATCTCAGGCTTATGCCAAGAGCGCTTCCATATGAAAGTCTGAG 1380  
1449 ACCAAGGTGAGACATTTGGCGTGAAGACGGTCCAGATCAATGGAAGATTCGCCAAG 1508  
1381 ACCAAGGTGAGACATTTGGCGTGAAGACGGTCCAGATCAATGGAAGATTCGCCAAG 1440  
1509 AGTGAGAGAAAGGTTATCTGCACTACACATCTTTTACCAAGCTGAAGGTGAGAAA 1568  
1441 AGTGAGAGAAAGGTTATCTGCACTACACATCTTTTACCAAGCTGAAGGTGAGAAA 1500  
1569 GGATTTCTCCAGACAGATTCAGATCTTGGAGTACAGAGGCTGAGAGTCCCTTAACAGA 1628  
1501 GGATTTCTCCAGACAGATTCAGATCTTGGAGTACAGAGGCTGAGAGTCCCTTAACAGA 1560  
1629 AAGACCTCTTACATTTGTCAGGTATGCGCCAGCACAGTGTGGGGGAACCAACGGGAC 1688  
1561 AAGACCTCTTACATTTGTCAGGTATGCGCCAGCACAGTGTGGGGGAACCAACGGGAC 1620  
1689 AAGATTAATTTCAAGACATTTGTCAGGTATGCGCCAGCACAGTGTGGGGGAACCAACGGG 1748  
1621 AAGATTAATTTCAAGACATTTGTCAGGTATGCGCCAGCACAGTGTGGGGGAACCAACGGG 1680  
1749 AATTGCTGAGAGGCTTCTTATATCTGATATCTGACATGAGATATGCTCAAAAACCC 1808  
1681 AATTGCTGAGAGGCTTCTTATATCTGATATCTGACATGAGATATGCTCAAAAACCC 1740  
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QY 1809 AACAAATGACTCTGTGTGGCCACCGTCCCAACCTGCTGANAAGTATAGCC 1868  
 |||||||  
 Db 1741 AACAAATGACTCTGTGTGGCCACCGTCCCAACCTGCTGANAAGTATAGCC 1800  
 |||||||  
 QY 1869 ACATGGCATGGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATCTGTG 1928  
 |||||||  
 Db 1801 ACATGGCATGGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATCTGTG 1860  
 |||||||  
 QY 1929 AACACAGAGACAGATCTTAAACCATGTTCCACCCCATGCAAGTGTGATTTGAC 1988  
 |||||||  
 Db 1861 AACACAGAGACAGATCTTAAACCATGTTCCACCCCATGCAAGTGTGATTTGAC 1920  
 |||||||  
 QY 1989 AAGTTGGTGTGATCTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAAG 2048  
 |||||||  
 Db 1921 AAGTTGGTGTGATCTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAAG 1980  
 |||||||  
 QY 2049 GGTGAGGAAAACAAATTTAGAGAGGGGAAAAGAAATGGTATGTGACCTGCCCCCTCAGGCCCT 2108  
 |||||||  
 Db 1981 GGTGAGGAAAACAAATTTAGAGAGGGGAAAAGAAATGGTATGTGACCTGCCCCCTCAGGCCCT 2040  
 |||||||  
 QY 2109 GATTGTCCTCCCTGGGGAAAAGTTTGAGAGAGCTCCCAAGTTTACCTGAGATTTCCGCCCA 2168  
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 Db 2041 GATTGTCCTCCCTGGGGAAAAGTTTGAGAGAGCTCCCAAGTTTACCTGAGATTTCCGCCCA 2100  
 |||||||  
 QY 2169 AATATCCCAATACCTACGTTGAGAGATGCGACAGAGGGAGCCGCCAGAAAGAGAGAG 2228  
 |||||||  
 Db 2101 AATATCCCAATACCTACGTTGAGAGATGCGACAGAGGGAGCCGCCAGAAAGAGAGAG 2160  
 |||||||  
 QY 2229 CTCTCTCTTTTGTGTCACAAAGTTTATGATACAGATCATCTGTGTGAGGAAGAGCCCCAAAT 2288  
 |||||||  
 Db 2161 CTCTCTCTTTTGTGTCACAAAGTTTATGATACAGATCATCTGTGTGAGGAAGAGCCCCAAAT 2220  
 |||||||  
 QY 2289 CCATATTTGAAAATTTAGTACAGCCAGGGAATTTCTGTGTGTAAGAACTCCAGAG 2348  
 |||||||  
 Db 2221 CCATATTTGAAAATTTAGTACAGCCAGGGAATTTCTGTGTGTAAGAACTCCAGAG 2280  
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 QY 2349 CACACCAAGGAGAGATCTTAATATCGACCATATGATGAGACCTCGGGGCTCA 2402  
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 Db 2281 CACACCAAGGAGAGATCTTAATATCGACCATATGATGAGACCTCGGGGCTCA 2334  
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 RESULT 4  
 AAD38772 standard; cDNA; 2480 BP.  
 ID AAD38772 standard; cDNA; 2480 BP.  
 XX AAD38772;  
 AC AAD38772;  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE Human haematopoietin receptor 1 (HPR1) cDNA.  
 XX  
 KW Human: haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;  
 KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;  
 KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
 KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;  
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
 KW osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;  
 KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;  
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
 KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
 KW ischaemic disease; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 132..2369  
 FT /tag- a  
 FT /product- "Human HPR1 protein"  
 FT /transl\_except- (pos:1680..1682, aa:Asn)  
 FT /note- "This region is specifically claimed as  
 FT SEQ ID NO: 5 in claim 6 of the specification"

FT sig\_peptide 191..227  
 FT /tag- b  
 FT mat\_peptide 228..2366  
 FT /tag- c  
 FT /product- "Human mature HPR1 protein"  
 FT /replace (278, G)  
 FT /tag- d  
 FT /replace (633, G)  
 FT /tag- e  
 FT /replace (691, G)  
 FT /tag- f  
 FT /replace (1212, G)  
 FT /tag- g  
 FT /replace (1216, G)  
 FT /tag- h  
 FT /replace (1660, G)  
 FT /tag- i  
 FT /replace (1680, G)  
 FT /tag- j  
 FT /replace (2166, G)  
 FT /tag- k  
 FT  
 PN WO200229060-A2.  
 PD 11-APR-2002.  
 PD 05-OCT-2001; 2001WO-US31634.  
 PE 06-OCT-2000; 2000US-238706F.  
 PR 13-OCT-2000; 2000US-240476P.  
 PR 20-FEB-2001; 2001US-270282P.  
 PR  
 PA (IMMUNEX CORP.  
 PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;  
 PL WPI; 2002-330172/36.  
 DR P-PSDB; AAE24024.  
 DR  
 XX  
 PT Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,  
 PT useful for treating cell proliferation, metabolic, and reproductive  
 PT hormone related conditions -  
 PT  
 PS  
 PS  
 PS  
 XX  
 CC Claim 6; Page 83-84; 136pp: English.  
 CC  
 CC The present invention relates to human and murine haematopoietin receptor  
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 CC resulting from a lack of bone-forming cells. They are also useful for  
 CC treating cell proliferation conditions such as leukaemia and tumour  
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
 CC cells. HPR sequences are also useful for treating medical conditions and  
 CC diseases such as cell proliferation, metabolic and reproductive hormone  
 CC related disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 CC oncologic conditions e.g., colon, stomach, prostate, renal cell,  
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 CC squamous cell carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 CC sarcoma), leiomyosarcoma, haematologic disorders, anemias (e.g., anaemia  
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such  
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis  
 CC resulting in tooth loosening or loss, prosthesis loosening after joint  
 CC replacement, neurodegenerative conditions (e.g., acute polynuropathy,  
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 CC myasthenia gravis, chronic neuronal degeneration, stroke including



QY 2178 TACCTACGTCGAGATGCGAGAGGAGCCGCCAGAACCCAAAGACAGCTTCTCTT 2237  
DB 2178 TACCTACGTCGAGATGCGAGAGGAGCCGCCAGAACCCAAAGACAGCTTCTCTT 2237  
QY 2238 TCTGCTCAAGTTTGTATCCAGATCATCTGTGTGAGAGAGAGCCCAATTCATATTTG 2297  
DB 2238 TCTGCTCAAGTTTGTATCCAGATCATCTGTGTGAGAGAGAGCCCAATTCATATTTG 2297  
QY 2298 AAAAATTGAGTACGACGAGGAAATTTCTGTGTGAGAGAGAGCCCAATTCATATTTG 2357  
DB 2298 AAAAATTGAGTACGACGAGGAAATTTCTGTGTGAGAGAGAGCCCAATTCATATTTG 2357  
QY 2358 GGAGAGTCTTAATGCGACATAGCATAGACCCCTGCGGCGCTCA 2402  
DB 2358 GGAGAGTCTTAATGCGACATAGCATAGACCCCTGCGGCGCTCA 2402  
RESULT 5  
ABQ83366  
ID ABQ83366 standard; cDNA: 3072 BP.  
AC ABQ83366;  
XX 20-JAN-2003 (first entry)  
DT 20-JAN-2003 (first entry)  
XX Human NR10.5 splicing variant encoding cDNA SEQ ID NO:7.  
DE Human NR10.5 splicing variant encoding cDNA SEQ ID NO:7.  
XX NR10: splicing variant; haematopoietic receptor; immunomodulator;  
KW haemostatic; haematopoietic factor; immunological disease;  
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 7.1890  
FT CDS /tag= a  
FT /product= "NR10.5"  
XX  
XX MO20027230-A1.  
XX  
XX 03-OCT-2002.  
XX 22-MAR-2002; 2002WO-JP02769.  
XX 26-MAR-2001; 2001JP-0087298.  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX Maeda M, Yaguchi N, Hasegawa M;  
PI WPI: 2003-018925/01.  
XX P-PSDB: ABP54366.  
XX NR10 splicing variants of hematopoietic receptor proteins and encoded  
PT genes, applicable in searching hematopoietic factors and developing  
PT remedies for immunological and hematopoietic diseases -  
XX  
XX Claim 1; Fig 10-12; 250pp; Japanese.  
XX  
XX The present invention describes haematopoietic receptor NR10 splicing  
CC variants (I). (i) have immunomodulator and haemostatic activities. The  
CC proteins and encoded genes are applicable in searching for novel  
CC haematopoietic factors. The developing remedies for immunological and  
CC haematopoietic diseases. The haematopoietic receptor genes participate  
CC in vivo immunomodulation and haematopoietic cell regulation, and in  
CC the search for haematopoietic factors capable of functionally binding  
CC to the receptors. The present sequence encodes the human NR10.5 protein  
CC from the present invention.  
XX  
XX Sequence 3072 BP; 849 A; 721 C; 755 G; 747 T; 0 other:  
XX  
XX Query Match 91.8%, Score 2204, DB 25; Length 3072;

Best Local Similarity 95.1%; Pred. No. 0;  
Matches 2334; Conservative 0; Mismatches 0; Indels 120; Gaps 1;  
QY 69 CTGGGAATGTGTCATCAGGCAACTAAGTTTTCACACAGCATGTGTCTGGAATGTCG 128  
DB 1 CTGGGAATGTGTCATCAGGCAACTAAGTTTTCACACAGCATGTGTCTGGAATGTCG 60  
QY 129 CAACAACATTCCTCTCCACGCTTCATGTGTAACTGGGGAGATGTGGACCTGGGCA 188  
DB 61 CAACAACATTCCTCTCCACGCTTCATGTGTAACTGGGGAGATGTGGACCTGGGCA 120  
QY 189 CTGTGATGCTCCCTCAGCTCTGCAAAATTCAGCTGAGCTGTCCAGCTAAGCTGAG 248  
DB 121 CTGTGATGCTCCCTCAGCTCTGCAAAATTCAGCTGAGCTGTCCAGCTAAGCTGAG 180  
QY 249 AACATTTCTGTGTCTACTATATAGGAAAAATTAACCTGTGACTTGGAGTCCAGGAAG 308  
DB 181 AACATTTCTGTGTCTACTATATAGGAAAAATTAACCTGTGACTTGGAGTCCAGGAAG 240  
QY 309 GAAACCAAGTTATACCCAGTACAGATTAGAGAACTTACGCTTTGGAGAAAAACATGAT 368  
DB 241 GAAACCAAGTTATACCCAGTACAGATTAGAGAACTTACGCTTTGGAGAAAAACATGAT 300  
QY 369 AATTGTACAAACCAATAGTTCTACAGTGAAGTGAATGCTGTGCTCTTTTTCCTTCCA 428  
DB 301 AATTGTACAAACCAATAGTTCTACAGTGAAGTGAATGCTGTGCTCTTTTTCCTTCCA 360  
QY 429 AGAATTAACGATCCAGATATATATACATTTGAGTGGAGAGCTGAAATTCAGATGCTGA 488  
DB 361 AGAATTAACGATCCAGATATATATACATTTGAGTGGAGAGCTGAAATTCAGATGCTGA 420  
QY 489 ATTAATCTCATATGATATGATGAGATTAGAGAACTAGAGAAACCTGAAACCTTAAG 548  
DB 421 ATTAATCTCATATGATATGATGAGATTAGAGAACTAGAGAAACCTGAAACCTTAAG 480  
QY 549 ATTTTCGCTGGAACAGTTTGGGATCAACAGAAATGATTCAAATTTGAATGATTAAG 608  
DB 481 ATTTTCGCTGGAACAGTTTGGGATCAACAGAAATGATTCAAATTTGAATGATTAAG 540  
QY 609 CCTGAGTTGGGGCTGTTTCACTGATTTAAATATACACCTTGCTGATTCAGAGACGTCAG 668  
DB 541 CCTGAGTTGGGGCTGTTTCACTGATTTAAATATACACCTTGCTGATTCAGAGACGTCAG 600  
QY 669 AGTACAGCTGATGATGATCAACTGCTAGAGAACCTGTAAGATTAAGAACCAACCTGAC 728  
DB 601 AGTACAGCTGATGATGATCAACTGCTAGAGAACCTGTAAGATTAAGAACCAACCTGAC 660  
QY 729 AACCTACAGGGGCTGACGCTTTTACAGAAATATGTCAATCTGCGATGTGCGGTCAAG 788  
DB 661 AACCTACAGGGGCTGACGCTTTTACAGAAATATGTCAATCTGCGATGTGCGGTCAAG 720  
QY 789 GAGTCAAAAGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848  
DB 721 GAGTCAAAAGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 849 CCATGTGCTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 908  
DB 781 CCATGTGCTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 840  
QY 909 GTGCGGTTGTTATGAGAAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 968  
DB 841 GTGCGGTTGTTATGAGAAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 969 AACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028  
DB 901 AACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
QY 1029 CAGCAGCTTAAGTCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1088  
DB 961 CAGCAGCTTAAGTCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1089 TCTCTGGGAAGTCTCAGTGGCCACCTGAGATTCACCTATTCAGAAAAATATCATTTT 1148  
DB 1089 TCTCTGGGAAGTCTCAGTGGCCACCTGAGATTCACCTATTCAGAAAAATATCATTTT 1148

Db 1021 TCCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCAGCTATTCAGAAAAATCATTTT 1080  
 QY 1149 CAGTGCATTTGAGTCATGACAGGCTGGTTGCTGAGAACACAGTAGTGGTGAATGGCAA 1208  
 Db 1081 CAGTGCATTTGAGTCATGACAGGCTGGTTGCTGAGAACACAGTAGTGGTGAATGGCAA 1140  
 QY 1209 AGCTCTGCTAGACGTGAACACTTGTGATGATTAATGATGTTCCGATGTTGAGATCCAGAG 1268  
 Db 1141 AGCTCTGCTAGACGTGAACACTTGTGATGATTAATGATGTTCCGATGTTGAGATCCAGAG 1200  
 QY 1269 CCCACCACTTTCTCTGGGAATCTGTCTCAGGCCAGAACTGAGATCCAGCAAGAT 1328  
 Db 1201 CCCACCACTTTCTCTGGGAATCTGTCTCAGGCCAGAACTGAGATCCAGCAAGAT 1260  
 QY 1329 AAATTAACCTTTCTGCTGCTATACATCTCTGATATCCAAATGTTGCATGAGCAAGTT 1388  
 Db 1261 AAATTAACCTTTCTGCTGCTATACATCTCTGATATCCAAATGTTGCATGAGCAAGTT 1320  
 QY 1389 GGGCAGCCATATTTCCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAAAGTCTGAG 1448  
 Db 1321 GGGCAGCCATATTTCCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAAAGTCTGAG 1380  
 QY 1449 ACCAAGTGGGAACATTGGCGGTGAAGAGGTCAAGATCACATGGAAGAGATTCACAG 1508  
 Db 1381 ACCAAGTGGGAACATTGGCGGTGAAGAGGTCAAGATCACATGGAAGAGATTCACAG 1440  
 QY 1509 AGTAGAGAAAGGGATCATCTGCACTACACCATCTTTTCCAGAGTGAAGAGTGGAAAG 1568  
 Db 1441 AGTAGAGAAAGGGATCATCTGCACTACACCATCTTTTCCAGAGTGAAGAGTGGAAAG 1500  
 QY 1569 GGATTTCTCCAGACAGTCAATTTCCAGATCTTGGCAGTACGGCGTGGATCCCTGAAACGA 1628  
 Db 1501 GGATTTCTCCAGACAGTCAATTTCCAGATCTTGGCAGTACGGCGTGGATCCCTGAAACGA 1560  
 QY 1629 AAGACCTTTCATATTGTTCAAGTATGAGCCAGCAGCAGTGTGGGGGAGAACACAGGGAGC 1688  
 Db 1561 AAGACCTTTCATATTGTTCAAGTATGAGCCAGCAGCAGTGTGGGGGAGAACACAGGGAGC 1620  
 QY 1689 AGCATTAATTTCAAGACATCTGTCAATTCAGTGTCTTGGATTAATCCATTAATCTCTGTG 1748  
 Db 1621 AGCATTAATTTCAAGACATCTGTCAATTCAGTGTCTTGGATTAATCCATTAATCTCTGTG 1680  
 QY 1749 ATTGGTGGAGGCGCTTCTTATTCATTAATTCAGTGTGAGTGTGCTCAAAAAAACC 1808  
 Db 1681 ATTGGTGGAGGCGCTTCTTATTCATTAATTCAGTGTGAGTGTGCTCAAAAAAACC 1740  
 QY 1809 AACCAATTTGACTATCTGTGTGTGGCCCAAGCTTCCCAACCTGCTGAAAGTAGTAGCC 1868  
 Db 1741 AACCAATTTGACTATCTGTGTGTGGCCCAAGCTTCCCAACCTGCTGAAAGTAGTAGCC 1800  
 QY 1869 ACATGGCATGAGATGATTTCAA----- 1891  
 Db 1801 ACATGGCATGAGATGATTTCAAAGTTTGAGCTTACAGCCGGCAGCTTATTATCACTCA 1860  
 QY 1892 ----- 1891  
 Db 1861 CTACATGCCAGTGTCTGGGCTAGGCCCTAGGGATACAATGACAAGTCACTGTCCCTGC 1920  
 QY 1892 -----GATTAAGCTAAACCTGAAAGGAGTCTGATGACTGTGTG 1928  
 Db 1921 CATGAGGCCACTTGTGATTTTCTGGATTAAGCTAAACCTGAAAGGAGTCTGATGACTGTGTG 1980  
 QY 1929 AACACAGAAAGAGATCTTAACACATGTTCCACCCCACTGACAGATTTGTGATTTGAC 1988  
 Db 1981 AACACAGAAAGAGATCTTAACACATGTTCCACCCCACTGACAGATTTGTGATTTGAC 2040  
 QY 1989 AAGTTGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAGCCAGAACG 2048  
 Db 2041 AAGTTGTGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTACAGATGAAGCCAGAACG 2100  
 QY 2049 GGTGAGGAAACATTTTGAAGGGGAAAGAAATGGGTATGTGAGTGTGAGTGTGAGGCTT 2108  
 Db 2101 GGTGAGGAAACATTTTGAAGGGGAAAGAAATGGGTATGTGAGTGTGAGTGTGAGGCTT 2160

QY 2109 GATTGTCCCTGGGGAAGATTTTGAAGAGTCCCATGTTACCTGATTCGAGATTCGCCGAGA 2168  
 Db 2161 GATTGTCCCTGGGGAAGATTTTGAAGAGTCCCATGTTACCTGATTCGAGATTCGCCGAGA 2220  
 QY 2169 AATGCCAATACCTACGCTTGGAGAGTCCAGAGGGAGCCGCCAGAGCAAGCAAGAGCAG 2228  
 Db 2221 AATGCCAATACCTACGCTTGGAGAGTCCAGAGGGAGCCGCCAGAGCAAGCAAGAGCAG 2280  
 QY 2229 CTTCCTTTTCTGTGTCAAAGTTTAGTACAGATCATCTGTGTGAGGAAGAGCCCAAT 2288  
 Db 2281 CTTCCTTTTCTGTGTCAAAGTTTAGTACAGATCATCTGTGTGAGGAAGAGCCCAAT 2340  
 QY 2289 CCATATTTGAAAAATTCAGTACAGCCAGGGAATTTCTGTGCTGAAAAAATTCACAGAG 2348  
 Db 2341 CCATATTTGAAAAATTCAGTACAGCCAGGGAATTTCTGTGCTGAAAAAATTCACAGAG 2400  
 QY 2349 CACACCAAGGAGGAAGTCTAAATGCGACCATATGATGAGACCCCTGGGGCCTCA 2402  
 Db 2401 CACACCAAGGAGGAAGTCTAAATGCGACCATATGATGAGACCCCTGGGGCCTCA 2454

RESULT 6  
 AB083367  
 ID AB083367 standard; cDNA; 2870 BP.  
 XX  
 AC AB083367;  
 XX  
 XX 20-JAN-2003 (first entry)  
 DT  
 XX  
 DE Human NR10.6 splicing variant encoding cDNA seq ID NO:9.  
 XX  
 KW NR10: splicing variant; haematopoietic receptor; immunomodulator;  
 KW haemostatic; haematopoietic factor; immunological disease;  
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH  
 FT Key Location/Qualifiers  
 FT CDS 7..1752  
 FT /tag= a  
 FT /product= "NR10.6"  
 FT  
 PN WO200272730-A1.  
 XX  
 PD 03-OCT-2002.  
 XX  
 XX 22-MAR-2002; 2002WO-JP02769.  
 PE  
 XX 26-MAR-2001; 2001JP-0087298.  
 PR  
 XX (CHUS ) CHUGAI SEIYAKU KK.  
 PA  
 XX Maeda M, Yaguchi N, Hasegawa M;  
 PI  
 XX WPI: 2003-018925/01.  
 DR P-PSDB: ABP54367.  
 XX  
 XX NR10 splicing variants of hematopoietic receptor proteins and encoded  
 PT genes, applicable in searching hematopoietic factors and developing  
 PT remedies for immunological and hematopoietic diseases  
 XX  
 XX Claim 1; Fig 13-15; 250pp; Japanese.  
 PS  
 CC The present invention describes haematopoietic receptor NR10 splicing  
 CC variants (I). (i) have immunomodulator and haemostatic activities. The  
 CC proteins and encoded genes are applicable in searching for novel  
 CC haematopoietic factors, and developing remedies for immunological and  
 CC haematopoietic diseases. The haematopoietic receptor genes participate  
 CC in in vivo immunomodulation and haematopoietic cell regulation, and in  
 CC the search for haematopoietic factors capable of functionally binding  
 CC to the receptors. The present sequence encodes the human NR10.6 protein  
 CC from the present invention.

xx Sequence 2870 bp; 799 A; 667 C; 709 G; 695 T; 0 other;  
SQ  
Query Match 89.9%; Score 2160; DB 25; Length 2870;  
Best Local Similarity 96.5%; Pred. No. 0;  
Matches 2252; Conservative 0; Mismatches 0; Indels 82; Gaps 1;  
QY 69 CTGGAAATGTGCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGAATGTCG 128  
DB 1 CTGGAAATGTGCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGAATGTCG 60  
QY 129 CAAAACATTCCTCTCCACCACCTTCATGTGTTAACTGGGAGATGATGACCTGGGCA 188  
DB 61 CAAAACATTCCTCTCCACCACCTTCATGTGTTAACTGGGAGATGATGACCTGGGCA 120  
QY 189 CTGTGATGTCCTCCCTCACTCTGCAAAATTCAGCCCTGGAGAGCTCTGCCAGCTTAG 248  
DB 121 CTGTGATGTCCTCCCTCACTCTGCAAAATTCAGCCCTGGAGAGCTCTGCCAGCTTAG 180  
QY 249 AACATTTCTGTCTACTACTATAGAAAAATTTAACTGCACCTGGAGTCAGAGAA 308  
DB 181 AACATTTCTGTCTACTACTATAGAAAAATTTAACTGCACCTGGAGTCAGAGAA 240  
QY 309 GAAACCACTTATACCCAGTACAGAGTAAAGAACTTACGCTTTTGGAGAAAAACATGAT 368  
DB 241 GAAACCACTTATACCCAGTACAGAGTAAAGAACTTACGCTTTTGGAGAAAAACATGAT 300  
QY 369 AATTGTACACCAATAGTTTACAAAGTAAATGCTGTGCTCTTTTTCCTTCCA 428  
DB 301 AATTGTACACCAATAGTTTACAAAGTAAATGCTGTGCTCTTTTTCCTTCCA 360  
QY 429 AGAATTAACGATCCAGATATATATACCATGAGTGAAGCTGAAATAGAGATGTGTA 488  
DB 361 AGAATTAACGATCCAGATATATATACCATGAGTGAAGCTGAAATAGAGATGTGTA 420  
QY 489 ATTAATCTCATATGACACTACTGGAGATTAGAGAAATGCGAAATCTGAACCTTAG 548  
DB 421 ATTAATCTCATATGACACTACTGGAGATTAGAGAAATGCGAAATCTGAACCTTAG 480  
QY 549 ATTTCCGCTGGAACCAAGTTTGGGCAATCAAGCAATGATTCAAATGAAATGATTAAG 608  
DB 481 ATTTCCGCTGGAACCAAGTTTGGGCAATCAAGCAATGATTCAAATGAAATGATTAAG 540  
QY 609 CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAAC 668  
DB 541 CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAAC 600  
QY 669 AGTACACACTGATGAGAGTCACTTCGCTAAGAACCTTAAGATAAAAACCAACCTTAG 728  
DB 601 AGTACACACTGATGAGAGTCACTTCGCTAAGAACCTTAAGATAAAAACCAACCTTAG 660  
QY 729 AACCTCAGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGCTAG 788  
DB 661 AACCTCAGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGCTAG 720  
QY 789 GAGTCAAAAGTTCTGAGTGAAGTGAAGCAAGAAAAATGGAAATGACTGAGGAAGAACCT 848  
DB 721 GAGTCAAAAGTTCTGAGTGAAGTGAAGCAAGAAAAATGGAAATGACTGAGGAAGAACCT 780  
QY 849 CCATGTGGCTTGAAGCTGTGAGAGTCTGAAACAGCTGAGGGGATGGAAGAAAGGCA 908  
DB 791 CCATGTGGCTTGAAGCTGTGAGAGTCTGAAACAGCTGAGGGGATGGAAGAAAGGCA 840  
QY 909 GTGGCGTGTATGGAAGAGCAAGAGAGCCGAGCTAGAGAAAAACCTTGGCTAG 968  
DB 841 GTGGCGTGTATGGAAGAGCAAGAGAGCCGAGCTAGAGAAAAACCTTGGCTAG 900  
QY 969 AACATATGTAATATCCAGAAAGCAACTAACTCAGAGAAACATGAACTACTATAC 1028  
DB 901 AACATATGTAATATCCAGAAAGCAACTAACTCAGAGAAACATGAACTACTATAC 960  
QY 1029 CAGCAGCTTGAATGATCTGAGGAGGAGAGCTTTGGGTGCTATGATTTCTTATAT 1088  
DB 1029 CAGCAGCTTGAATGATCTGAGGAGGAGAGCTTTGGGTGCTATGATTTCTTATAT 1088

DB 961 CAGCAGCTTGAATGATCTGAGGAGGAGAGAGCTTTGGGTGCTATGATTTCTTATAT 1020  
QY 1089 TCTCTTGGAGAGTCTCCAGTGGCCACCTGAGATTCACAGTATTCAGAAATCAATT 1148  
DB 1021 TCTCTTGGAGAGTCTCCAGTGGCCACCTGAGATTCACAGTATTCAGAAATCAATT 1080  
QY 1149 CAGTGCATATGAGTCAATGACAGGCTTGGCTGAGAACCAAGTATGATGTAAGTGGCAA 1208  
DB 1081 CAGTGCATATGAGTCAATGACAGGCTTGGCTGAGAACCAAGTATGATGTAAGTGGCAA 1140  
QY 1209 AGCTCTGCTTAGACGTGACACTTGGATGATTAATGTTTCCGATGTGACATGAG 1268  
DB 1141 AGCTCTGCTTAGACGTGACACTTGGATGATTAATGTTTCCGATGTGACATGAG 1200  
QY 1269 CCCACACCCCTTCTGGGAATCTGTCTCAGGCGACGAACTGAGATCCACCAAGAT 1328  
DB 1201 CCCACACCCCTTCTGGGAATCTGTCTCAGGCGACGAACTGAGATCCACCAAGAT 1260  
QY 1329 AAATTTAAACCTTTCTGTGCTATACATCTCTGTATCCCAATGTTGCATGACAAAGTT 1388  
DB 1261 AAATTTAAACCTTTCTGTGCTATACATCTCTGTATCCCAATGTTGCATGACAAAGTT 1320  
QY 1389 GCGGAGCCATATTCATTCAGGCTTATGCCAAAGAGCGTTCATAGAAAGTCTGAG 1448  
DB 1321 GCGGAGCCATATTCATTCAGGCTTATGCCAAAGAGCGTTCATAGAAAGTCTGAG 1380  
QY 1449 ACCAAGGTGAGAACATTTGGCGTGAAGCGGTACAGATCAGATGAAAGAGATTCGCAAG 1508  
DB 1381 ACCAAGGTGAGAACATTTGGCGTGAAGCGGTACAGATCAGATGAAAGAGATTCGCAAG 1440  
QY 1509 AGTGAAGAAAGGATATCATCTGCACTACACATCTTTTACCAAGCTGAAGTGA 1568  
DB 1441 AGTGAAGAAAGGATATCATCTGCACTACACATCTTTTACCAAGCTGAAGTGA 1500  
QY 1569 GGATTTCCCAAGACATCAATTCAGACATCTTGGAGTACGCGCTGAGATCCCTAAGCA 1628  
DB 1501 GGATTTCCCAAGACATCAATTCAGACATCTTGGAGTACGCGCTGAGATCCCTAAGCA 1560  
QY 1629 AAGACCTCTTCAATGTTGACGATGCGCCAGCACAGTGTGGGGGAACCAACGGGACC 1688  
DB 1561 AAGACCTCTTCAATGTTGACGATGCGCCAGCACAGTGTGGGGGAACCAACGGGACC 1620  
QY 1689 AGCATTAATTTCAAGACATTCATTCAGTGTCTTTGAGATTTATCTATACCTTCTGT 1748  
DB 1621 AGCATTAATTTCAAGACATTCATTCAGTGTCTTTGAGATTTATCTATACCTTCTGT 1680  
QY 1749 ATGTGTGAGGCGCTTATATCTATATCTGACAGTGGATGATGATCAAAACCC 1808  
DB 1681 ATGTGTGAGGCGCTTATATCTATATCTGACAGTGGATGATGATCAAAACCC 1740  
QY 1809 AACAAATTTGACTCATCTGTGTGGCCCAACGCTTCCCAACCTGCTGAAGTATAGCC 1868  
DB 1741 AA----- 1742  
QY 1869 ACATGCGATGAGATGATTTCAAGATTAAGTAACTGAAGAGTCTGATGACTGTGTG 1928  
DB 1743 -----GATTAAGCTTAACCTGAAGGAGTCTGATGATGACTGTGTG 1778  
QY 1929 AACACAGAGACAGATCTTAAACCAATGTTCCACCCCGCAGTGCAGATGCTGATGAC 1988  
DB 1779 AACACAGAGACAGATCTTAAACCAATGTTCCACCCCGCAGTGCAGATGCTGATGAC 1838  
QY 1889 AAGTTGGTGGAGACTTGGGAATGTCTGCAAGAAATTTTCAAGATGAAAGCCAGAAC 2048  
DB 1839 AAGTTGGTGGAGACTTGGGAATGTCTGCAAGAAATTTTCAAGATGAAAGCCAGAAC 1888  
QY 2049 GGTGAGGAAAACAATTTAGAGGGGAAAAAGAAATGGTATGTGACCTGCCCTTCAAGGCT 2108  
DB 1889 GGTGAGGAAAACAATTTAGAGGGGAAAAAGAAATGGTATGTGACCTGCCCTTCAAGGCT 1958  
QY 2109 GATGTGCTCCCTGGGAAAAAGTTTGGAGAGTCCCAAGTTTACCTGAGATTCGCCCCAGA 2168  
DB 1959 GATGTGCTCCCTGGGAAAAAGTTTGGAGAGTCCCAAGTTTACCTGAGATTCGCCCCAGA 2018

Oy	2169	AAATCCCAATACCCATGACGTGGAGATGCGAGAGGGGACCCGCCCAAGAACCAAGACGAC	2228
Dd	2019	AAATCCCAATACCCATGACGTGGAGATGCGAGAGGGGACCCGCCCAAGAACCAAGACGAC	2078
Oy	2229	CTTCTCTTTCTGGTCAAAAGTTTGTAGTACAGATCATCTGTGTGTGAGGAAGAGGCCCAAT	2288
Dd	2079	CTTCTCTTTCTGGTCAAAAGTTTGTAGTACAGATCATCTGTGTGTGAGGAAGAGGCCCAAT	2138
Oy	2289	CCATATTTTGAAGAAATTCAGTGCACAGCCAGGGAATTTCTGTCTGTAAGAAAATTCACAG	2348
Dd	2139	CCATATTTTGAAGAAATTCAGTGCACAGCCAGGGAATTTCTGTCTGTAAGAAAATTCACAG	2198
Oy	2349	CACACCAAGGAGAGAGTCTAAATCCGACCCATAGCATGAGACCCGCGGCGCTCA	2402
Dd	2199	CACACCAAGGAGAGAGTCTAAATCCGACCCATAGCATGAGACCCGCGGCGCTCA	2252
RESULT 7			
ID	ABQ83368	standard; CDNA; 2858 BP.	
XX	ABQ83368;		
AC			
XX			
DT	20-JAN-2003	(first entry)	
XX			
DE	Human NR10.7	splicing variant encoding CDNA SEQ ID NO:11.	
XX			
KW	NR10; splicing variant; haematopoietin receptor; immunomodulator;		
KW	haemostatic; haematopoietic factor; immunological disease;		
KW	haematopoietic disease; haematopoietic cell regulation; gene; ss.		
OS	Homo sapiens.		
XX			
EH	Key	Location/Qualifiers	
FT	CDS	7..1656	
FT		/*tag= a	
FT		/product= "NR10.7"	
XX			
PN	WO20027230-A1.		
XX			
PD	03-OCT-2002.		
XX			
PE	22-MAR-2002; 2002WO-JP02769.		
XX			
PR	26-MAR-2001; 2001JP-0087298.		
XX			
PA	(CHUS ) CHUGAI SEIYAKU KK.		
XX			
PI	Maeda M, Yaguchi N, Hasegawa M;		
XX			
DR	WPI: 2003-018925/01.		
DR	P-PSDB: ABP54368.		
XX			
PT	NR10 splicing variants of hematopoietin receptor proteins and encoded		
PT	genes, applicable in searching hematopoietic factors and developing		
PT	remedies for immunological and hematopoietic diseases		
XX			
PS	Claim 1; Fig 16-18; 250pp; Japanese.		
XX			
CC	The present invention describes haematopoietic receptor NR10 splicing		
CC	variants (I). (i) have immunomodulator and haemostatic activities. The		
CC	proteins and encoded genes are applicable in searching for novel		
CC	haematopoietic factors, and developing remedies for immunological and		
CC	haematopoietic diseases. The haematopoietin receptor genes participate		
CC	in in vivo immunomodulation and haematopoietic cell regulation, and in		
CC	the search for haematopoietic factors capable of functionally binding		
CC	to the receptors. The present sequence encodes the human NR10.7 protein		
CC	from the present invention.		
XX			
SO	Sequence 2858 BP; 798 A; 667 C; 710 G; 683 T; 0 other;		
Query Match	88.9%; Score2136; DB 25; Length 2858;		

	Bast Local Similarity	96.0%	Pred No.	0:	Mismatches	0:	Indels	94:	Gaps	1:
	Matches	2240:	Conservative	0:						
OY	69	CTGGGAATGTGCATTCAGGCAACTCACAATTTTTTACACACGGCANGTGCTGTGAATGCCG	128							
Db	1	CTGGGAATGTGCATTCAGGCAACTCACAATTTTTTTCACCACGGCANGTGCTGTGAATGCCG	60							
OY	129	CAAAACATTCTCTCCCGCCAGCTTCTATGTGTTAATCTGGGGATGATGTGGACCTGGCCA	188							
Db	61	CAAAACATTCTCTCCCGCCAGCTTCTATGTGTTAATCTGGGGATGATGTGGACCTGGCCA	120							
OY	189	CTGTGATGTGCCCTCACCTCGAATAATTCAGCTGGCAGCTCTGCCAGCTAACGCCTAG	248							
Db	121	CTGTGATGTGCCCTCACCTCTACTGTGCATAATTCAGCTGGCAGCTCTGCCAGCTAACGCCTAG	180							
OY	249	AACATTTCCGTGTCTACTACTATAGGAAAAATTTAACTGCACCTTGAGCTCCAGCAAG	308							
Db	181	AACATTTCCGTGTCTACTACTATAGGAAAAATTTAACTGCACCTTGAGCTCCAGCAAG	240							
OY	309	GAAPACCATTAATACCCAGTACACAGTTAAAGAACTTAGCCTTTTGGAGAAAAACATGAT	368							
Db	241	GAAPACCATTAATACCCAGTACACAGTTAAAGAACTTAGCCTTTTGGAGAAAAACATGAT	300							
OY	369	AATTGTACAACCATTAATTTCTACAGAAGAAATCGTCTCTGCTCTTTTTCCTTCCA	428							
Db	301	AATTGTACAACCATTAATTTCTACAGAAGAAATCGTCTCTCTTTCCTTTCCTTCCA	360							
OY	429	AGAATAACGATCCCAGATTAATTTATACATTGAGGTGGAGCTGAAATTCAGATGTGTA	488							
Db	361	AGAATAACGATCCCAGATTAATTTATACATTGAGGTGGAGCTGAAATTCAGATGTGTA	420							
OY	489	ATTAAATCTCATATGACATCTGGAGATTAGAGAACTTAGCGAAACTGAACCCACTAAG	548							
Db	421	ATTAAATCTCATATGACATCTGGAGATTAGAGAACTTAGCGAAACTGAACCCACTAAG	480							
OY	549	ATTTCCGCTGGAACACAGTTTGGGATCAACAGATGATTCAAATTTGATGGATTAAG	608							
Db	481	ATTTCCGCTGGAACACAGTTTGGGATCAACAGATGATTCAAATTTGATGGATTAAG	540							
OY	609	CCGTGATTTGGCGCTGTTTCATCTGATTTAAATATACACACTTCATTCCAGACAGCTAAC	668							
Db	541	CCGTGATTTGGCGCTGTTTCATCTGATTTAAATATACACACTTCATTCCAGACAGCTAAC	600							
OY	669	AGTACACAGCTGATGAGAGTCAACTTGGCTPAAGAACCGTAAAGATTAACCAACCTAC	728							
Db	601	AGTACACAGCTGATGAGAGTCAACTTGGCTPAAGAACCGTAAAGATTAACCAACCTAC	660							
OY	729	AACCTCACGGGGCTGCAGCTTTTACAGAAATATGTCTATAGCTCTGCGATGTGGGCTAAG	788							
Db	661	AACCTCACGGGGCTGCAGCTTTTACAGAAATATGTCTATAGCTCTGCGATGTGGGCTAAG	720							
OY	789	GAGTCAAAAGTTCTTSGAATGACTGGAGGCAAGAAAAATGGGAATGACTGAGGAAAGAGCT	848							
Db	721	GAGTCAAAAGTTCTTSGAATGACTGGAGGCAAGAAAAATGGGAATGACTGAGGAAAGAGCT	780							
OY	849	CCATGTGGCCCTGGAACCTGTGGAGAGTCTCTAATAACACACTGAGCGCGATGGAAGAAGCCA	908							
Db	781	CCATGTGGCCCTGGAACCTGTGGAGAGTCTCTAATAACACACTGAGCGCGATGGAAGAAGCCA	840							
OY	909	GTCGCGTTGTTATGGAAGAAGGCAAGAGAGGCCCACTCTTGAAGAAACCTTGGCTAC	968							
Db	841	GTCGCGTTGTTATGGAAGAAGGCAAGAGAGGCCCACTCTTGAAGAAACCTTGGCTAC	900							
OY	969	AACATATGTGATCTATCCAGAAAGCAACATTAACCTCACAGAAACAATGAACACTACTAAC	1028							
Db	901	AACATATGTGATCTATCCAGAAAGCAACATTAACCTCACAGAAACAATGAACACTACTAAC	960							
OY	1029	CAGCAGCTTAACTGCATCTGGAGGAGGAGAGCTTTGGGTGTATGATTTCTTATAT	1088							
Db	961	CAGCAGCTTGAACCTGCATCTGGAGGAGGAGAGCTTTGGGTGTATGATTTCTTATAT	1020							
OY	1089	TCTCTGGGAAGTCTCCAGTGGGCCACCTGAGAGTTCCAGCTATTTCAAGAAAAATCATTT	1148							



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D 1021 TCTCTGGGAAGTCTCCAGTGGCCACCCTGAGATTCCAGTATTCAGAAAAATCATTT 1080
O 1149 CAGTGCATTTAGAGTCATGCAGCCCTGGTGTGAGSACGACTAGTGGTAAGTGGCAA 1208
D 1081 CAGTGCATTTAGAGTCATGCAGCCCTGGTGTGAGSACGACTAGTGGTAAGTGGCAA 1140
O 1209 AGCTGTGCTAGAGTCGTAACACTTGGATGATGATGATGATGATGATGATGATGATGAT 1268
D 1141 AGCTGTGCTAGAGTCGTAACACTTGGATGATGATGATGATGATGATGATGATGATGAT 1200
O 1269 CCCACCACTCTTCTGGGATCTGTGTCTCAGGCCACGAACTGGAGCATCCAGCAAGAT 1328
D 1201 CCCACCACTCTTCTGGGATCTGTGTCTCAGGCCACGAACTGGAGCATCCAGCAAGAT 1260
O 1329 AAATTAACCTTCTGTGCTATACATCTGTGTATCCATGTTTCATGACAAAGTT 1388
D 1261 AAATTAACCTTCTGTGCTATACATCTGTGTATCCAAATGTTTCATGACAAAGTT 1320
O 1389 GCGCAGCCATATTCATCCATCCAGGCTTATGCCAAGAAGGCGTTCCATCAGAAGTCTGAG 1448
D 1321 GCGCAGCCATATTCATCCATCCAGGCTTATGCCAAGAAGGCGTTCCATCAGAAGTCTGAG 1380
O 1449 ACCAAGGTGAGACATTTGGGTGTAAGCGGTCAAGCATCATGTAAGAAAGATTCCTCAG 1508
D 1381 ACCAAGGTGAGACATTTGGGTGTAAGCGGTCAAGCATCATGTAAGAAAGATTCCTCAG 1440
O 1509 AGTGAAGAAAGGGATCATCTGCACATCAACATCTTTTACCAAGCTGAAGTGGAAAA 1568
D 1441 AGTGAAGAAAGGGATCATCTGCACATCAACATCTTTTACCAAGCTGAAGTGGAAAA 1500
O 1569 GGATTTCTCAAGACAGTCAATTCACGATCTTGCAGTACGCGCTGGAGTCCCTGAAACGA 1628
D 1501 GGATTTCTCAAGACAGTCAATTCACGATCTTGCAGTACGCGCTGGAGTCCCTGAAACGA 1560
O 1629 AAGACCTCTCATTTGTTGAGTCAAGCATGCGCAGCAACCATGTTGGGGGAAACCAAGGAGCC 1688
D 1561 AAGACCTCTCATTTGTTGAGTCAAGCATGCGCAGCAACCATGTTGGGGGAAACCAAGGAGCC 1620
O 1689 AGCATAAATTTCAAGACATGTCATTCAGTGTCTTTGAGATTATCCATTAACCTTCTCTG 1748
D 1621 AGCATAAATTTCAAGACATGTCATTC----- 1647
O 1749 ATTGTGAGGCGCTTCTTATTCATTAATCTGACAGTGCATATGCTCAAAAAACC 1808
D 1648 ----- 1647
O 1809 AACAAATGACTCANCTGTGTGTGGCCACCGTCCCAACCTGCTGAAAGTATATACC 1868
D 1648 -ACAATTTGACTCANCTGTGTGTGGCCACCGTCCCAACCTGCTGAAAGTATATACC 1706
O 1869 ACATGCGATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTGTGATGACTCTGTG 1928
D 1707 ACATGCGATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTGTGATGACTCTGTG 1766
O 1929 AACACAGAACAGAGATCTTAAACCATGTTCCACCCCACTGACAAAGTGTGATTTGAC 1988
D 1767 AACACAGAACAGAGATCTTAAACCATGTTCCACCCCACTGACAAAGTGTGATTTGAC 1826
O 1889 AAGTTGGTGAAGCTTTGGGAATGTCTGCAAGAAATTTTCAAGATGAGAGCCAGAACG 2048
D 1827 AAGTTGGTGAAGCTTTGGGAATGTCTGCAAGAAATTTTCAAGATGAGAGCCAGAACG 1886
O 2049 GGTGAGGAAAACAATTTAGAGGGGAAAAAAGATGGTATGTGACTGCTGCCCTTCAGGCT 2108
D 1887 GGTGAGGAAAACAATTTAGAGGGGAAAAAAGATGGTATGTGACTGCTGCCCTTCAGGCT 1946
O 2109 GATTGTCCCTTGGGAAAAAGTTTGGAGAGTCCCAAGTTTACTGAGATTCGCCCCAGA 2168
D 1947 GATTGTCCCTTGGGAAAAAGTTTGGAGAGTCCCAAGTTTACTGAGATTCGCCCCAGA 2006
O 2169 AAATCCCAATACCTACGTTGAGAGTGCACAGGGGAGCCGCCCAAGAAAGCCAAAGAGCAG 2228
D 2007 AAATCCCAATACCTACGTTGAGAGTGCACAGGGGAGCCGCCCAAGAAAGCCAAAGAGCAG 2066
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O 2229 CTCTCTTTTCTGGCAAGTTTATACACATCATCTGTGTGAGGAAGAGCCCAAT 2288
D 2067 CTCTCTTTTCTGGCAAGTTTATACACATCATCTGTGTGAGGAAGAGCCCAAT 2126
O 2289 CCATATTTGAAAAATTCAGTACGACGACGAGGAATTTCTGTGTGAAAAATTCAGAG 2348
D 2127 CCATATTTGAAAAATTCAGTACGACGACGAGGAATTTCTGTGTGAAAAATTCAGAG 2186
O 2349 CACACCAAGGAGAGATCTTAATGCGACCATAGCATAGACCTTCGGGCGCTCA 2402
D 2187 CACACCAAGGAGAGATCTTAATGCGACCATAGCATAGACCTTCGGGCGCTCA 2240

RESULT 8
ABA93803
ID ABA93803 standard; cDNA: 2529 BP.
XX
XX ABA93803;
AC
XX
DT 01-MAY-2002 (first entry)
XX
DE Human zcytor17 cDNA sequence SEQ ID NO:45.
XX
KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
OS Homo sapiens.
XX
PN WO20020721-A2.
PD
XX 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
PR 26-JUN-2000; 2000US-214282P.
PR 29-JUN-2000; 2000US-214955P.
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kujper JL;
PI Maurer MP;
XX
DR WI: 2002-090519/12.
DR P-PSDB: ABB05738.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
PS Claim 2; Page 190-194; 235pp; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antinflammatory, antiviral, cyostatic,
CC antirheumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
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XX Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 other;  
SQ

Query Match	86.48;	Score 2075;	DB 24;	Length 2529;
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2075; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	10	TGTTGTGCAAGTATGAAAATTTGAGACAGAGAAAGCGAGAGTGTCACTTGTTCCTCCACTAGC	69
Db	1	TGTGTGTGCAAGTATGAAAATTTGAGACAGAGAAAGCGAGAGTGTCACTTGTTCCTCCACTAGC	60
QY	70	TGGGAATGTGCATCAGGCAACTCAAGTTTTTTCACACAGGCAATGTCTGTGTAAATGTCCGC	129
QY	61	TGGGAATGTGCATCAGGCAACTCAAGTTTTTTCACACAGGCAATGTCTGTGTAAATGTCCGC	120
Db	130	AAAAATTCTCTCTCCCGAGCTTCAATGTGTTAACTGTGGGAGTATGTGGACCTGGCCAC	189
QY	121	AAAAATTCTCTCTCCCGAGCTTCAAGTTTTTTCACACAGGCAATGTCTGTGTAAATGTCCGC	180
Db	190	TGTGTATGTCTCCCTCACTCTGCAGAAATTCAGACCTGGGAGCTGTCCGAGCTAAGCTGAGA	249
QY	181	TGTGTATGTCTCCCTCACTCTGCAGAAATTCAGACCTGGGAGCTGTCCGAGCTAAGCTGAGA	240
Db	250	ACATTTTCTGTGTCTACTACTATAGAAAAATTTTAACTGCACATTGTGAGTCCAGGAAGG	309
QY	241	ACATTTTCTGTGTCTACTACTATAGAAAAATTTTAACTGCACATTGTGAGTCCAGGAAGG	300
Db	310	AAACCAATTATATACCACTACACACTTTAAGAACTTACGCTTTTGGAGAAAAATATGATA	369
QY	301	AAACCAATTATATACCACTACACACTTTAAGAACTTACGCTTTTGGAGAAAAATATGATA	360
Db	370	ATTGTACAAACCAATAGTTCATACAGTAAATATCTGTGCTGTCTTTTTCCTTCCAA	429
QY	361	ATTGTACAAACCAATAGTTCATACAGTAAATATCTGTGCTGTCTTTTTCCTTCCAA	420
Db	430	GAATTAAGATCCCGATATATATATACCAATGTAGGTGAGAACTGAAAAATGAGATGCTGTAA	489
QY	421	GAATTAAGATCCCGATATATATATATACCAATGTAGGTGAGAACTGAAAAATGAGATGCTGTAA	480
Db	490	TTAATATCTCATATATACATACTGAGATGTAGAGACATAGCGAAAACTGAACACACTTAGA	549
QY	481	TTAATATCTCATATATACATACTGAGATGTAGAGACATAGCGAAAACTGAACACACTTAGA	540
Db	550	TTTTCCGTGTGAAACCAAGTTTTGGGCAATCAACGATGATTCAAATTTGAATGATYAAAGC	609
QY	541	TTTTCCGTGTGAAACCAAGTTTTGGGCAATCAACGATGATTCAAATTTGAATGATYAAAGC	600
Db	610	CTGAGTTGGGGCCCTGTTTCACTCATATTTAAATATACACTTCGATTGACAGCACTCAACA	669
QY	601	CTGAGTTGGGGCCCTGTTTCACTCATATTTAAATATACACTTCGATTGACAGCACTCAACA	660
Db	670	GTACCACTGTGATGGAAGTCAACTTGTGCTTAAGAACGCTAAGGATTAAGAAAAACCAACGTACA	729
QY	661	GTACCACTGTGATGGAAGTCAACTTGTGCTTAAGAACGCTAAGGATTAAGAAAAACCAACGTACA	720
Db	730	ACCTCAGAGGGGCTCCAGCCTTTTACAAATATGTGCATATAGCTCTCGCATGTGCGGTCAAG	789
QY	721	ACCTCAGAGGGGCTCCAGCCTTTTACAAATATGTGCATATAGCTCTCGCATGTGCGGTCAAG	780
Db	790	AGTCAAGATTCTGAGATGACTGAGAGCCAGAGAAAAATTTGGCAATATACAGAGAGAAAGCTC	849
QY	781	AGTCAAGATTCTGAGATGACTGAGAGCCAGAGAAAAATTTGGCAATATACAGAGAGAAAGCTC	840
Db	850	CATGTGGCTGTGGAAGTGTGGAAGTCTGTGAACCAAGCTGAGGCGGATGTGAAGAAAGCCAG	909
QY	841	CATGTGGCTGTGGAAGTGTGGAAGTCTGTGAACCAAGCTGAGGCGGATGTGAAGAAAGCCAG	900
Db	910	TGCGGTTGTTATGGAAGAGGCAAGAGAGCCCGAGTCTGAGAAAAACATTGGCTACA	969
QY	901	TGCGGTTGTTATGGAAGAGGCAAGAGAGCCCGAGTCTGAGAAAAACATTGGCTACA	960
Db	970	ACATATGGTACTATCCAGAAAGCAACATACTCTACAGAAACATGAACTACTATACC	1029

Db	961	ACATATGCTACTATCCAGAAAGCACACTTAACCTCACAGAAACAATGAAACACTACTPACC	1020
QY	1030	AGCAGCTTGAACCTCATCTGGGAGGCGAGAGCTTTTGGGTGCTATGATTTCTTAAAT	1089
Db	1021	AGCAGCTTGAACCTCATCTGGGAGGCGAGAGCTTTTGGGTGCTATGATTTCTTAAAT	1080
QY	1090	CTCTTGGGAAGTCTCCAGTGGCCACCCCTGAGAGATTCAGCTATTCAAGAAAATCATTTTC	1149
Db	1081	CTCTTGGGAAGTCTCCAGTGGCCACCCCTGAGAGATTCAGCTATTCAAGAAAATCATTTTC	1140
QY	1150	AGTCATTGAGGTATATCGAGGCCGCTGCTGTAGAGACACAGCTAGTGTGAAGTGGCAAA	1209
Db	1141	AGTCATTGAGGTATATCGAGGCCGCTGCTGTAGAGACACAGCTAGTGTGAAGTGGCAAA	1200
QY	1210	GCTCGCTCTGAGAGCTGAACCTTGGATGATTAATGATTTCCGGATGTGGACTCAGAGC	1269
Db	1201	GCTCTGCTCTGAGAGCTGAACCTTGGATGATTAATGATTTCCGGATGTGGACTCAGAGC	1260
QY	1270	CCACACACCTTTCTGGGAATCTGTGCTCAGGCCACAGAACTGGACGATCCAGACAGATA	1329
Db	1261	CCACACACCTTTCTGGGAATCTGTGCTCAGGCCACAGAACTGGACGATCCAGACAGATA	1320
QY	1330	AATTAAACCTTTTGTGCTATATACATCTCTGTATTCCAATGTTGCATGACAAAGTTG	1389
Db	1321	AATTAAACCTTTTGTGCTATATACATCTCTGTATTCCAATGTTGCATGACAAAGTTG	1380
QY	1390	GGGAGCCATATTCATCCAGGCTTATGCGCAAGAAAGGCGTTCCATCGAAGGTCGTGAGA	1449
Db	1381	GGGAGCCATATTCATCCAGGCTTATGCGCAAGAAAGGCGTTCCATCGAAGGTCGTGAGA	1440
QY	1450	CCAAGGTGAGAACATTTGGCTGTAAGACGGTGCACAGATCACATGGAAAAGATTTCCCAAGA	1509
Db	1441	CCAAGGTGAGAACATTTGGCTGTAAGACGGTGCACAGATCACATGGAAAAGATTTCCCAAGA	1500
QY	1510	GTGAGAGAAAGGATATCTCTGCACTACACCATCTTTTACCAAGCTGAAGGTGGAAGAAG	1569
Db	1501	GTGAGAGAAAGGATATCTCTGCACTACACCATCTTTTACCAAGCTGAAGGTGGAAGAAG	1560
QY	1570	GATTCTCCAAACAGTCAATTCCAGCATCTTGGCATGAGGCTGGATTCCTCGTAAGACGA	1629
Db	1561	GATTCTCCAAACAGTCAATTCCAGCATCTTGGCATGAGGCTGGATTCCTCGTAAGACGA	1620
QY	1630	AGACCTCTTACATTGTTCAGGTGCATGTGCGACACACACAGTGTGGGGGAACCAACGCGACCA	1689
Db	1621	AGACCTCTTACATTGTTCAGGTGCATGTGCGACACACACAGTGTGGGGGAACCAACGCGACCA	1680
QY	1690	GCATTAATTTCAAGACATTTGTCAATTCAGTGTCTTTGAGATTTATTCCTATTAATCTTCTGTA	1749
Db	1681	GCATTAATTTCAAGACATTTGTCAATTCAGTGTCTTTGAGATTTATTCCTATTAATCTTCTGTA	1740
QY	1750	TTGGTGGAGGCGCTTATTTCTCATTTATCCGACAGTGGCATATNGTCTCAAAAAACCCA	1809
Db	1741	TTGGTGGAGGCGCTTATTTCTCATTTATCCGACAGTGGCATATNGTCTCAAAAAACCCA	1800
QY	1810	ACAAATTTACATCTGTGTGGGCCACACCGTTCCCAACCCGTCGTAAGTAGATATAGCA	1869
Db	1801	ACAAATTTACATCTGTGTGGGCCACACCGTTCCCAACCCGTCGTAAGTAGATATAGCA	1860
QY	1870	CATGGCATGAGATGATTTCAAGATTAAGCTTAACCTGGAAGAGTCTGATGACTCTGTGA	1929
Db	1861	CATGGCATGAGATGATTTCAAGATTAAGCTTAACCTGGAAGAGTCTGATGACTCTGTGA	1920
QY	1930	ACACAGAAAGAGAGATCTTAAACCAATGTTCCACCCCAAGTGAACAAATTTGGTATTTGACA	1989
Db	1921	ACACAGAAAGAGAGATCTTAAACCAATGTTCCACCCCAAGTGAACAAATTTGGTATTTGACA	1980
QY	1990	AGTTGTGTGTAACCTTTGGGAATGTTCTGCAAGAATTTTTCACAGATGAAGCCGGAAGCG	2049
Db	1981	AGTTGTGTGTAACCTTTGGGAATGTTCTGCAAGAATTTTTCACAGATGAAGCCGGAAGCG	2040
QY	2050	GTCAAGAAAACATTTAGAGGGGGAAGAAATGGG	2084
Db	2041	GTCAAGAAAACATTTAGAGGGGGAAGAAATGGG	2075

```
RESULT 9
ID ABQ83363
AB ABQ83363 standard; cDNA: 4315 BP.
XX
AC ABQ83363;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.3 splicing variant encoding cDNA SEQ ID NO:1.
XX
KW NR10; splicing variant; haematopoietic receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 7..2052
FT CDS /*tag= a
FT /product= "NR10.3"
XX
PN WO200277230-A1.
XX
PD 03-OCT-2002.
XX
PE 22-MAR-2002; 2002WO-JP02769.
XX
PR 26-MAR-2001; 2001JP-0087298.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
DR WPI: 2003-018925/01.
DR P-PSDB: ABP54363.
XX
XX
PT NR10 splicing variants of hematopoietic receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases
XX
XX
PS Example 2; Fig 1-2; 250pp: Japanese.
XX
XX
CC The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (i) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietic receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence encodes the human NR10.3 protein
CC from the present invention.
XX
SQ Sequence 4315 BP: 1187 A; 1008 C; 1061 G; 1059 T; 0 other;
Query Match 83.9%; Score 2016; DB 25; Length 4315;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2016; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 69 CTGGGAATGTCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGAATGCCG 128
DB 1 CTGGGAATGTCATCAGGCACTCAAGTTTTCACACAGGCGATGTCGTGAATGCCG 60
QY 129 CAAACATTCCTCTCCCGACCTTCATGTGTTAACTGGGAGATGTGGACCTGGGCA 188
DB 61 CAAACATTCCTCTCCCGACCTTCATGTGTTAACTGGGAGATGTGGACCTGGGCA 120
QY 189 CTGTGATGCTCCCGTCACTGTGCAATTCAGCTGGAGCTGGCCAGCTAAGCTGAG 248
DB 121 CTGTGATGCTCCCGTCACTGTGCAATTCAGCTGGAGCTGGCCAGCTAAGCTGAG 180
QY 249 AACATTTCTGTGTCTACTACTATAGGAAAAATTTAACTGCACCTGGAGTCCAGAAAG 308
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DB 181 AACATTTCTGTGTCTACTACTATAGGAAAAATTTAACTGCACCTGGAGTCCAGAAAG 240
QY 309 GAAACCGATTTATCCCGATACAGGTTTAAGAACTTACGCTTTTGGAGAAAAACATGAT 368
DB 241 GAAACCGATTTATCCCGATACAGGTTTAAGAACTTACGCTTTTGGAGAAAAACATGAT 300
QY 369 AATTGTACACCAATAGTCTTACAGTGAAGTGAAGTGTGCTGCTGCTTTTTCCTTCCA 428
DB 301 AATTGTACACCAATAGTCTTACAGTGAAGTGAAGTGTGCTGCTGCTTTTTCCTTCCA 360
QY 429 AGAATTAACGATCCAGATTAATTAATACATTTAGAGTGAAGCTGAAAATGAGATGTGTA 488
DB 361 AGAATTAACGATCCAGATTAATTAATACATTTAGAGTGAAGCTGAAAATGAGATGTGTA 420
QY 489 ATTAATTCATATAGCATCTGAGATTTAGAGAACTAGAGAACTGAACCCCTAG 548
DB 421 ATTAATTCATATAGCATCTGAGATTTAGAGAACTAGAGAACTGAACCCCTAG 480
QY 549 ATTTCCGTTGGAACACAGTTTGGGATCAAAACGAATGATTCAAATTTGAATGATTAAG 608
DB 481 ATTTCCGTTGGAACACAGTTTGGGATCAAAACGAATGATTCAAATTTGAATGATTAAG 540
QY 609 CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATATACACACTTCGATTCAGGACAGTCAAC 668
DB 541 CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATATACACACTTCGATTCAGGACAGTCAAC 600
QY 669 AGTACCAAGTGTGATGGAAGTCACTTGGCTTAAGAACCTTAAGATTAATAAACCAACGTCAC 728
DB 601 AGTACCAAGTGTGATGGAAGTCACTTGGCTTAAGAACCTTAAGATTAATAAACCAACGTCAC 660
QY 729 AACCTCACGGGGCTGCAGCCCTTTTACAGAAATATGTACCTGCGATGCGCGTCAAG 788
DB 661 AACCTCACGGGGCTGCAGCCCTTTTACAGAAATATGTACCTGCGATGCGCGTCAAG 720
QY 789 GAGTCAAGATTTCTGAGTCACTGAGGCCAAGAAAAATGGAATGACTGAGGAAGAAGCT 848
DB 721 GAGTCAAGATTTCTGAGTCACTGAGGCCAAGAAAAATGGAATGACTGAGGAAGAAGCT 780
QY 849 CCATGTGCGCTGGAACTGTGAGAGTCTGAANCCACTGAGCGGATGGAAGAACGCCA 908
DB 781 CCATGTGCGCTGGAACTGTGAGAGTCTGAANCCACTGAGCGGATGGAAGAACGCCA 840
QY 909 GTGGCGTTGTTATGGAAGCAAGCGCAAGAGACCCCATCTAGAGAAACATCTTGCGTAC 968
DB 841 GTGGCGTTGTTATGGAAGCAAGCGCAAGAGACCCCATCTAGAGAAACATCTTGCGTAC 900
QY 969 AACATATGTTACTATCCAGAAAGCAACACTTACCTACAGAAACATGAACACTACTAAC 1028
DB 901 AACATATGTTACTATCCAGAAAGCAACACTTACCTACAGAAACATGAACACTACTAAC 960
QY 1029 CAGCAGCTTAACATGCACTGTGGAGGCGAGACGCTTTGGTGCTATGATTTCTTAAT 1088
DB 961 CAGCAGCTTAACATGCACTGTGGAGGCGAGACGCTTTGGTGCTATGATTTCTTAAT 1020
QY 1089 TCTCTTGGGAAGTCTCAGTGGCCACCTTAGATTCACATTAATCAAGAAAAATCAATT 1148
DB 1021 TCTCTTGGGAAGTCTCAGTGGCCACCTTAGATTCACATTAATCAAGAAAAATCAATT 1080
QY 1149 CAGTGCATTAAGTCAATGACAGGCGCTGCTGCTGAGAGCAGCTAGTGTGAAGTGCA 1208
DB 1081 CAGTGCATTAAGTCAATGACAGGCGCTGCTGCTGAGAGCAGCTAGTGTGAAGTGCA 1140
QY 1209 AGCTCTGCTCTAAGACGTGAACACTTGTGATTAATGATTTCCGAGATGTGACCTCAG 1268
DB 1141 AGCTCTGCTCTAAGACGTGAACACTTGTGATTAATGATTTCCGAGATGTGACCTCAG 1200
QY 1269 CCCAGCACCCCTTTCCTGGGAATGTGTCCAGGCCAGAACTGGAGATCCAGCAAGAT 1328
DB 1201 CCCAGCACCCCTTTCCTGGGAATGTGTCTCAGGCCAGAACTGGAGATCCAGCAAGAT 1260
QY 1329 AAATTAACCTTTCCTGCTCTATACATCTGTGTATCAATGTTCATGACAAAGTT 1388
DB 1329 AAATTAACCTTTCCTGCTCTATACATCTGTGTATCAATGTTCATGACAAAGTT 1388
```

Db	1261	AAATTAACACCTTTCTGTCCTATACATCTCTGTGTATCCAAATGTTGCATGACAAAGTT	1320
QY	1389	GGGAGGCCAATATTCATCCAGGCTTATGCCAAGAGGCGTTCATCAGAGGCTCGAG	1448
Db	1321	GGGAGGCAATATTCATCCAGGCTTATGCCAAGAGGCGTTCATCAGAGGCTCGAG	1380
QY	1449	ACCAAGGTGAGAACATTTGGCGTGAAGACGGTCACGATCAATGAAAAGATTTCCAG	1508
Db	1381	ACCAAGGTGAGAACATTTGGCGTGAAGACGGTCACGATCAATGAAAAGATTTCCAG	1440
QY	1509	AGTGAAGAAAAGGTTATCATCTGCACTAACACCATCTTTTACCAAGCTGAAGGTGAAAA	1568
Db	1441	AGTGAAGAAAAGGTTATCATCTGCACTAACACCATCTTTTACCAAGCTGAAGGTGAAAA	1500
QY	1569	GGATTCCTCCAAAGACAGTCAATTCACAGATCTTGGAGTACGCGCTGGAGTCCCTGAACGA	1628
Db	1501	GGATTCCTCCAAAGACAGTCAATTCACAGATCTTGGAGTACGCGCTGGAGTCCCTGAACGA	1560
QY	1629	AAGACCTCTTACATTTGTTCAAGTCAATGGCCAGCACACAGTCTGGGGGAACCAAGGAGCC	1688
Db	1561	AAGACCTCTTACATTTGTTCAAGTCAATGGCCAGCACACAGTCTGGGGGAACCAAGGAGCC	1620
QY	1689	AGCATTAATTTCAAGACATTTGTCAATTAAGTGTCTTTAGATTAATTCCTATTAATCTCTGTG	1748
Db	1621	AGCATTAATTTCAAGACATTTGTCAATTAAGTGTCTTTAGATTAATTCCTATTAATCTCTGTG	1680
QY	1749	ATTGTTGGAGGCGCTCTTATTCATATTCCTGACAGTGGAGATTTGGTCTCCAAAACCC	1808
Db	1681	ATTGTTGGAGGCGCTCTTATTCATATTCCTGACAGTGGAGATTTGGTCTCCAAAACCC	1740
QY	1809	AACAAATTTGACTCATCTGTGTGTTGGCCACCGTTTCCCAACCTGCTGGAAGTAGTAGCC	1868
Db	1741	AACAAATTTGACTCATCTGTGTGTTGGCCACCGTTTCCCAACCTGCTGGAAGTAGTAGCC	1800
QY	1869	ACATGCGATGAGATGATTTTCAGAGATTAAGTAACTGAAGAGTGTGATGACTCTGTG	1928
Db	1801	ACATGCGATGAGATGATTTTCAGAGATTAAGTAACTGAAGAGTGTGATGACTCTGTG	1860
QY	1929	AACACAGAGACAGATCTTAAAAACATGTCCACCCCGCAGTGCAGTAGTTGGTATTTGAC	1988
Db	1861	AACACAGAGACAGATCTTAAAAACATGTTCACACCCCGCAGTGCAGTAGTTGGTATTTGAC	1920
QY	1989	AAGTTGGTGTGAACCTTTGGGAATGTCTGCAGAATAATTTTCACAGATGAAGCCGACAGC	2048
Db	1921	AAGTTGGTGTGAACCTTTGGGAATGTCTGCAGAATAATTTTCACAGATGAAGCCGACAGC	1980
QY	2049	GGTCAGGAAAACAATTTAGAGGGGAAAAAGATGGG	2084
Db	1981	GGTCAGGAAAACAATTTAGAGGGGAAAAAGATGGG	2016

RESULT	10
ABO83369	
ID	ABO83369 standard; cDNA; 2776 bp.
XX	
XX	
AC	
ABO83369;	
XX	
DT	20-JAN-2003 (first entry)
XX	
DE	Human NR10.8 splicing variant encoding CDNA SEQ ID NO:13.
XX	
KM	NR10: splicing variant: haematopoietin receptor; immunomodulator;
KM	haemostatic; haematopoietic factor; immunological disease;
KM	haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX	
OS	Homo sapiens.
XX	
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	7..1653
FT	/4Tag= a
FT	/product= "NR10.8"
XX	
PN	MO200277230-A1.

03-OCT-2002.  
22-MAR-2002; 2002WO-JP02769.  
26-MAR-2001; 2001JP-0087298.  
(CHUS ) CHUGAI SEIYAKU KK.  
Maeda M, Yaguchi N, Hasegawa M;  
WPI: 2003-018925/01.  
P-PsDB: ABP54369.  
NR10 splicing variants of hematopoietin receptor proteins and encoded  
genes, applicable in searching hematopoietic factors and developing  
remedies for immunological and hematopoietic diseases -  
Claim 1; Fig 19-21; 250pp; Japanese.  
The present invention describes hematopoietic receptor NR10 splicing  
variants (1). (1) have immunomodulator and haemostatic activities. The  
proteins and encoded genes are applicable in searching for novel  
haematopoietic factors, and developing remedies for immunological and  
haematopoietic diseases. The haematopoietin receptor genes participate  
in vivo immunomodulation and haematopoietic cell regulation, and in  
the search for hematopoietic factors capable of functionally binding  
to the receptors. The present sequence encodes the human NR10.8 protein  
from the present invention.

Query	Match	82.1%	Score 1972:	DB 25:	Length 2776:
Best Local	Similarity	92.5%:	Pred. No. 0:		
Matches 2158:	Conservative	0:	Mismatches	0:	Indels 176: Gaps 1
QY	69	CTGGAAATGTGCATAGGCAACCTCAAGTTTTTCACCACGACATGTGCTGTAATGTCCG	128		
Db	1	CTGGAAATGTGCATAGGCAACCTCAAGTTTTTCACCACGACATGTGCTGTAATGTCCG	60		
QY	129	CAAAACATTTCTCTCCCCAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGGCA	188		
Db	61	CAAAACATTTCTCTCCCCAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGGCA	120		
QY	189	CTGTGGATGTCTCCCTCACTCTGCAAAATTCAGCCTTGCGACGTCTCCACGTAGCTGAG	248		
Db	121	CTGTGGATGTCTCCCTCACTCTGCAAAATTCAGCCTTGCGACGTCTCCACGTAGCTGAG	180		
QY	249	AACATTTCTCTGTGTACTACTATATGAGAAAATTTAACTGTGACTTGGAGTCCAGAGAA	308		
Db	181	AACATTTCTCTGTGTACTACTATATGAGAAAATTTAACTGTGACTTGGAGTCCAGAGAA	240		
QY	309	GAACACAGTTATACCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAACATGAT	368		
Db	241	GAACACAGTTATACCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAACATGAT	300		
QY	369	AATTGTACACCAATAGTCTTCAAGAGTGAATTCGTGCTCTCTTTTCTTCTTCCA	428		
Db	301	AATTGTACACCAATAGTCTTCAAGAGTGAATTCGTGCTCTCTTTTCTTCTTCCA	360		
QY	429	ACAATAACGATCCGATTAATATATACCATGTGAGTGGAGAACTGAAAATGAGAGATGTGA	488		
Db	361	ACAATAACGATCCGATTAATATATACCATGTGAGTGGAGAACTGAAAATGAGAGATGTGA	420		
QY	489	ATTAAATCTCATATGACATACTGAGATTAGAGACATATAGCAAAAACGTGAACCTCAAG	548		
Db	421	ATTAAATCTCATATGACATACTGAGATTAGAGACATATAGCAAAAACGTGAACCTCAAG	480		
QY	549	ATTTTCCTGTGTAACCAAGTCTTTGGGCGATCAACAGCAATGATTTCAATATGATGATTAAG	608		
Db	481	ATTTTCCTGTGTAACCAAGTCTTTGGGCGATCAACAGCAATGATTTCAATATGATGATTAAG	540		
QY	609	CCTGAGTTGGGCGCTGTTTCATCTGATTTAAATCACACTGTGATTCAGGCACTCAAC	668		

```

Db      |||||
541 CCTGAGTTGGCCCGCTTTTCATCTGATTTAAATACACACTTCGATTCAGGACACTCAAC 600
Oy      |||||
669 AGTACACAGCTGGATGAGTCACTTGGCTAGAGACCGTAAGGATTAACCAACCAACGAC 728
Db      |||||
601 AGTACACAGCTGGATGAGTCACTTGGCTAGAGACCGTAAGGATTAACCAACCAACGAC 660
Oy      |||||
729 AACCTCAGCGGGCTGACGCTTTTACAGAAATATGTCAATAGCTCTGCGATGCGGCTCAG 788
Db      |||||
661 AACCTCAGCGGGCTGACGCTTTTACAGAAATATGTCAATAGCTCTGCGATGCGGCTCAG 720
Oy      |||||
789 GAGTAAAGTTCTGAGAGTACTGGAGCCAGAGAAAATGGGAATGACTGAGAGAGAGCT 848
Db      |||||
721 GAGTAAAGTTCTGAGAGTACTGGAGCCAGAGAAAATGGGAATGACTGAGAGAGAGCT 780
Oy      |||||
849 CCATGTGCGCTGAGACTGTGAGAGTCTGAAACCAGCTGAGGCGGATGAGAAAGGGCA 908
Db      |||||
781 CCATGTGCGCTGAGACTGTGAGAGTCTGAAACCAGCTGAGGCGGATGAGAAAGGGCA 840
Oy      |||||
909 GTGCGGTTGTTATGGAAGAGGCAAGAGAGGCCAGTCTAGAGAAAACACTTGGCTAC 968
Db      |||||
841 GTGCGGTTGTTATGGAAGAGGCAAGAGAGGCCAGTCTAGAGAAAACACTTGGCTAC 900
Oy      |||||
969 AACATATGCTACTATCCAGAAAGCAACACTAATCTCAGAGAAACATAGACACTATAC 1028
Db      |||||
901 AACATATGCTACTATCCAGAAAGCAACACTAATCTCAGAGAAACATAGACACTATAC 960
Oy      |||||
1029 CAGCAGCTTTGAACTCATCTGAGGAGCGAGAGCTTTGGGTGTCATGATTTCTATAT 1088
Db      |||||
961 CAGCAGCTTTGAACTCATCTGAGGAGCGAGAGCTTTGGGTGTCATGATTTCTATAT 1020
Oy      |||||
1089 TCTCTGGGAAAGTCTCAGTGGCCACCTGAGAGATTCAGAGTATCAAGAAAATCATTT 1148
Db      |||||
1021 TCTCTGGGAAAGTCTCAGTGGCCACCTGAGAGATTCAGAGTATCAAGAAAATCATTT 1080
Oy      |||||
1149 CAGTGCATGAGTGCATCAGGCGCTGCTGAGAGCAAGCTATGCTGTAAGTGGCAA 1208
Db      |||||
1081 CAGTGCATGAGTGCATCAGGCGCTGCTGAGAGCAAGCTATGCTGTAAGTGGCAA 1140
Oy      |||||
1209 AGCTCTGCTAGACGTGACACTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1268
Db      |||||
1141 AGCTCTGCTAGACGTGACACTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Oy      |||||
1269 CCCACACACCTTTCTCTGGGAATCTGTGCTCAGGCGCACGAATGGAGCATCCAGCAAT 1328
Db      |||||
1201 CCCACACACCTTTCTCTGGGAATCTGTGCTCAGGCGCACGAATGGAGCATCCAGCAAT 1260
Oy      |||||
1329 AAATTAACCTTCTGCTGCTATACATCTGTGTATCCAAATGTTGCATGACAAAGTT 1388
Db      |||||
1261 AAATTAACCTTCTGCTGCTATACATCTGTGTATCCAAATGTTGCATGACAAAGTT 1320
Oy      |||||
1389 GCGGAGCCATATTCATCCAGGCTTATGCGCAAGAGGCGTTCCATCAGAGTCTGAG 1448
Db      |||||
1321 GCGGAGCCATATTCATCCAGGCTTATGCGCAAGAGGCGTTCCATCAGAGTCTGAG 1380
Oy      |||||
1449 ACCAAGGTGGAGAACATTTGGCGTGAAGCGTCAAGATCACAATGGAAGAGATTCACAG 1508
Db      |||||
1381 ACCAAGGTGGAGAACATTTGGCGTGAAGCGTCAAGATCACAATGGAAGAGATTCACAG 1440
Oy      |||||
1509 AGTGAGAGAAAGGATATCATGTGCAACATCAATCTTTTCCAAAGCTGGAAGGTGGAAA 1568
Db      |||||
1441 AGTGAGAGAAAGGATATCATGTGCAACATCAATCTTTTCCAAAGCTGGAAGGTGGAAA 1500
Oy      |||||
1569 GGATTTCTCAAGACAGTCAATTCAGCATCTTGGAGTACGGCGCTGAGATCCCTGAACGA 1628
Db      |||||
1501 GGATTTCTCAAGACAGTCAATTCAGCATCTTGGAGTACGGCGCTGAGATCCCTGAACGA 1560
Oy      |||||
1629 AAGACCTCTTACATTTGTCAGGTCATGGCCAGCACCACTGCTGGGGGCAACCAACGGGACC 1688
Db      |||||
1561 AAGACCTCTTACATTTGTCAGGTCATGGCCAGCACCACTGCTGGGGGCAACCAACGGGACC 1620
Oy      |||||
1689 AGCATTAATTTCAAGACATTTGTCATGAGTCTTTGAGATTATTCATCAATCTTCTGTG 1748

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Db      |||||
1621 AGCATTAATTTCAAGACATTTGTCATTTCA----- 1648
Oy      |||||
1749 ATGTGAGAGGCGCTTCTATTCCTATTCCTGACAGTGGCATATGCTCTCAAAAACCC 1808
Db      |||||
1649 ----- 1648
Oy      |||||
1809 AACAAATAGCATCATCTGTGTGGCCACCGCTTCCCAACCGCTGTAAGATATATACC 1868
Db      |||||
1649 ----- 1648
Oy      |||||
1869 ACATGGCATGGAGATGATTTAAGGATTAAGCTAAACCTGAAAGAGCTGTGATGACTCTGTG 1928
Db      |||||
1649 -----GATTAAGCTAAACCTGAAAGAGTGTGATGACTCTGTG 1684
Oy      |||||
1929 AACACAGAGACAGATCTTAAACCATGTTCCACCGCCACGTCACAAATGTTGGTATAC 1988
Db      |||||
1685 AACACAGAGAGAGATCTTAAACCATGTTCCACCGCCACGTCACAAATGTTGGTATAC 1744
Oy      |||||
1989 AAGTTGCTGTAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACG 2048
Db      |||||
1745 AAGTTGCTGTAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACG 1804
Oy      |||||
2049 GGTACAGAAACATTTTGAAGGGGAAAGATGGGTATGTGACCTGCCCTTCAGGCTT 2108
Db      |||||
1805 GGTACAGAAACATTTTGAAGGGGAAAGATGGGTATGTGACCTGCCCTTCAGGCTT 1864
Oy      |||||
2109 GATTGTCCTCCCTGGGGAAAGTTTGTGAGAGCTCCAGTTCCAGCTGAGATTCGCCGCCAGA 2168
Db      |||||
1865 GATTGTCCTCCCTGGGGAAAGTTTGTGAGAGCTCCAGTTCCAGCTGAGATTCGCCGCCAGA 1924
Oy      |||||
2169 AAATCCCAATACCTTTCAGAGTGCAGAGGGGACCCGCCAGAAAGCCAAAGAGACG 2228
Db      |||||
1925 AAATCCCAATACCTTTCAGAGTGCAGAGGGGACCCGCCAGAAAGCCAAAGAGACG 1984
Oy      |||||
2229 CTTCCTTTTCTGTCGAAGTGTAGTACCAATCATCTGTGTGAGAAAGAGCCCAAT 2288
Db      |||||
1985 CTTCCTTTTCTGTCGAAGTGTAGTACCAATCATCTGTGTGAGAAAGAGCCCAAT 2044
Oy      |||||
2289 CCATATTTGAAGAAATTCAGTACAGAGCCAGGAATTTCTGTGTCGAAGAACTTCACAG 2348
Db      |||||
2045 CCATATTTGAAGAAATTCAGTACAGAGCCAGGAATTTCTGTGTGTCGAAGAACTTCACAG 2104
Oy      |||||
2349 CACACCAAGGAGAGATCTAATAGCGACCATAGATGAGACCTCTGGGGCTCTCA 2402
Db      |||||
2105 CACACCAAGGAGAGATCTAATAGCGACCATAGATGAGACCTCTGGGGCTCTCA 2158

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RESULT 11  
 AAC92350  
 ID AAC92350 standard; cDNA: 2119 BP.  
 XX  
 AC AAC92350;  
 XX  
 DT 26-MAR-2001 (first entry)  
 XX  
 DE Human haemopoietin receptor protein NR10.3 encoding cDNA SEQ ID NO:16.  
 XX  
 KW Human; haemopoietin receptor: NR10.1; NR10.2; NR10.3; NR10;  
 KW immunoregulation; haematopoietic cell regulation; transmembrane;  
 KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;  
 KW metal allergy; pollen allergy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200075314-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 01-JUN-2000; 2000WO-JP03556.  
 XX  
 PR 02-JUN-1999; 99JP-0155797.  
 PR 30-JUL-1999; 99JP-0217797.  
 XX

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE, INC.  
XX  
PI Maeda M, Yaguchi N;  
XX  
DR WPI: 2001-061720/07.  
DR P-PSDB: AAB51244.  
XX  
XX Hematopoietin receptor protein NR10 for screening potential ligands for  
PT treatment of immune and hematopoietic disorders such as autoimmune  
PS diseases and allergies -  
XX  
PS Claim 1; Fig 13-14; 127pp; Japanese.  
XX  
XX The present sequence encodes a human haemopoietin receptor protein  
CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane  
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule  
CC which participates in immunoregulation and haematopoietic cell  
CC regulation in vivo, and is useful in searching for haematopoietic  
CC factors capable of binding to the receptor. NR10 can be used for the  
CC identification of substances for the treatment and prevention of immune  
CC and haematopoietic disorders including autoimmune diseases and allergies  
CC such as metal and pollen allergy.  
XX  
SO Sequence 2119 BP; 643 A; 459 C; 504 G; 513 T; 0 other;

Query Match 81.1%; Score 1947; DB 22; Length 2119;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 CTCCTCCCAAGCCTTATGTTAACTGGGGATGATGGACCTGGGCACTGTGATG 197  
DB 17 CTCCTCCCAAGCCTTATGTTAACTGGGGATGATGGACCTGGGCACTGTGATG 76  
OY 198 CTCCTCCCAAGCCTTATGTTAACTGGGGATGATGGACCTGGGCACTGTGATG 257  
DB 77 CTCCTCCCAAGCCTTATGTTAACTGGGGATGATGGACCTGGGCACTGTGATG 136  
OY 258 TGTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGTCCAGAAAGAAACAGT 317  
DB 137 TGTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGTCCAGAAAGAAACAGT 196  
OY 318 TATACCCAGTACAGATTAGAGAACTTACGCTTTGGAGAAAAACATGATATTGTACA 377  
DB 197 TATACCCAGTACAGATTAGAGAACTTACGCTTTGGAGAAAAACATGATATTGTACA 256  
OY 378 ACACATAGTTTACAGTAAATCGTCTGCTCTTTTCTTCTTCCCAAGATACG 437  
DB 257 ACACATAGTTTACAGTAAATCGTCTGCTCTTTTCTTCTTCCCAAGATACG 316  
OY 438 ATCCAGATATTTATACCATTTAGGTGAGAGCTGAAATGAGATGATGATTAATCT 497  
DB 317 ATCCAGATATTTATACCATTTAGGTGAGAGCTGAAATGAGATGATGATTAATCT 376  
OY 498 CATATGACATCTGAGAGTTAGAGAACTAGCAAACTGAAACCACTTAACATTTCCGT 557  
DB 377 CATATGACATCTGAGAGTTAGAGAACTAGCAAACTGAAACCACTTAACATTTCCGT 436  
OY 558 GTGAACACAGTTTGGGATCAAAAGATGATCAAAATGAAATGAAATGAAATGAAATG 617  
DB 437 GTGAACACAGTTTGGGATCAAAAGATGATCAAAATGAAATGAAATGAAATGAAATG 496  
OY 618 GCGCCTGTTTCATGATTTAAATATACACACTTGATTCAGAGACAGTCAACAGTACAGC 677  
DB 497 GCGCCTGTTTCATGATTTAAATATACACACTTGATTCAGAGACAGTCAACAGTACAGC 556  
OY 678 TGGATGGAAGTCACTTCGCTAAGACGTAAGATTAATAACCAAGCTACAACTCAGC 737  
DB 557 TGGATGGAAGTCACTTCGCTAAGACGTAAGATTAATAACCAAGCTACAACTCAGC 616  
OY 738 GGGGTGACGCTTTTACAGATATGTCATGCTGCGATGCGCGGTCAAGAGTCAAG 797  
DB 617 GGGGTGACGCTTTTACAGATATGTCATGCTGCGATGCGCGGTCAAGAGTCAAG 676

OY 798 TTCTGAGTAGCTAGGAGCCAGAAAAATGGGAATGACTGAGAGAAAGCTCCATGTGCG 857  
DB 677 TTCTGAGTAGCTAGGAGCCAGAAAAATGGGAATGACTGAGAGAAAGCTCCATGTGCG 736  
OY 858 CTGGAACGTGTGAGAGTCTTAAACACAGCTAGGCGGATGGAAGAGGCCAGTGGGTTG 917  
DB 737 CTGGAACGTGTGAGAGTCTTAAACACAGCTAGGCGGATGGAAGAGGCCAGTGGGTTG 796  
OY 918 TTATGGAAGAGGCAAGAGAGGCCAGTCTAGAGAAACACTTGGCTACACATATAG 977  
DB 797 TTATGGAAGAGGCAAGAGAGGCCAGTCTAGAGAAACACTTGGCTACACATATAG 856  
OY 978 TACTATCCAGAAAGCAACACTTAACCTCAGAGAAACAAATGAACACTACTAACACAGCTT 1037  
DB 857 TACTATCCAGAAAGCAACACTTAACCTCAGAGAAACAAATGAACACTACTAACACAGCTT 916  
OY 1038 GAACATGATCTGGGAGGCGAGACGCTTTGGGTGCTATGATTTCTTATATTTCTTGGG 1097  
DB 917 GAACATGATCTGGGAGGCGAGAGGCTTTGGGTGCTATGATTTCTTATATTTCTTGGG 976  
OY 1098 AAGTCTCAGTGGCCACCCCTGAGATTCACGATTTCAAGAAATATCTTACAGTGCATT 1157  
DB 977 AAGTCTCAGTGGCCACCCCTGAGATTCACGATTTCAAGAAATATCTTACAGTGCATT 1036  
OY 1158 GAGTCATGACAGGCGCTGCTGAGAGACGAGTGTGAGTGAAGTGGCAAGCTCTGCT 1217  
DB 1037 GAGTCATGACAGGCGCTGCTGAGAGACGAGTGTGAGTGAAGTGGCAAGCTCTGCT 1096  
OY 1218 CTAGACGTGAACACTTGGATGATGATGTTCCGGATGTGAGCTCAGACCCACAC 1277  
DB 1097 CTAGACGTGAACACTTGGATGATGATGTTCCGGATGTGAGCTCAGACCCACAC 1156  
OY 1278 CTTTCCTGGGAACTGTGCTCAGGCGCAAGCTGAGATCCAGCAAGATTAATTA 1337  
DB 1157 CTTTCCTGGGAACTGTGCTCAGGCGCAAGCTGAGATCCAGCAAGATTAATTA 1216  
OY 1338 CTTTCCTGGGAACTGTGCTCAGGCGCAAGCTGAGATCCAGCAAGATTAATTA 1397  
DB 1217 CTTTCCTGGGAACTGTGCTCAGGCGCAAGCTGAGATCCAGCAAGATTAATTA 1276  
OY 1398 TATTCATCCAGGCTTATGCCAAGAGGCTTGCATAGAAAGTCTCTGAGAACCAAGTG 1457  
DB 1277 TATTCATCCAGGCTTATGCCAAGAGGCTTGCATAGAAAGTCTCTGAGAACCAAGTG 1336  
OY 1458 GAGAACATTTGGCGGAAGAGGCTCAGATCCATGGAAGAGATTTCCCAAGTGAAGGA 1517  
DB 1337 GAGAACATTTGGCGGAAGAGGCTCAGATCCATGGAAGAGATTTCCCAAGTGAAGGA 1396  
OY 1518 AAGGTATCATCTGCAACTACACATCTTTACCAAGCTGAAGGTGAAGAAAGATTC 1577  
DB 1397 AAGGTATCATCTGCAACTACACATCTTTACCAAGCTGAAGGTGAAGAAAGATTC 1456  
OY 1578 AAGACAGTCAATTCAGAGATCTTGGCAGTAGGCGCTGGAGTCCCTGAAACGAAGACCT 1637  
DB 1457 AAGACAGTCAATTCAGAGATCTTGGCAGTAGGCGCTGGAGTCCCTGAAACGAAGACCT 1516  
OY 1638 TACATTTTTCAGGATCAGGAGCCAGACACAGTCTGGGAGCAACAGGAGCAGCTAAT 1697  
DB 1517 TACATTTTTCAGGATCAGGAGCCAGACACAGTCTGGGAGCAACAGGAGCAGCTAAT 1576  
OY 1698 TTCAAGACATTTGATTCAGTGTCTTTGAGATTTATCTCATTAATCTCTGATTTGGTGA 1757  
DB 1577 TTCAAGACATTTGATTCAGTGTCTTTGAGATTTATCTCATTAATCTCTGATTTGGTGA 1636  
OY 1758 GGCCTTCTTATTTCTATTTATCTGACATGAGATGAGTCTGCAAAAAACCAACAAATG 1817  
DB 1637 GGCCTTCTTATTTCTATTTATCTGACATGAGATGAGTCTGCAAAAAACCAACAAATG 1696  
OY 1818 ACTCATCTGTGTTGGCCACGCTTCCCAACCTGCTGAAATAGATAGCCACATGGCAT 1877  
DB 1697 ACTCATCTGTGTTGGCCACGCTTCCCAACCTGCTGAAATAGATAGCCACATGGCAT 1756  
OY 1878 GGAGATGATTTTCAAGATTAAGCTTAACCTGAAGAGTCTGATGATGATGATGATGATG 1937

|||||  
DB 1757 GGAGATGATTCAAGATAGCTAAACCTGAAGAGTCTGATGACTGTGTAACACAGAA 1816  
QY 1938 GACAGATCTTAAACCATGTTCCACCCCACTGACCAAGTGTGATGACAAAGTTGGTG 1997  
DB 1817 GACAGATCTTAAACCATGTTCCACCCCACTGACCAAGTGTGATGACAAAGTTGGTG 1876  
QY 1998 GTGAAGTGTGGGATGTTCTGCAAGAAATTTTCACAGATGAGCAGAACGGGTGAGGAA 2057  
DB 1877 GTGAAGTGTGGGATGTTCTGCAAGAAATTTTCACAGATGAGCAGAACGGGTGAGGAA 1936  
QY 2058 AACCAATTTAGAGGGGAGAAAGATGGG 2084  
DB 1937 AACCAATTTAGAGGGGAGAAAGATGGG 1963  
RESULT 12  
ABA93808  
ID ABA93808 standard; cDNA: 2903 BP.  
AC ABA93808;  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE Human zcytor17 cDNA sequence SEQ ID NO:53.  
XX  
KM zcytor17: chromosome 5; 5q11: cytokine receptor; immunomodulatory;  
KM antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;  
KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KM inflammatory disease; pancreatitis; inflammatory bowel disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200200721-A2.  
XX  
PD 03-JAN-2002.  
XX  
PE 26-JUN-2001; 2001WO-US20484.  
XX  
PR 26-JUN-2000; 2000US-214282P.  
PR 29-JUN-2000; 2000US-214955P.  
PR 08-FEB-2001; 2001US-267963P.  
XX  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;  
PI Maurer MF;  
XX  
DR WPI: 2002-090519/12.  
DR P-PSDB; ABB05741.  
XX  
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
PT splenic, blood or bone disorders -  
XX  
XX  
PS Example 1: Page 199-203; 235pp; English.  
XX  
CC The present invention describes a cytokine receptor designated zcytor17.  
CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
CC antirheumatic, antiarthritic and muscular activities. The zcytor17  
CC proteins are useful for treating and diagnosing lymphoid, immune,  
CC inflammatory, splenic, blood or bone disorders. Agonists or  
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
CC immunity and for stimulating lymphocyte proliferation, such as in the  
CC treatment of infections involving immunosuppression, including certain  
CC viral infections. They are also useful for inducing cytotoxicity and  
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to  
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to

CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 other:  
Query Match 81.0%; Score 1945.4; DB 24; Length 2903;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1946; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 138 CTCTCTCCCAAGCCTTTCATGTTTAACTGAGGATGATGTGACCTGGGCACTGTGATG 197  
DB 503 CTCTCTCCCAAGCCTTTCATGTTTAACTGAGGATGATGTGACCTGGGCACTGTGATG 562  
QY 198 CTCCCTCAGCTGCAAAATTCAGCTGGCAGCTGCGCAGCTAACCTGAGAACCTTTCC 257  
DB 563 CTCCCTCAGCTGCAAAATTCAGCTGGCAGCTGCGCAGCTAACCTGAGAACCTTTCC 622  
QY 258 TGTGTCTACTACTATAGGAAAAATTTAACTGCTGACCTGGAGTCCAGAAAGGAAACAGT 317  
DB 623 TGTGTCTACTACTATAGGAAAAATTTAACTGCTGACCTGGAGTCCAGAAAGGAAACAGT 682  
QY 318 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATTAATTGTACA 377  
DB 683 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATTAATTGTACA 742  
QY 378 ACCAATAGTCTACAAAGTAAATGCTGCTGCTCTTTTCTTCCCAAGATTAACG 437  
DB 743 ACCAATAGTCTACAAAGTAAATGCTGCTGCTCTTTTCTTCCCAAGATTAACG 802  
QY 438 ATCCACAGATTAATTAATCACTTGTAGGTGAGAGTGAAGATGATGATTAATTAATCT 497  
DB 803 ATCCACAGATTAATTAATCACTTGTAGGTGAGAGTGAAGATGATGATTAATTAATCT 862  
QY 498 CATATGACATCTGAGAGTTAGAGAACTAGCGAAACCTGAACCTTAAGATTTCCGT 557  
DB 863 CATATGACATCTGAGAGTTAGAGAACTAGCGAAACCTGAACCTTAAGATTTCCGT 922  
QY 558 GTGAACACAGTTTGGGATCAAAACGATGATTTCAATTTGAATGATTAAGCTGAGTTG 617  
DB 923 GTGAACACAGTTTGGGATCAAAACGATGATTTCAATTTGAATGATTAAGCTGAGTTG 982  
QY 618 GCGCCTGTTTCATGATTTTAAATATACACACTTGCATTCAGAGACAGTACAGTACAGC 677  
DB 983 GCGCCTGTTTCATGATTTTAAATATACACACTTGCATTCAGAGACAGTACAGTACAGC 1042  
QY 678 TGGATGGAAGTCAACTTGGCTTAAGAACCGTAAAGATTAATAACCAAGCTAACACTCAGC 737  
DB 1043 TGGATGGAAGTCAACTTGGCTTAAGAACCGTAAAGATTAATAACCAAGCTAACACTCAGC 1102  
QY 738 GGGCTGACAGCTTTTACAGAAATATGTCATAGCTGCGATGCGGCTCAAGAGTCAAG 797  
DB 1103 GGGCTGACAGCTTTTACAGAAATATGTCATAGCTGCGATGCGGCTCAAGAGTCAAG 1162  
QY 798 TTCTGGAAGTCAAGTGGAGGCAAGAAAAATGGGAATGACTGAGGAAGAAAGTCTAGTGGC 857  
DB 1163 TTCTGGAAGTCAAGTGGAGGCAAGAAAAATGGGAATGACTGAGGAAGAAAGTCTAGTGGC 1222  
QY 858 CTGGAAGTGTGGAAGTCTTGAACCAAGCTAGGCGGATGGAAGAAAGGCCAGTGGCTTG 917  
DB 1223 CTGGAAGTGTGGAAGTCTTGAACCAAGCTAGGCGGATGGAAGAAAGGCCAGTGGCTTG 1282  
QY 918 TTATGGAAGAGCAAGAGAGAGCCCAAGTCTAGAGAAACACTTGGCTAACACATATG 977  
DB 1283 TTATGGAAGAGCAAGAGAGAGCCCAAGTCTAGAGAAACACTTGGCTAACACATATG 1342  
QY 978 TACTATCCAGAAACCACTAACCTCAAGAAACATGAACACTACTAACACAGCTT 1037  
DB 1343 TACTATCCAGAAACCACTAACCTCAAGAAACATGAACACTACTAACACAGCTT 1402  
QY 1038 GAAGTGCATCTGGAGAGGAGAGAGCTTTGGGTGCTATGATTTCTTAAATTTCTTGGG 1097  
DB 1403 GAAGTGCATCTGGAGAGGAGAGAGCTTTGGGTGCTATGATTTCTTAAATTTCTTGGG 1462

QY	1098	AAGCTCCAGAGGGCCACCCGAGGATTCGAGCTTTCAGAGAAATATCTTCACTGACATT	1157
Db	1463	AAGCTTCAGTGGCCACCCCTGAGGATTCACACTATTCAGAGAAATATCTTCACTGACATT	1522
QY	1158	GAGGTTCATGACAGGCCCTCGTTGCTGAGAGACCAGCTAGTGTGTAAGTGGCAAGCTCTGCT	1217
Db	1523	GAGGTTCATGACAGGCCCTCGTTGCTGAGAGACCAGCTAGTGTGTAAGTGGCAAGCTCTGCT	1582
QY	1218	CTAAGCTGAACACTTGGATGATTTGAATGGTTTCCGGATGTGGACTCAGAGCCACACACC	1277
Db	1583	CTAAGCTGAACACTTGGATGATTTGAATGGTTTCCGGATGTGGACTCAGAGCCACACACC	1642
QY	1278	CTTTCCCTGGGATCTGTGCTCAGGCCACGAACTGAGAGATCCAGCAAGATTAATTTAAA	1337
Db	1643	CTTTCCCTGGGATCTGTGCTCAGGCCACGAACTGAGAGATCCAGCAAGATTAATTTAAA	1702
QY	1338	CCTTTCTGGTGCTATTAACATCTCTGTATTCCAATGTTTCATGACAAAAGTTGGCGAGCCA	1397
Db	1703	CCCTTTCTGGTGCTATTAACATCTCTGTATTCCAATGTTTCATGACAAAAGTTGGCGAGCCA	1762
QY	1398	TATTCATTCACAGGCTTATGCCAAAGAAGGCGCTTCATCAGAAAGTCCGTGAGACCAGGTG	1457
Db	1763	TATTCATTCACAGGCTTATGCCAAAGAAGGCGCTTCATCAGAAAGTCCGTGAGACCAGGTG	1822
QY	1458	GAGAACATTTGGCGTGAAGAAGCGTTCAGATCAATGAAAGAGATTCCCAAGATGAGAGAGA	1517
Db	1823	GAGAACATTTGGCGTGAAGAAGCGTTCAGATCAATGAAAGAGATTCCCAAGATGAGAGAGA	1882
QY	1518	AAGGTTATCATCTGCAACTACACATCTTTTACCACAGCTGAAGGTGGAAAAGATTTCTCC	1577
Db	1883	AAGGTTATCATCTGCAACTACACATCTTTTACCACAGCTGAAGGTGGAAAAGATTTCTCC	1942
QY	1578	AAGACAGTCAATTCACACATCTTCACATAGCGCGCTGAGAGTCCCTGAAACGAAACAGCTCT	1637
Db	1943	AAGACAGTCAATTCACACATCTTCACATAGCGCGCTGAGAGTCCCTGAAACGAAACAGCTCT	2002
QY	1638	TACATTTGTTCAAGTTCATGCGCCAGCACAGTGTCTGGGGAAACCAACGGGACCAGCATTAAT	1697
Db	2003	TACATTTGTTCAAGTTCATGCGCCAGCACAGTGTCTGGGGAAACCAACGGGACCAGCATTAAT	2062
QY	1698	TTCAAGACATTTGTCATTCAGTTCAGTCTTTGAGATTTATCCCATTAACCTTCCTGATTTGGTGA	1757
Db	2063	TTCAAGACATTTGTCATTCAGTTCAGTCTTTGAGATTTATCCCATTAACCTTCCTGATTTGGTGA	2122
QY	1758	GGCCTCTTATTTCTCATATTATCTGACAGTGGCATATGTGTCTCAAAAAACCCACAATAATG	1817
Db	2123	GGCCTCTTATTTCTCATATTATCTGACAGTGGCATATGTGTCTCAAAAAACCCACAATAATG	2182
QY	1818	ACATCATGTGTTGGCCACCCTGCCAACCCCTCTGAAAGTAACTATATAGCCACATGGCAT	1877
Db	2183	ACATCATGTGTTGGCCACCCTGCCAACCCCTCTGAAAGTAACTATATAGCCACATGGCAT	2242
QY	1878	GGAGATCATTTTCAAGATTAAGCTAAACCTGAAAGAGTCTGATGACTCTGTGAACACAGAA	1937
Db	2243	GGAGATCATTTTCAAGATTAAGCTAAACCTGAAAGAGTCTGATGACTCTGTGAACACAGAA	2302
QY	1938	GACAGGATCTTTAAACAATGTTCCACCCACAGTGAACAAGTTGTGATTGACAAAGTGGTG	1997
Db	2303	GACAGGATCTTTAAACAATGTTCCACCCACAGTGAACAAGTTGTGATTGACAAAGTGGTG	2362
QY	1998	GTGAACCTTTGGGAATGTTTGCACAGAATTTTCCACAGTGAAGCCAGAGGGGTCAAGAA	2057
Db	2363	GTGAACCTTTGGGAATGTTTGCACAGAATTTTCCACAGTGAAGCCAGAGGGGTCAAGAA	2422
QY	2058	AACAAATTTAGAGGGGAAAAAGAAATGGG 2084	
Db	2423	AACAAATTTAGAGGGGAAAAAGAAATGGG 2449	

Query Match	Best Local Similarity	80.5%	Score 1932.8	DB 22	Length 2969
Matches 1945	Conservative	0	Mismatches	2	Indels 1
					Gaps 1
AC	ACG92337,				
XX	26-MAR-2001 (first entry)				
DT					
XX					
DE	Human haemopoietin receptor protein NR10.1 encoding cDNA SEQ ID NO:1.				
XX					
KW	Human: haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10:				
KM	immunoregulation; hematopoietic cell regulation; transmembrane;				
KW	immune disorder; haematopoietic disorder; autoimmune disease; allergy;				
KM	metal allergy; pollen allergy; ss.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200075314-A1.				
XX					
PD	14-DEC-2000.				
XX					
PF	01-JUN-2000; 2000WO-JP03556.				
XX					
PR	02-JUN-1999; 99JP-0155797.				
PR	30-JUL-1999; 99JP-0217797.				
XX					
PA	(CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.				
XX					
PI	Maeda M, Yaguchi N;				
DR	WPI: 2001-061720/07.				
DR	P-PSDB; AAB51242.				
XX					
PT	Hematopoietin receptor protein NR10 for screening potential ligands for				
PT	treatment of immune and hematopoietic disorders such as autoimmune				
PT	diseases and allergies -				
XX					
PS	Claim 1; Fig 3-5; 12pp; Japanese.				
XX					
CC	The present sequence encodes a human haemopoietin receptor protein				
CC	(NR10), specifically designated NR10.1. NR10 occurs as a transmembrane				
CC	protein and a soluble protein. NR10 is a haemopoietin receptor molecule				
CC	which participates in immunoregulation and hematopoietic cell				
CC	regulation in vivo, and is useful in searching for hematopoietic cell				
CC	factors capable of binding to the receptor. NR10 can be used for the				
CC	identification of substances for the treatment and prevention of immune				
CC	and hematopoietic disorders including autoimmune diseases and allergies				
CC	such as metal and pollen allergy.				
XX					
XX					
SQ	Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 other;				
Query Match	80.5%	Score 1932.8	DB 22	Length 2969	
Best Local Similarity	99.8%	Freq. No. 0			
Matches 1945	Conservative	0	Mismatches	2	Indels 1
					Gaps 1
QY	138 CTCTCTCCCCCGCTTCATGTTGTTAACTGGGATGATGTGGACCTGGCACTGTGATG	197			
Db					
	529 CTCTCTCCCCCGCTTCATGTTGTTAACTGGGATGATGTGGACCTGGCACTGTGATG	588			
QY	198 CTCCCTCTCTCTGCAAAATTCAGCTGCGACCTCTGCCAGCTTAAGCTGAGAACATTTCC	257			
Db					
	589 CTCCCTCTCTCTGCAAAATTCAGCTGCGACCTCTGCCAGCTTAAGCTGAGAACATTTCC	648			
QY	258 TGTGTCTACTCTATAGAAAAATTTAACTGCACTTGAGAGTCGAGAAAGGAACCACT	317			
Db					
	649 TGTGTCTACTCTATAGAAAAATTTAACTGCACTTGAGAGTCGAGAAAGGAACCACT	708			
QY	318 TATACCCAGTACACAGTTAAGAACTTACGCTTTTGGAGAAAAACATGATTAATGTACA	377			
Db					
	709 TATACCCAGTACACAGTTAAGAACTTACGCTTTTGGAGAAAAACATGATTAATGTACA	768			
QY	378 ACCAATAGTTCTACAAGTGAAGTGTGCTGCTGCTTTTCTTCTTCCCAAGATTAACG	437			
Db					
	769 ACCAATAGTTCTACAAGTGAAGTGTGCTGCTGCTTTTCTTCTTCCCAAGATTAACG	828			
QY	438 ATCCAGATTAATTTATACATTCAGCTGAGTGAACCTGAAATGAGATGATTAATTAATCT	497			



Db 829 ATCCAGATTAATTATACCATTTGAGGTGGAAAGCTGAAAATGGAGATGTTAATTAAATCT 888  
QY 498 CATATGACATCTGAGAGATTAGAGACATAGCAAACTGAAACCACTTAATTTTCCGT 557  
Db 889 CATTTGACATATCTGAGATTAGAGACATAGCAAACTGAAACCACTTAATTTTCCGT 948  
QY 558 GTGAACACAGTTTGGGATCAAAAGATGATCAAAATGGAATGATTAAGCCGTGATG 617  
Db 949 GTGAACACAGTTTGGGATCAAAAGATGATCAAAATGGAATGATTAAGCCGTGATG 1008  
QY 618 GCGCCTGTTTATCTGATTTAAATTACACACTTGATTCAGACATCAACAGTACAC 677  
Db 1009 GCGCCTGTTTATCTGATTTAAATTACACACTTGATTCAGACATCAACAGTACAC 1068  
QY 678 TGGATGGAAGTCACTTCGCTAAGACCGTAAAGATTAACCAAGTACACCTCAGC 737  
Db 1069 TGGATGGAAGTCACTTCGCTAAGACCGTAAAGATTAACCAAGTACACCTCAGC 1128  
QY 738 GGGCTGACGCTTTTACAGAAATATGTATAGCTCTGGATGTGGGTCAAGAGTCAAG 797  
Db 1129 GGGCTGACGCTTTTACAGAAATATGTATAGCTCTGGATGTGGGTCAAGAGTCAAG 1188  
QY 798 TTCTGAGATGCTGGAGCCCAAGAAAATGGAAATGACTGAGAAAGAGTCCATGTGGC 857  
Db 1189 TTCTGAGATGCTGGAGCCCAAGAAAATGGAAATGACTGAGAAAGAGTCCATGTGGC 1248  
QY 858 CTGGAACCTGTGAGAGTCTGTAACCAAGCTGAGCGGATGGAAGAGCCGCTGCGGTG 917  
Db 1249 CTGGAACCTGTGAGAGTCTGTAACCAAGCTGAGCGGATGGAAGAGCCGCTGCGGTG 1308  
QY 918 TTATGAGAAGAGGCAAGAGAGCCCAAGTCTCTAGAGAAAACACTTGGCTACACATATG 977  
Db 1309 TTATGAGAAGAGGCAAGAGAGCCCAAGTCTCTAGAGAAAACACTTGGCTACACATATG 1368  
QY 978 TACTATCCAGAAACCAACACTTAACCTACAGAAAACATGAACACTACTTAACACACTT 1037  
Db 1369 TACTATCCAGAAACCAACACTTAACCTACAGAAAACATGAACACTACTTAACACACTT 1428  
QY 1038 GAATGCAATCTGGAGGCGAGAGCTTTGGTGTCTATGATTTTAAATTTCTTGGG 1097  
Db 1429 GAATGCAATCTGGAGGCGAGAGCTTTGGTGTCTATGATTTTAAATTTCTTGGG 1488  
QY 1098 AAGTCTCCAGTGGCCACCTGAGGATTCAGACTATTCAGAAAATCATTTTCACTGCAAT 1157  
Db 1489 AAGTCTCCAGTGGCCACCTGAGGATTCAGACTATTCAGAAAATCATTTTCACTGCAAT 1548  
QY 1158 GAGGTCAATGAGGCGCTGCTGCTGAGACACGTAATGTTGTTGAGTGGCAAGCTCTGCT 1217  
Db 1549 GAGGTCAATGAGGCGCTGCTGCTGAGACACGTAATGTTGTTGAGTGGCAAGCTCTGCT 1608  
QY 1218 CTAGACGTGAACACTTGGATGATTAATGTTCCGATGTGAGCTGAGAGCCACCAACC 1277  
Db 1609 CTAGACGTGAACACTTGGATGATTAATGTTCCGATGTGAGCTGAGAGCCACCAACC 1668  
QY 1278 CTTTCTGGAATCTGTGCTCAGGCCAGAACTGAGCATCCAGCAAGATTAATTAATA 1337  
Db 1669 CTTTCTGGAATCTGTGCTCAGGCCAGAACTGAGCATCCAGCAAGATTAATTAATA 1728  
QY 1338 CTTTCTGGAATCTGTGCTGATCAATGTTGATCAATGTTGATGAGCAAGTGGGAGCA 1397  
Db 1729 CTTTCTGGAATCTGTGCTGATCAATGTTGATGAGCAAGTGGGAGCA 1788  
QY 1398 TATTCATCCAGGCTTATGCCAAAGAGGCTTCATCAGAAAGTCTGAGACCAAGTG 1457  
Db 1789 TATTCATCCAGGCTTATGCCAAAGAGGCTTCATCAGAAAGTCTGAGACCAAGTG 1848  
QY 1458 GAGAACAATTTGGCGTGAAGAGCTCAGATCAGATGAGAAAGATTTCCCAAGAGTGAGA 1517  
Db 1849 GAGAACAATTTGGCGTGAAGAGCTCAGATCAGATGAGAAAGATTTCCCAAGAGTGAGA 1908  
QY 1518 AAGGTATCATCTGCAACTACACATCTTTTACCAACTAGAGTGGAAAAAGATTTCTCC 1577  
Db 1909 AAGGTATCATCTGCAACTACACATCTTTTACCAACTAGAGTGGAAAAAGATTTCTCC 1968

QY 1578 AAGACAGTCAATTCACATCTTGCAGTACGCGCTGGAGTCCCTGAAACGAAAGACCTCT 1637  
Db 1969 AAGACAGTCAATTCACATCTTGCAGTACGCGCTGGAGTCCCTGAAACGAAAGACCTCT 2028  
QY 1638 TACATTTGTCAGTTCATGCGCAGCAGCAGTCTGGGGAACCAACGGGACGATTAAT 1697  
Db 2029 TACATTTGTCAGTTCATGCGCAGCAGCAGTCTGGGGAACCAACGGGACGATTAAT 2088  
QY 1698 TTCAAGCATTTGTATTCAGTGTCTTTGAGATTAATCTCATTAATCTTCTGATTTGTTGA 1757  
Db 2089 TTCAAGCATTTGTATTCAGTGTCTTTGAGATTAATCTCATTAATCTTCTGATTTGTTGA 2148  
QY 1758 GGCCTGTATTTATTCATTAATTCATGAGTGCATATGCTCAAAAACCAACCAATTTG 1817  
Db 2149 GGCCTGTATTTATTCATTAATTCATGAGTGCATATGCTCAAAAACCAACCAATTTG 2208  
QY 1818 ACTCATCTGTGTGGCCACCCTTCCCAACCTGCTGAAGTACTATAGCCACATGSCAT 1877  
Db 2209 ACTCATCTGTGTGGCCACCCTTCCCAACCTGCTGAAGTACTATAGCCACATGSCAT 2268  
QY 1878 GGAGATATTTTCAAGGATTAAGCTTAACCTGAGAGAGTCTGATGACTTGTGAACACGAA 1937  
Db 2269 GGAGATATTTTCAAGGATTAAGCTTAACCTGAGAGAGTCTGATGACTTGTGAACACGAA 2328  
QY 1938 GACAGATCTTAAACCATGTTCCACCCCAAGTGACAGTGAAGTGGATTTGACAAAGTTGGTG 1997  
Db 2329 GACAGATCTTAAACCATGTTCCACCCCAAGTGACAGTGAAGTGGATTTGACAAAGTTGGTG 2388  
QY 1998 GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAGCGGTACAG -A 2056  
Db 2389 GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAGCGGTACAGAA 2448  
QY 2057 AACAATTTAGAGGGGAAAAAAGATGGG 2084  
Db 2449 AACAATTTAGAGGGGAAAAAAGATGGG 2476

RESULT 14  
ABA93768  
ID ABA93768 standard; DNA: 2196 BP.  
XX ABA93768;  
AC  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE Human zcytor17 protein encoding degenerate DNA SEQ ID NO:4.  
XX  
KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cycostatic;  
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KW inflammatory disease; pancreatitis; inflammatory bowel disease; ds.  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
PN MO200200721-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 26-JUN-2001; 2001MO-US20484.  
XX  
PR 26-JUN-2000; 2000US-214282P.  
PR 29-JUN-2000; 2000US-214955P.  
PR 08-FEB-2001; 2001US-267963P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuitper JL;  
PI Maurer MF;  
XX





OY		1911	GAGTCGTATGACTCTGTGGAAACACAGGAAGACAGATCTTAAAACCATGTTCACCCCCAGT	1970
Dd		1741	GARNSSNAYGVGSWNGTNNAAYCACGAGAAYVGNATHHTNAARCCNTGWSNACCNCMWSN	1800
OY		1971	GACAAAGTTGGGATTGACAAGTTGGTGSTGTAACCTTTGGGAAATGTTCTGCAGAATAATTTTC	2030
Dd		1801	GAYAAARTTNGNATHGAAVAARYTMGTNGTNNAAAYTTYGMAAAYGTYNTINCARGAATHTTY	1860
OY		2031	ACAGATGAAGCCAGAACGGGTCAAGAAACAATTTAGAGGGGAAAAGAATGGTATGTG	2090
Dd		1861	ACNNAVYARGNMGNACNGNCACAGAAAYAAAYTTNGNGNGNGRARAAYVGCGTAAVTN	1920
OY		2091	ACCTGCCCTTCAGAGCCTGATGTGCCCTGGGGGAAAAGTTTGGAGAGCTCCCAGTTTC	2150
Dd		1921	ACNTGYCCNTTYMGNCNGATYTGCCTTYTNGNAAHRMSNTTTYGARGARITYTCCNGTWSN	1980
OY		2151	CCTGAGATTCCGCCCAAGAAATCCCAATACCTACGTTGAGAGATGCCAGAGGGAGCCGC	2210
Dd		1981	CCNGARATHCCNCCNMGNAAARWSNCARTAYTYTNMNSNMGNATGCCNGARGNACNMGN	2040
OY		2211	CCAGAAGCAAAGAGACGACTCTCTTTTCGTCGCTAAAGTTTAGTACCAAGATCANCTGTG	2270
Dd		2041	CCNGARCNMARGARCARITYTNTTWTYSNGNCARRMSNTYTNCCNGAICAYTYTMGY	2100
OY		2271	GAGGAAGGAGCCCCCAATTCATATTTTGAAAAATCACTGACAGCCAGAGGATTTCTTGTG	2330
Dd		2101	GARGARGSGNGCNCNAAYCCMTAYTYTNAARAAYSNTGNACNCGMNGARTYYTNGTN	2160
OY		2331	TCTGAAAAACTTCCAGAGCACACCAAGGAGAGT	2365
Dd		2161	WSNGARAARYTNCNGARCAIYACNAAGAGMGARGT	2195

RESULT 15
ABA93821
ID ABA93821 standard; cDNA; 2295 BP.
XX
AC ABA93821;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human zcytor17-FC4 fusion polynucleotide SEQ ID NO:68.
XX
KW zcytor17; chromosome 5; Sgll; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cyostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001MO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
XX
PR 29-JUN-2000; 2000US-214955P.
XX
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kulper JL;
PI Maurer MF;
XX
DR WPI: 2002-090519/12.
XX
DR P-PDB: ABB05743.
XX
TJ Isolated polynucleotide encoding a cytokine receptor zcytor17 which is

PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
 PT splenic, blood or bone disorders -  
 XX  
 PS Example 11: Page 216-221, 235pp; English.

CC The present invention describes a cytokine receptor designated zycytor17.  
CC Zycytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
CC antitumematic, antithalritic and muscular activities. The zycytor17  
CC proteins are useful for treating and diagnosing lymphoid, immune,  
CC inflammatory, splenic, blood or bone disorders. Agonists or  
CC anti-zycytor17 antibodies are useful in stimulating cell-mediated  
CC immunity and for stimulating lymphocyte proliferation, such as in the  
CC treatment of infections involving immunosuppression, including certain  
CC viral infections. They are also useful for inducing cytotoxicity and  
CC for treating leukopenias. Antagonist of zycytor17 polypeptides are useful  
CC for treating autoimmune diseases (e.g. Rheumatoid arthritis and multiple  
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
CC pancreaticitis, and inflammatory bowel disease. Zycytor17 was mapped to  
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
CC exemplification of the present invention.

Sequence 2295 BP; 659 A; 578 C; 565 G; .493 T; 0 other;

Query Match	66.1%	Score 1586.8	DB 24	Length 2295
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1588	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

138 CTCTCTCCCGAGCCTTCATGTGTTAACCTGGGATGATGTGGACCTGGGCACCTGTGGATG 197

Db 7 CTCTCTCCCGCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGCACTGTGGATG 66

QY 198 CTCCTCACTCTGCAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGACATTTCC 257

Db 67 CTCCTTCACTCTGCAATTCAGCCTGGCAGCTCTGCCAGCTAAGCCTGAGACATTTCC 126

QY 258 TGTGCTACTACTATAGGAAATTTAACCTGCACCTTGGAGTCCAGGAAGGAACCACT 317

Db 127 TGTGCTACTACTATAGGAAAAATTAACTGCACCTTGAGATCCAGGAAGGAACCACT 186

318 TATACCACTACACAGTTAGAGAACTTACGCTTTTGAGAGAAACATGATATTTGTACA 377

Db 187 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGAGAGAAACATGATTAATTGTACA 245

378 ACCAATAGTTCATACAAAGTAGAAATTCTGCGCCTCCGTCTGGTTCTGCCTCAAGAAATAAAC  
437

[illegible]

A 30 AAAAAAAAAAAAAAAAAAAAAA  
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[illegible][illegible]

48 / GCGCCIGTTCATCTGATTTAAATAACACACTTCGATTCAGGACAGTCAACAGTACCGC 348

QY 6/8 TGGATGGAGTCAACTTCGCTAAGAACCGTAAGGATAAAACCAACGTACAACTTCAG /3/

Db 54 / TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAACCAACGTACAACTCACC 606

738 GGGCTGCAGCCTTTACAGAATATGTCATAGCTCTGCATGTGGGTCGAAGAGTCAAC 797

Db 607 GGGCTGCAGCCTTTTACAGATATGTCATAGCTCTCGGATGTGGGTCAGGAGTCAAG 666

2Y 798 TTCTGAGTGA CTGGAGCC AAGAAAAA ATGGGA TGACTGAG GAGAAG CTCCAT GTGGC 857



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OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 18:18:26 ; Search time 141 Seconds

(without alignments)  
7519.165 Million cell updates/sec

Title: US-09-892-949-1

Perfect score: 2402  
Sequence: 1 ggcacagatgtgtgtgcag.....atgagacccctgggacctca 2402

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_MN:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96.6	4.0	2369	1	US-07-797-556-1 Sequence 1, Appli
2	96.6	4.0	2369	1	US-08-308-881-1 Sequence 1, Appli
3	96.6	4.0	2369	2	US-09-058-283-1 Sequence 1, Appli
4	96.6	4.0	2369	2	US-09-058-283-1 Sequence 1, Appli
5	96.6	4.0	2369	3	US-09-058-283-1 Sequence 1, Appli
6	96.6	4.0	2369	4	US-09-058-283-1 Sequence 1, Appli
7	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
8	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
9	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
10	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
11	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
12	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
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14	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
15	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
16	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
17	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
18	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
19	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
20	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
21	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
22	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
23	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
24	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
25	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli
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27	96.6	4.0	2369	5	US-09-058-283-1 Sequence 1, Appli

28	35.4	1.5	580073	4	US-08-545-528D-1	Sequence 1, Appli
29	35	1.5	3312	4	US-09-669-751-259	Sequence 259, App
C 30	34.8	1.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
C 31	34.2	1.4	14602	1	US-08-597-236-1	Sequence 1, Appli
C 32	34.2	1.4	14602	1	US-08-746-682A-1	Sequence 1, Appli
C 33	34	1.4	2634	3	US-08-949-386-26	Sequence 26, Appli
C 34	34	1.4	2634	3	US-08-450-562-26	Sequence 26, Appli
C 35	34	1.4	2634	4	US-08-984-709A-26	Sequence 26, Appli
C 36	34	1.4	2634	4	US-08-450-272-26	Sequence 26, Appli
C 37	34	1.4	2712	3	US-08-949-386-38	Sequence 38, Appli
C 38	34	1.4	2712	3	US-08-450-562-38	Sequence 38, Appli
C 39	34	1.4	2712	4	US-08-984-709A-38	Sequence 38, Appli
C 40	34	1.4	2712	4	US-08-450-272-38	Sequence 38, Appli
C 41	34	1.4	2970	3	US-08-949-386-37	Sequence 37, Appli
C 42	34	1.4	2970	3	US-08-450-562-37	Sequence 37, Appli
C 43	34	1.4	2970	4	US-08-984-709A-37	Sequence 37, Appli
C 44	34	1.4	2970	4	US-08-450-272-37	Sequence 37, Appli
C 45	33.6	1.4	4223	3	US-09-541-782-5	Sequence 5, Appli

#### ALIGNMENTS

RESULT 1  
US-07-797-556-1  
Sequence 1, Application US/07797556  
Patent No. 5262522  
GENERAL INFORMATION:  
APPLICANT: Geating, David P.  
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia  
TITLE OF INVENTION: Inhibitory Factor  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/797,556  
FILING DATE: 19911122  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2607  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
TELEFAX: 206-587-0606  
INFORMATION FOR SEQ ID NO.: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2369 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
TISSUE TYPE: human placenta  
IMMEDIATE SOURCE:  
CLONE: B10G/pDC303  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 244..2369  
FEATURE:

NAME/KEY: mat\_peptide  
 LOCATION: 310..2369  
 FEATURE:  
 NAME/KEY: sig\_peptide  
 LOCATION: 244..309  
 US-07-797-556-1

Query Match 4.0%; Score 96.6; DB 1; Length 2369;  
 Best Local Similarity 44.6%; Pred. No. 7.4e-20;  
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

724 CGTACACCTCAGCGGCTGACCTTTACAGATATGTCATCTGCGATGGG 783  
 1091 CATTACCTGTCACACCTTAAACCTTTACAGATATGTTTGAATGCGCTATGA 1150  
 784 TCAGAGTCAAG---TTCTGAGTGCAGCGCCAGAAAATGGGAATGACTGAG 840  
 1151 AGGAAGATGTTAGAGGATAGTGAAGTGAAGCAAGCAAGTGGATCAGCTATG 1210  
 841 AAGAAGCTCAGTGT---GGCTGGAACCTGTGAGAGTCTCTGAACCACTGAGGAGT 897  
 1211 AAGATAGACCTTAAACCCAGCTTCTGTATTAATAGATCCATCCATCTCAG 1270  
 898 GAAGAAGCCAGTGGGCTTGTATGGAAGCAAGCAAGGAGCCAGTCCCTAGAGAA 957  
 1271 GCTACAGACGTACACCTGCTGTGAGACATTTGCCCTTTTGAACCAATGAAAA 1330  
 958 CACTTGGCTACACATATGTTACTATCCAGAAAGCACATTAACCTCAGAAACATGA 1017  
 1331 TCTTGATTAATGAAGTGAAGTCTCAGAGATGAATCAGATTTACAAATTTACACAGTTA 1390  
 1018 ACACCTACTAACACAGCTTGAACCTGCTGGGAGGAGAGAGCTTTGGTGTCTATGA 1077  
 1391 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATCCGTATTTAGCAACCTTAA 1444  
 1078 TTTCTTAATATCTCTTGGGAAGTCTCCAGTGGCCACCTGAGATTCACCTATTCAG 1137  
 1445 CAGTAAGAAATCTTGTGGCAATCAGATGACGCTGTTTAAGTATCCCTGCTGACT 1504  
 1138 AAAATCATTTTCAAGCATGAGTCATGACGAGGCTGGCTGCTGAGAGACCACTAGTGG 1197  
 1505 TTCAAGCTACTACCCCTGTAATGATCTTAAAGCATTCCTCCAAAGATTAACGTTGGG 1564  
 1198 TGAAGTGGCAAGCTCTGCTCTAGACGTGAACACTTGGATGTAATGAACTTCCGATG 1257  
 1565 TGGATGAGCTACTACCAAGGAAATCTGTAAGAAATATATCTTGAAGTGTGTAT 1624  
 1258 TGGAGTGGAGCCACACCTTTCCGAGGAACTGTGTCTCAGGCCACGAACTGGACGA 1317  
 1655 CAGATTAAGCACCTCTGTATCAGACATGGAACAAAGATGATGATGATGACCT 1684  
 1318 TCAGCAAGATTAATTAACCTTTCTGTGCTATTAACATCTGTGTATCCATGTTGC 1377  
 1685 ATTTAAGAGGAACTTGGCAGAGCAAAATGCTATTGTAATACAGTTACTCAGTATATG 1744  
 1378 ATGACAAAGTTGGCGACCATATTCATCCAGCTTATGCCAAGAAAGGCGTTCCATGAG 1437  
 1745 CTGATGAGCAAGGAGCCCTGAATCATTAAGGATCACTTAAACAGCTCCACCTTCA 1804  
 1438 AAGTCTGAGACCAAGTGGAGAAATTTGGCTGAGAGAGGCTACAGTACATGAGGAAG 1497  
 1805 AAGGACCTACTGCTGGACAAAAAAGTAGGAAAAAGAAAGCTGCTTTAGATGGAGCC 1864  
 1498 AGATTCCCAAGAGTGAAGAAAGGATTCATCTGCAACTACACCATCTTTTACCAACTG 1557  
 1865 AACTTCTGTTGATGTTTACAGATGATTTATCAGAAATTTATATTTTATGAGCA 1924  
 1558 AAGGTGAAAAAGATTTCCAAAGCATCTTCCAGATCTTCCATGAGCCCTGAGT 1617  
 1925 TCATTGAAATGAAGTGTGTGATGATGATTTCTCCACACAGATATACATTTGCT 1984  
 1618 CCCTGAACGAAGACCTTACATTTGAGGTCATGGCAGACAGTGTGGGGAA 1677

DB 1985 CTTTGACTAGTACACATTTGATCATGTGACAAATGGCAGCATACACAGATGAGTGGGA 2044  
 QY 1678 CCACGGGACACGATTAATTTTCAAGACATTTGCTATTAGTGTCTTTGAGTTATCCCA 1737  
 DB 2045 AGGATGGTCCAGAAATTCATTTTACTACCCCAAGATTGGCTCAAGAGAAATTTGAAGCA 2104  
 QY 1738 TAACCTCTGATTTGGTGGAGCCCTTCTTATTCATATTCCTGACAGTGCATATGCTC 1797  
 DB 2105 TAGTCGTGCTGTTTGTCTTACATTTCTTATGACACACTTCTGTGGAGTGTCTGTCT 2164  
 QY 1798 TCAAAAAACCAACAAATTTGATCATCTGTGTGGCCACCGCTTCCCAACCTGCTGAA 1857  
 DB 2165 TTAATTAACGAGACCTTAATTAATAAACACATCTGCTTAATGTTCCAGATCTTCAAGA 2224  
 QY 1858 GTAGTATGCCACATGG 1874  
 DB 2225 GTCATATTGCCAGTGG 2241

## RESULT 2

US-08-881-1

Sequence 1, Application US/08308881

Patent No. 5783672

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2369 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TISSUE TYPE: human placenta

IMMEDIATE SOURCE:

CLONE: B10G/PDC303

FEATURE:

NAME/KEY: CDS

LOCATION: 244..2369

FEATURE:

NAME/KEY: mat\_peptide  
 LOCATION: 310..2369  
 FEATURE:  
 NAME/KEY: sig\_peptide.  
 LOCATION: 244..309  
 US-08-308-881-1

Query Match 4.0%: Score 96.6; DB 1; Length 2369;  
 Best Local Similarity 44.6%; Pred. No. 7.4e-20;  
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CTTACACCTGACGGGCTGACGCTTTTACAGAAATGTCATAGCTGTGGATGTCGG 783  
 DB 1091 CATTCACCTGTCAGAGACCTTAACCTTTACAGAAATGTCATAGCTGTGGATGTCGG 1150  
 QY 784 TCAAGAGTCAAG---TTCTGGAGTACGTGAGCCCAAGAAAAATGGAATGCTAGG 840  
 DB 1151 AGGAAGATGTTAAGGATGCTGAGTGAAGAGCAAGTGGGATCACCTATG 1210  
 QY 841 AAGAAGCTCCATG---GGCCTGGAAGTGGAGAGTCTGAAACAGCTGAGCGGATG 897  
 DB 1211 AAGATTAACCATCTAAAGCACCAAGTTTCTGTATTAATATGATCCATCTCATAG 1270  
 QY 898 GAAGAAGGCCAGTGGGCTTTTATGAGAAGGCAAGAGAGCCCAAGCTCCAGAGAAA 957  
 DB 1271 GCTACAGACCTGTACACTGCTGTGGAAGACATTTGCCCTTTTGAAGCCATGGAATA 1330  
 QY 958 CACTTGGCTACACATATGTCATCTCAGAAAGCAACACTAACCTACAGAAACAATGA 1017  
 DB 1331 TCTTGAATTTGAAGTACTCTCAGAAAGTGAATACATTTCAAAATTTACACATTA 1390  
 QY 1018 ACACCTACTAACACAGCTTGAAGTCTGGAGGCGAGAGGCTTTTGGTGTCTATGA 1077  
 DB 1391 ATGCCACAAAAGT-----CAGTAAATCTCACAATGATCGCTATCTAGCAACCTAA 1444  
 QY 1078 TTTCTTAATTTCTTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGCTATTCAG 1137  
 DB 1445 CAGTAAGAAATCTTGTGGCAAAATCAGATGAGCTGTTTAACTATCCCTGCTGACT 1504  
 QY 1138 AAAATATCTTCACTGATGAGTTCATGCAAGGCTCGCTTGGAGACAGCTAGTGG 1197  
 DB 1505 TTCAAGTACTCACCCTGTATGATCTTAAAGCATTCGCCCAAGAAATACATGCTTGG 1564  
 QY 1198 TGAAGTGGCAAGCTGCTCTAGAGCTGAACACTTGATGATGAATGTTCCGGATG 1257  
 DB 1565 TGAATGAGTACTCTCCAGGAATCTGTAAGAAATATATCTGAGTGGTGTGTAT 1624  
 QY 1258 TGAAGTGAAGCCGACACCTTCTGGAATCTGTGTCTCAGGCCAGAACTGAGCA 1317  
 DB 1625 CAGATTAAGCACCTGTATCACAGCTGGCAACAAGAAATGATACCGTGCATGCACT 1684  
 QY 1318 TCCAGCAAGATTAATTAACCTTTCTGCTATTAACATCTCTGTATCAATGTTGC 1377  
 DB 1685 ATTTAAGAGGAACTTGGCAGAGCAAAATGCTATTTGATTAACAGTTACTCTCATATATG 1744  
 QY 1378 ATGACAAAGTTGGGAGCATATTCATTCACAGGCTTATGCAAGAGGCGTTCATCAG 1437  
 DB 1745 CTGATGAGACCGAGAGCCCTGAATCCATTAAGGCATACCTTAAACAGCTCCACCTTCA 1804  
 QY 1438 AAGTCTCTGAGACCAAGGTGAGAAATGCGCTGAAGACGTCACGATCATGGAAG 1497  
 DB 1805 AAGGACCTACTGTCGCAAAAAGAAAGTAGGAAAGAGAGCTGTCTTAAGTGGGACC 1864  
 QY 1498 AGATTCCCAAGAGTGAAGAAAGGTATCATCTGCACACTACACCATCTTTTACCAAGCTG 1557  
 DB 1865 AACTTCCTGTTGATGATGATGATTAATGAGAAATATATATATTTTATGAACCA 1924  
 QY 1558 AAGTGAAGAAAGATTTCTCAAGACAGTCAATTCAGACATTTCCAGTAGCGCTGAGGT 1617  
 DB 1925 TCATTGGAAATGAACGTCTGTGATGTGATTTCTTCCACACAGAAATATCATGTGCT 1984  
 QY 1618 CCTGAAGCAAGAAAGCTTTACATTTGTCAGGTATGCGCAGCAACGATGCTGGGGAA 1677

DB 1985 CTTTACTAGTGAACATATGCTATAGTGTAGCAATGGCAGCATACACAGATGAAGTGGGA 2044  
 QY 1678 CCAACGGACAGCATTAATTTCAAGACATTTGTCATCTGCTTTGAAATATCTCA 1737  
 DB 2045 AGGATGGTCCAGAAATTCATCTTACTACCCCAAGATTGTGTCAGAGGAATTAAGAACCA 2104  
 QY 1738 TAACCTCTGATTTGGTGGAGGCTTCTTATTTCTCATTTATCTGACAGTGGCATATGTC 1797  
 DB 2105 TAGTCGTCCTGTTTGTGCTTATGACATCTCTATTTGACAACTCTTGGAGTGTCTGTCT 2164  
 QY 1798 TCAAAAAACCAACAAATGACTCATCTGTGTGGCCACCCTTCCCAACCTGCTGAAA 1857  
 DB 2165 TTAATTAAGCAGACCTTAATTAATAAACACATCTGCGCTAATGTTCCAGATCTTCAAGA 2224  
 QY 1858 GTAGTATAGCCACATGG 1874  
 DB 2225 GTCAATTTGCCCACTGG 2241

## RESULT 3

US-09-058-263-1  
 ; Sequence 1, Application US/09058263  
 ; Patent No. 5891997  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mosley, Bruce  
 ; APPLICANT: Cosman, David J.  
 ; TITLE OF INVENTION: Receptor for Oncostatin M  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Macintosh  
 ; OPERATING SYSTEM: Apple 7.1  
 ; SOFTWARE: Microsoft Word, Version 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/058, 263  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/308, 881  
 ; FILING DATE: 12-SEP-1994  
 ; APPLICATION NUMBER: US 08/249, 553  
 ; FILING DATE: 26-MAY-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Seese, Kathryn A.  
 ; REGISTRATION NUMBER: 32,172  
 ; REFERENCE/DOCKET NUMBER: 2614-A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 587-0430  
 ; TELEFAX: (206) 233-0644  
 ; TELEX: 756822  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2369 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 ; ORIGINAL SOURCE:  
 ; TISSUE TYPE: human placenta  
 ; IMMEDIATE SOURCE:  
 ; CLONE: B106/pDC303  
 ; FEATURE:  
 ; NAME/KEY: CDS

LOCATION: 244..2369  
FEATURE:  
NAME/KEY: mat..peptide  
LOCATION: 310..2369  
FEATURE:  
NAME/KEY: sig..peptide  
LOCATION: 244..309  
US-09-058-263-1

Query Match 4.0% Score 96.6; DB 2: Length 2369;  
Best Local Similarity 44.6%; Pred. No. 7.4e-20;

Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CGTACAACTCAGCGGCTGCGAGCTTTACAGAAATATGCTACCTGCGATGCGG 783  
DB 1091 CATTCACGTGTCAGAGCTTTAACTTTACAGAAATATGCTTTAGATGCTGTATGA 1150  
QY 784 TCAGAGAGTCAAG---TTCTGAGTGTAGTGTAGAGCCAGAAAGAAATGGAATGACTGAG 840  
DB 1151 AGGAAGATGTAGAGGATCTGAGTGTAGTGTAGAGCAAGTGTGATCACTGATG 1210  
QY 841 AAGAAGTGTGATGT---GGCTGGAAGTGTGAGAGTGTGAGTGTGAGTGTGAGTGTG 897  
DB 1211 AAGATAGACCATCTAAGCACCAGATTCTGTGTATTAATAGATCCATCCATCTCAAG 1270  
QY 898 GAAGAAGGCCAGAGTGGGCTGTGTATGAGAAAGCAAGAGAGAGCCAGTCTAGAGAAA 957  
DB 1271 GCTACAGAACTGTACAACTGCTGTGAGAGACATGCTCCCTTTGAGCCAAATGAGAAA 1330  
QY 958 CACTTGGCTACAACTATGTGTACTATCCAGAAAGCAACATCACTCAGAAACATGA 1017  
DB 1331 TCTTGGATTAAGAGTGTACTCTACAAAGATGAAATCACTTTACAAATTTACACAGTTA 1390  
QY 1018 ACACACTAATCAGAGAGCTTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077  
DB 1391 ATGCCACAAACTGA-----CAGTAAATCTCACAATAGATGCTATTTACAAACCTTAA 1444  
QY 1078 TTTCTTAATATCTCTTGGGAAGTCTCCAGTGGCCAGCCCTGAGATTTCCAGTATTTCAAG 1137  
DB 1445 CAGTAAAGAAATCTTGTGGCAATCAGATGACAGTGTTTAACTATCCCTGCTGCTGACT 1504  
QY 1138 AAAAATCTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197  
DB 1505 TTCAAGTGTACTGACCTGTATGATGATGATGATGATGATGATGATGATGATGATG 1564  
QY 1198 TGAAGTGTGCAAGGCTGTCTGTAGAGTGTGATGATGATGATGATGATGATGATGATG 1257  
DB 1565 TGGATGTGACTACTCCAGAGGATCTGTAAAGAAATATATCTGTAGTGTGTGTAT 1624  
QY 1258 TGGACTGAGAGCCAGCAGCCCTTCTGGAATCTGTGTCTCAGGCCAGAACTGAGCA 1317  
DB 1625 CAGATTAAGGACCCCTGTATCAGAGCTGCAACAAAGATGATGATGATGATGATG 1684  
QY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGTCTATACATCTGTGTATCCAAATGTC 1377  
DB 1685 ATTTAAGGAGAACTTTAGCAGAGCAATATCTATTTGATTAACAGTTACTCAGTATATG 1744  
QY 1378 ATGACAAAGTTGGGAGGACATATTCATCCAGGCTTATGCCAAGAGAGGCTTCCATAG 1437  
DB 1745 CTGATGTGACAGAGAGCCCTTAATTCATTAAGGCACTTAAACAGAGCTTCCACCTTCA 1804  
QY 1438 AAGTGTCTGAGACCAAGGTGAGAACATTTGCGTGAAGACGTCAGATCAATCAAGAAAG 1497  
DB 1805 AAGGACCTACTGTTGCGACAAAGAAAGTAAAGGAAAGAAAGGAGTGTCTTAAGTGGAG 1864  
QY 1498 AGATTCCAGAGTGTAGAGAAAGGTATCATCTGCACTACATCACTTTTACCAAGCTG 1557  
DB 1865 AACTTCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1924  
QY 1558 AAGGTGAAAGGATTTTCCAGAGCAATTCAGATTCAGATTCAGATTCAGATTCAGAT 1617  
DB 1925 TCATTGGAAATGAAGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATG 1984

QY 1618 CCTGAAGAGAAAGACCTCTTACATTTGTTCAGTGTATGCGCAGCAGCAGCAGCAGCAG 1677  
DB 1985 CTTTGACATGTGACACATTTGACATGTGACAAATGCGCAGATFACAGATATAGCTGGA 2044  
QY 1678 CCAAGGAGCAGCAGATTAATTTCAAGACATTTGATGATGATGATGATGATGATGATG 1737  
DB 2045 AGGATGTGTCAGAAATTCATCTTTACTACCCAAAGTTGTGCAAGAGAAATGAGCA 2104  
QY 1738 TAACCTCTGATGTGTGAGAGCCCTCTTATTCATATTCAGATGAGTGCATATGTC 1797  
DB 2105 TAGTGTGCTGCTGTGTGCTTACATTTCTATTGACAACTCTTCTGGAGTGTGTGCT 2164  
QY 1798 TCAAAAAACCAACAAATTTGATCATCTGTGTGAGCCAGCAGTGTGCAACCTGCTGAA 1857  
DB 2165 TTAATTAAGGAGACCTATTTAAAAACACATCTGTGCTTAATGTTCCAGATCTTCAAGA 2224  
QY 1858 GTAGTATAGCCATG 1874  
DB 2225 GTCATATGCCCCAGTGG 2241

## RESULT 4

US-09-059-099-1

Sequence 1, Application US/09059099

Patent No. 5925740

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

APPLICANT: Cosman, David J.

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059, 099

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/308, 881

FILING DATE: 12-SEP-1994

APPLICATION NUMBER: US 08/249, 553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 755822

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2369 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

TISSUE TYPE: human placenta

IMMEDIATE SOURCE:

CLONE: B10G/PC303



FEATURE: CDS  
NAME/KEY: 244..2369  
LOCATION: 244..2369  
FEATURE: mat-peptide  
NAME/KEY: 310..2369  
LOCATION: 310..2369  
FEATURE: sig-peptide  
NAME/KEY: 244..309  
LOCATION: 244..309  
US-09-059-099-1

Query Match 4.0%; Score 96.6; DB 2; Length 2369;  
Best Local Similarity 44.6%; Pred. No. 7.4e-20;  
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CGTACACCTGACGCGGCTGACGCGCTTTTACAGAAATGTCATGCTGCTGCGG 783  
DB 1091 CATTCTGCTGACGAGCTTAACCTTTTACAGAAATGCTTTAGGATTGCTGTATGA 1150  
QY 784 TCAAGAGTCAAG---TTCTGAGTACTGAGAGCCAGAAAAAATGGAAATGACTGAG 840  
DB 1151 AGGAGATGTAAGGATGACTGAGTGAAGTGAAGAGCAAGTGGATGACCTATG 1210  
QY 841 AAGAGCTCATGT---GGCTGGAAGTGTGAGAGTCTGAAACCACTGAGCGGATG 897  
DB 1211 AAGATGACCATCTTAAGCACCAGTTTCTGTATTAATAGATCCATCCATACCTAAG 1270  
QY 898 GAAGAGGCGAGTGGCTGTATGAGAGAGCAGAGGAGCCGCTCTAGAGAAA 957  
DB 1271 GCTACGAAAGTGTACACTGCTGTGTGAGAGCAATGCTCTTGAAGCAATGAGAAAA 1330  
QY 958 CACTTGGCTACAAATATGCTACTATCCAGAAAGCAACATACTCACAGAAACAATGA 1017  
DB 1331 TCTTGATTTATGAAGTACTCTCAAAAGATGAAATACATTTACAAATTAACAGTTA 1390  
QY 1018 ACCTCTTACACGAGCTTGAAGTCAATCTGGAGGCGAGAGCTTTGGGTCTATGA 1077  
DB 1391 ATGCCACAAACGA-----CAGTAAATCTCAAAATGATCCCTATCTAGCAACCTAA 1444  
QY 1078 TTTCTATATCTCTGGGAATCTCCAGTGGCCACCCGAGAGATTCACGATATTCAG 1137  
DB 1445 CAGTAAGAAATCTTGTGGCAATTCAGATGACCTGTTTAACTATCCCTGCTGTACT 1504  
QY 1138 AAAAATCAATTCAGTCAATGAGTCATGAGCGCTGCTGCTGAGAGCAGCTAGTGG 1197  
DB 1505 TTCAAGCTACTCACCCTGTAATGATCTTAAGCATTCGCCAAGTAATATCTTTGG 1364  
QY 1198 TGAAGTGGCAAGCTCTGCTCTAGAGCTGAACCTTGATGATGATGTTCCGGATG 1257  
DB 1565 TGGAAATGGAATCTCCAGGGAATCTGTAAGAAATATATCTGAGTGTGTGTAT 1624  
QY 1258 TGGACTCAGAGCCACACCTCTTCTGGGAATCTGTCTCAGGCGCAGCAATGAGCA 1317  
DB 1625 CAGATTAAGACCTCTATTCACAGACTGGCAACAAGATGTACCTGTCATCGACCT 1684  
QY 1318 TCCAGCAAGTAATTAACCTTTCTGTGCTATAACATCTGTGTATCAATGTTG 1377  
DB 1685 ATTTAGAGGGAATCTAGCAGAGAGCAATGCTATTGTAATAGTACTCCAGTATAG 1744  
QY 1378 ATGACAAAGTTGGCGGACCATATTCATCCAGCTTATGCCAAGAAGCGCTTCATAG 1437  
DB 1745 CTGATGACAGGAGACCTCTGATTAAGGCAATACCTTTAAACAAGCTCCACTTCA 1804  
QY 1438 AAGTCTGAGACCAAGGAGGAGATGCGCTGGAAGCGTCAAGATACATGGAAG 1497  
DB 1805 AAGGACCTACTGTTGGACAAAAAAGTGAAGAAAAAGGAGTGTCTTAGAGTGGACC 1864  
QY 1498 AGATTCACAGAGTGAAGAGGATATCATCTGCAACTACACATCTTTTACCAAGCTG 1557  
DB 1865 AACTTCTGTGATGTTCAAGATGATTTATCGAAATATTTATATTTTATAGAACCA 1924  
QY 1558 AAGTGAAGAAAGATTTCTCCAGACAGTCAATTCAGATCTTTCAGATGAGGCTGAGT 1617

DB 1925 TCATTGAAATGAAGTACTGTGAATGTGATTCCTCCACAGATAATACATTCCT 1984  
QY 1618 CCCTGAAGCAAGACCTCTTACATGCTTACAGTCAATGGCCAGCAGCTGGGGGA 1677  
DB 1985 CTTTGACTGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2044  
QY 1678 CCAAGGAGACACATTAATTTCAAGACATTTGATTCATGATGATGATGATGATGAT 1737  
DB 2045 AGATGCTCAGATTCATCTTACTACCCCAAGTTGCTCAAGAGAAATGAGGCCA 2104  
QY 1738 TAACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1797  
DB 2105 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2164  
QY 1798 TCAAAAACCCCAAAATGATCATCTGTGTGGCCACCCCTCCCAACCTGCTGAAA 1857  
DB 2165 TTATTAAGGAGAGCTTAATTAATAAACATCTGCTGCTTAATGTCAGATCTTCAAGA 2224  
QY 1858 GTAGTATAGCCACATG 1874  
DB 2225 GTCATATGCGCAGTGG 2241

RESULT 5  
US-09-058-264-1  
Sequence 1, Application US/09058264  
Patent No. 6010886  
GENERAL INFORMATION:  
APPLICANT: Mosley, Bruce  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: Receptor for Oncostatin M  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/058,264  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,881  
FILING DATE: 12-SEP-1994  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-A  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2369 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
TISUE TYPE: human placenta

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IMMEDIATE SOURCE:
CLONE: B10G/pdc303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-058-264-1

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Query Match      4.0%; Score 96.6; DB 3; Length 2369;
Best Local Similarity 44.6%; Pred. No. 7.4e-20;
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

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QY 724 CGTCAACCTGACGGGCTGACGCTTTTACAGAAATGTCATAGCTCTGCGATGCGGG 783
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Db 1091 CATTCACTGTCACAGACCTTAAACCTTTACAGAAATGTTGTAGGATTCGTGTATGA 1150
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 784 TCAGGAGTCAAG---TTCTGAGTACTGAGCCCAAGAAAATGGGATGACTGAG 840
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1151 AGGAGATGCTAAGGAGTACTGAGTACTGAGTGAAGAGCAAGTGGGATCACTATG 1210
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QY 841 AAGAGCTCATGT---GGCCTGGAAGTGAAGAGTCTGAACACAGCTGAGCGGATG 897
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1211 AAGTATAGACCATTAAGACCAACCAAGTTCTGTGTTAAATATGATCCATCTCAAG 1270
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QY 898 GAAGAGGCCAGTCGGCTGTTGTTATGAGAAAGCAAGAGAGCCAGTCTAGAGAAA 957
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Db 1271 GCTACAGACACTGTCAACTGCTGTGGAAGACATTCCTCTTTTGAAGCCAAATGAAAA 1330
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QY 958 CACTTGGCTACACATATGTGACTATCCAGAAACACACATACCTCAGAAACATGA 1017
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Db 1331 TCTTGGATTATGAGTACTCTCAAGATGGAATACATTTACAAATTTACACACTTA 1390
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QY 1018 ACACCTACTAACAGACAGCTTGAACTGATCGAGAGGCGAGAGCTTTGGGTCTATGA 1077
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Db 1391 ATGCCACAAAACCTGA-----CAGTAATCTCACAAATGATCGCTATCTGACACCTTA 1444
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QY 1078 TTTCTTTAATCTCTTGGGAAGTCTCAGTGGCCACCTGAGGATTCAGCTATTCAG 1137
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Db 1445 CAGTAAAGAAATCTTGGGCAAAATCAGATGAGTGTTTAACTATCCCTGCTGACT 1504
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QY 1138 AAAATATCTTCAGTCACTGATGAGTCAATGACAGCCCTGCTGAGAGACAGCTAGTG 1197
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Db 1505 TTCAAGCTACTCACCTCTGTATGATGATTTAAAGCATTCGCCAAGATTAACATGCTTGGG 1564
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QY 1198 TGAAGTGGCAAGCTCTGCTCTAGACGTGAACACTTGATGATGAATGGTTTCCGGATG 1257
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Db 1565 TGAATGTGACTACTCAAGGGAATCTGTAAAGAAATATTAATCTGAGTGGTGTGTAT 1624
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QY 1258 TGGACTAGAGCCACCACTTCTCTGGGAATGTGTCTCAGGCCACGAACGTGACGA 1317
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Db 1625 CAGATTAAGCAACCTGTATCACAACACTGGCAACAAAGATGTGATCGCATCGCACT 1684
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QY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGCTATACATCTCTGTATCCATATGTGC 1377
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Db 1685 ATTTAAGAGGAACTTATGACAGAGCAAAATGCTATTTGATTAACAGTTACTCCATATATG 1744
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QY 1378 ATGCAAAAGTTGGCGACCATATTCATCCAGGCTTATGCAAGAGGCGTTCATCAG 1437
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Db 1745 CTGATGACAGCAAGCCCTGAATCCATTAAGGATACCTTAAGCAAGATCCACCTTCCA 1804
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1438 AAGTCTCTGAGACCAAGGTGAGAAACATTTGGCGTGAAGACGCTACATCATGAGAA 1497
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1805 AAGGACCTTACTGTTCGACAAAAGTGAAGAAAAGCAAGCTGTCTTAGAGTGGAGCC 1864
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1498 AGATTTCCAGAGTGAAGAGGATCATCTGCACTACACCATTTTACCAACCTG 1557
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Db 1865 AACTTCTCTGTGATGTTCAAGAAATGATTTATCAGAAATTAATTTATATGAACCA 1924
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QY 1558 AAGTGGAAAAGATTCACAGACAGTCAATTCACAGATCTGACAGTGGCGTGGAGT 1617
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Db 1925 TCATTGGAATGAATGAAACCTGCTGATATGATGATTTCTTCCACACAGAAATATCATTTGCT 1984
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QY 1618 CCTTGAAGCAAGACCTTTACATTTGTCAGGTGATGCGCAGCAGCAGTCTGGGGAA 1677
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Db 1985 CTTTGACTAGTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2044
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QY 1678 CCAAGGAGCAGATTAATTTCAAGACATTTGATTCATTCAGTGTCTTTGAGATTTCTCA 1737
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Db 2045 AGGATGTGCGGAATTCATTTACTACCCCAAGATTTGCTCAAGAGAAATGAAGCCA 2104
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QY 1738 TAACCTCTGATTTGTTGAGAGGCGCTTCTTATTCATTTATCTGACAGTGGCATATGTC 1797
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Db 2105 TAGTGTGCGCTGTTTGTCTTACATTTCTATTTGACACACTTCTTGAGAGTGTCTTCTCT 2164
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1798 TCAAAAAACCAACAAATTCATCTGCTGTGGCCCAACCGTTCCCAACCTGCTGAAA 1857
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Db 2165 TTAATTAAGCAGACCTTAATTAATAAACACATCTGCGCTAATGTCTCAGATCTTCAAGA 2224
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1858 GTAGTATAGCCACATGG 1874
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 2225 GTCAATTTGCCAGTGG 2241
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

RESULT 6
US-09-455-962-1
Sequence 1, Application US/09455962
Patent No. 6524817
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,962
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,264
FILING DATE:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-May-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

```

	ORIGINAL SOURCE:	TISSUE TYPE:	human placenta
	IMMEDIATE SOURCE:		
	CLONE:	B10G/PDC303	
	FEATURE:		
	NAME/KEY:	CDS	
	LOCATION:	244..2369	
	FEATURE:		
	NAME/KEY:	mat.peptide	
	LOCATION:	310..2369	
	FEATURE:		
	NAME/KEY:	sig.peptide	
	LOCATION:	244..309	
	US-09-455-962-1		
Query Match	4.0%	Score 96.6:	DB 4: Length 2369:
Best Local Similarity	44.6%	Pred. No. 7.4e 20:	
Matches	516: Conservative	0: Mismatches 629: Indels	12: Gaps 3:
QY	724	CGTACCAACCTTCACGGGGCTGCAGCCCTTTTACAGATATGTCATAGCTCTGCGATGTCGG	783
Db	1091	CATTACAGTGTCCAGACACTTAACCTTTTACAGATATGTCATAGCTCTGCGATGTCGG	1150
QY	784	TCAAGAGTCAAG---TTCTGAGTGACTGTGGAGCCAAAGAAAATGGGAATGACTGAGG	840
Db	1151	AGGAAGATGTGAAGGAGTACTGGAGTGACTGGAGTGAAGGAAGCAAGTGGGATTCACCTATG	1210
QY	841	AAGAAGCTCCACTGT---GGCCTGGACGTGGAGAGTCTGAACCCACTGAGGCGGATG	897
Db	1211	AAGATTAGACCATCTTAAGACCAAGTTTCTGTATTAATATGATTCACATCTACTACAG	1270
QY	898	GAAGAAGGCCAGTGCGGTTGTTATGGAAGAAAGGAAGAGAGAGCCCACTCCTAGAGAAA	957
Db	1271	GCTACAGAACTGTCAACACTCGTGGAGAGACATTGCCCTCTTTGAAGCCAAATGGAAAA	1330
QY	958	CACTTGGCTCAACATATGATGACTATATCCAGAAAGCACACTAACCCTCACAGAAACATGA	1017
Db	1331	TCCTTGATTTATGAAGTGACTCTCAACAGATGGAATCACTTTACAAATTTACACAGTTA	1390
QY	1018	ACACTTACTAACACAGCAGCTTGAATGTCATCTGGAGGAGGAGAGAGCTTTGGGTGTCATGA	1077
Db	1391	ATGCCACAAAACCTGA-----CACTAATATCTCACAAATAGATCGCATCTACCAACCCCTAA	1444
QY	1078	TTTCTTATATTCCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCACAGCTATTCAG	1137
Db	1445	CAGTAAAGAAATCTGTTGGCAAAATCAGATGAGCGTGTTTTAACATACCTCCCTGCTGACT	1504
QY	1138	AAAATATCATTTTCAGTGCATTTGAGGTCATGACGACGAGGCGCTGGTCTGAGAGCACAGCTAGTG	1197
Db	1505	TTCAAGCTACTACCCCTGTATATGATCTTTAAGACATTTCCCAAGATTAACATGCTTTTGGG	1566
QY	1198	TGAAGTGGCAAGCTCTGCTCTAGACGTGAACACTTGGATGATGATGATTTCCGGATG	1257
Db	1565	TGGATGACTACTACCTCAAGGGAAATCTGAAGAAATATATATCTTGAGTGGTGTGTTAT	1624
QY	1258	TGGACTCGAGCCCAACCACTTCCTCGGGGAATCTGTCTCAGGCCACAGACTGGAGCA	1317
Db	1625	CAGATTAAAGCACCTCTGTATCAAGACTGGCAACAAAGAAAGATGTAACCTGTGATGCACT	1684
QY	1318	TCCAGCAAGATTAATTAACCTTTCTGCTCTTAACATCTCTGCTGATCCAAATGTTGC	1377
Db	1685	ATTTAAGAGGGAACTTACAGAGCAAGCAATGCTATTGATTAACGTTACTCCAGATATATG	1744
QY	1378	ATGACAAAGTTGGCGAGCATATTCATCCAGGCTTATGCCAAGAGAGGCGTTCCATCAG	1437
Db	1745	CTGATGGACCAAGGAAGCCCTGAATTCATAAAGGACATTAACCAACCTCCACCTTCCA	1804
QY	1438	AAGGTTCCGAGACCAAGCTGTGAGAAACATTTGGCTGTGAAGACGTACACATCATAGGAAG	1497
Db	1805	AAGGACCTACGTTTCGGACAAAATAAGTAAAGGAAAACGAAGCTGTCTTAAAGTGGAC	1866
QY	1498	AGATTCCCAAGAGTGAAGAAAGGGTATCATCTGCACATCAACATCTTTTACCAAGCTG	1557

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Db      1865  AACTTCCTGTTGATGTTACAGATGATTTATACAAATTTATACATATTTTATATGAAACA 1924
QY      1588  AAGGTGAAAAAGATTTCTCCAGACAGTCAATTTCCAGCATCTTGACAGTACGCCCTGAGT 1617
Db      1925  TCATTGGAAATGAAACATGCTGTGTGAATGTGGATTTCTCCACACAGAAATATACATTTGCT 1984
QY      1618  CCCGAAACGAAACACCTCTTACATTTGTTCAGGTCATTCAGGACGACGACGAGTGGGGGAA 1677
Db      1985  CTTTGACTAGTACACATTTGTACATTTGTAGCAATGCGACGATPACACAGATGAAAGTGGGA 2044
QY      1678  CCAACGGACAGCATTAATTTCAAGACATTTGTCATTCATTCAGTGTCTTTGAGATATTCCTCA 1737
Db      2045  AGAGTGTCCAGAAATTCACATTTTACTACCCCAAGTTTGGTCAGAGGAAATGAAACCA 2104
QY      1738  TAACTTCTGATTTGGTGGAGGCCCTTCTTATTCATTATTCATTCAGTGGCATATGTC 1797
Db      2105  TAGTCGTGCGCTGTTTGTCTTAGCATTTAGTACACATCTTCTTGAGAGTGTGTCTGCT 2164
QY      1798  TCAAAAAACCCACAAATTTGATCATTGTTGGTGGCCACCGTCCCAACCTGCTGAAA 1857
Db      2165  TTATTAAGCGAGACCTTATTTAAAAACACATCTGTGCCAATGTTCCAGATCTCTTAAGA 2224
QY      1858  GTAGTATAGCCACATGG 1874
Db      2225  GTCATATTGGCCCACTGG 2241

RESULT 7
PCT-US95-06530-1
: Sequence 1, Application PC/TUS9506530
: GENERAL INFORMATION:
: APPLICANT: Mosley, Bruce
: APPLICANT: Cosman, David J.
: TITLE OF INVENTION: Receptor for Oncostatin M
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/06530
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/308,881
: FILING DATE: 09-SEP-1994
: APPLICATION NUMBER: US 08/249,553
: FILING DATE: 26-MAY-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Anderson, Kathryn A.
: REGISTRATION NUMBER: 32,172
: REFERENCE/DOCKET NUMBER: 2614-WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 587-0430
: TELEFAX: (206) 233-0644
: TELEX: 756822
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2369 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO

```

FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
TISSUE TYPE: human placenta  
IMMEDIATE SOURCE:  
CLONE: B106/pDC303  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 244..2369  
FEATURE: mat.peptide  
NAME/KEY: 310..2369  
LOCATION: 310..2369  
FEATURE: sig.peptide  
NAME/KEY: 244..309  
LOCATION: 244..309  
PCT-US95-06530-1

Query Match 4.0%; Score 96.6; DB 5; Length 2369;  
Best Local Similarity 44.6%; Pred. No. 7.4e-20;  
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3:

QY 724 GGTACACCTCAGCGGCTGAGACCTTTTACAGATATGTCATACCTCTGGGATGGCG 783  
DB 1091 CATTCACGTCCAGACCTTTAACTTTTACAGATATGTTTGAATGCGCTGATGA 1150  
QY 784 TCAAGAGTCAAG--TTCTGAGTACTGAGCCAGAAAAAATGGGAATGACTGAG 840  
DB 1151 AGAAGATGTAAGGAGTACTGAGAGTGAAGCAAGTGGATCACCATTG 1210  
QY 841 AAGAAGCTCCATGT---GGCCTGAGACTGTGAGAGTCTGAACCACTGAGCGGATG 897  
DB 1211 AAGATAGACCATCTAAACCCAGATTCTGTATTAATAGATCCATCCATCTCAAG 1270  
QY 898 GAAGAGGCCAGTGGGTTGTTATGAGAAAGCAAGAGAGCCAGTCTAGAGAAA 957  
DB 1271 GCTACAGACGTACAACTCGTGTGAGAGACATTGCCCTTTGAGCCATGAAAAA 1330  
QY 958 CACTTGGCTACACATATGTAATGTAATCCAGAAACCACTACCTCAGAAACATGA 1017  
DB 1331 TCTTGATTAAGAACTGACTCTCAGAAAGTGAATCAATTTACAAATTAACAGTGA 1390  
QY 1018 ACACACTAACAGCAGCTTGAACTGATCTGGGAGGAGAGCTTTGGGTGCTGTATGA 1077  
DB 1391 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATGCGTATCTAGCAACCTAA 1444  
QY 1078 TTTCTTAATATCTCTTGGGAAGTCTCCAGTGGCCACCTGAGATTCACATTAATCAAG 1137  
DB 1445 CAGTAAGAAATCTTGTGGCAATCAGATGCAAGCTTTTAACATACCTCGCTGTGACT 1504  
QY 1138 AAAAATCTTTCAGTCAATGATGATGACAGCCCTGCTGCTGAGAGACCACTAGTGG 1197  
DB 1505 TTCAAGCTACACCTCTGTAATGATCTTAAGACATCCCAAGATTAACATGCTTTGGG 1564  
QY 1198 TGAAGTGCAGAAAGCTCTGCTAGACGTAACACTGATGATGAATGAATGTTCCGAGT 1257  
DB 1565 TGGATGAGACTACTCTCAAGGAATCTGTAAGAAATATATCTTGAGTGGTGTGTTAT 1624  
QY 1258 TGAAGTCAAGCCCAACCCCTTTCTGGGAATCTGTCTCAGGACCAAGTGGAGCA 1317  
DB 1625 CAGATTAAGCAACCGTATTCACAGACTGCAACAAGAGATGTAACCTGATGCACT 1684  
QY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGCTATACATCTCTGTATCAATGTTGC 1377  
DB 1685 ATTTAAGAGGAACTTACAGAGCAATATCTATTTGATTAACAGTTACTCAGATATG 1744  
QY 1378 ATGACAAAGTTGGGAGGCAATATCCATCCAGGCTTATGCCAAGAAAGCGTTCCATAG 1437  
DB 1745 CTGATGGACCAAGAGCCCTGAATCCATAAAGGCACTTAAACAACTCCACCTTCCA 1804  
QY 1438 AAGTCTCGAGACCAAGGTGGAACATTTGGCTGAAGACGTCACATCATGGAAG 1497  
DB 1805 AAGGACCTACTGTTGGACAAAAAAGTAGGAAAAAGAAAGAGCTGTCTTAAGTGGACC 1864  
QY 1498 AGATTCCCAAGAGTGAAGAAAGGATATCTGTCAACTACACATCTTTTACCAAGCTG 1557

DB 1865 AACTTCTGTGATGTTCAGAAATGATTTATCAGAAATTAATATATTTATATACCA 1924  
QY 1558 AAGTGAAGAAAGATTTCTCCAGACAGTCAATTCAGATCTTGGAGTACGCCCTGGAGT 1617  
DB 1925 TCATTGGAATGAAGAACTCTGTGATGATGATGATGATGATGATGATGATGATGAT 1984  
QY 1618 CCGTGAAGAAAGACCTCTTACATTTGTCAGGTGATGATGATGATGATGATGATGATGAT 1677  
DB 1985 CTTTGACTAGTACACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2044  
QY 1678 CCAAGGAGCAGCAGATTAATTTCAAGACATTTGTCAGTGTCTTTGAGATTAATCTCA 1737  
DB 2045 AGATGCTCCAGAAATTAATCTTTTACTACCCCAAGTTTGTCAAGAGAAATGAAGCA 2104  
QY 1738 TAACCTCTGATTTGTTGAGAGCCCTTCTTATTTCTATTTCTGACAGTGCATATGCTC 1797  
DB 2105 TAGTGTGCTGCTTTGCTTACATTTCTTACATTTCTTACATTTCTTACATTTCTTAC 2164  
QY 1798 TCAAAAAACCCCAAAATTTGATCTGCTGTGAGCCAGCCAGTCCCAACCTGCTGA 1857  
DB 2165 TTAATTAAGCAGACCTTAATTTAAAAACATCTGTGCTTAATTTTCCAGATCTTTCA 2224  
QY 1858 GTAGTATAGCCACATG 1874  
DB 2225 GTCATATTGCCAGTGG 2241

RESULT 8  
US-08-825-558-5  
Sequence 5, Application US/08825558  
Patent No. 5965724  
GENERAL INFORMATION:  
APPLICANT: SHARKEY, ANDREW  
APPLICANT: SMITH, STEPHEN K.  
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/825.558  
FILING DATE: 19-MAR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: ESMOND, ROBERT W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0623.0530001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2754 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2754  
US-08-825-558-5

Query Match 4.0%; Score 96.6; DB 2; Length 2754;  
 Best Local Similarity 44.6%; Pred. No. 8.1e-20;  
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CGTCAACCTGACGGGCTGCAGCCTTTTACAGAAATGTCATAGCTCTGCGATGCGG 783  
 DB 848 CATTCACTGTCACAGACCTTAACCTTTTACGAATATGTTTGGATTCGCTATGA 907  
 OY 784 TCAAGAGTCAAG---TTCTGAGTGTGAGTGCACCAAGAAAATGGAAATGACTGAG 840  
 DB 908 AGGAAGATGTGAAGGATACGTGAGTGTGAGTGAAGAGCAAGTGGATCCACTATG 967  
 OY 841 AAGAAGTCCATGT---GGCCTGGAAGTGTGAGAGTCTGGAACCAAGCTGAGCGGATG 897  
 DB 968 AAGATAGACCATTAAGACACAGTTTCTGTATTAATAATGATTCATCCATFCTCAAG 1027  
 OY 898 GAAGAAGCCAGTCCGGTGTGTATGGAAGAAGCAAGAGAGCCCACTCTAGAGAAA 957  
 DB 1028 GCTACAGACCTGTCAACACTCGTGTGGAAGACATTCCTCTTTTGAAGCCAAATGAAAA 1087  
 OY 958 CACTTGGCTCAACATATGTACTATCCAGAAAGCAACACTAACCTCACAAGAAACATGA 1017  
 DB 1088 TCTTGATATTAAGAGTACCTCTCACAAGATGGAATACATTTTCAAAATTTACACAGTTA 1147  
 OY 1018 AACTACTAACCAAGCTTGAACTGATGAGAGGAGAGAGCTTTTGGTGTCTATGA 1077  
 DB 1148 ATGCCACAAAACCTGA-----CAGTAATCTCACAAATGATCGCTATCTACCAACCTTA 1201  
 OY 1078 TTTCTTAAATCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCACCTATTCAG 1137  
 DB 1202 CAGTAAGAAATCTTGTGGCAAAATCAATGACAGCTGTTTAACTATCCCTGCTGCTACT 1261  
 OY 1138 AAAATCATTTTCAGTGAATGAGTCATGACAGGCTGTGTCGAGAGACCAAGTATGAG 1197  
 DB 1262 TTCAAGCTACTACCCCTGTATGATCTTTAAAGCATTCCTCCAAAGATTAACATGCTTGGG 1321  
 OY 1198 TGAAGTGGCAAGGCTGTGCTCTAGACGTGAACACTTGGATGATGAATGGTTCCGAGATG 1257  
 DB 1322 TGAATGAGTACTATCCAAAGGAAATCTGTAAGAAATATATCTTGAAGGTGTGTAT 1381  
 OY 1258 TGAAGTCAAGAGCCCAACCTTTCTGGAATCTGTCTCAGAGCCACGAACTGAGCA 1317  
 DB 1382 CAGATTAAGGACCCCTGTATCAGACGTGGCAACAAAGATGATCCCTGATGCACT 1441  
 OY 1318 TCCAGCAAGATTAATTAACCTTTCTGCTGTATACATCTGTGTATCCAAATGTGC 1377  
 DB 1442 ATTTAAGAGGAACTTAGCAGAGCAAAATCTTATGATTAACAGTTACTCCAGATATG 1501  
 OY 1378 ATGACAAAGTTGGAGGACCATTTCCATCCAGGCTTATGCCAAGAAAGGCGTTCATCAG 1437  
 DB 1502 CTGATGAGCCAGAAAGCCCTGAATCCAAAGCATACCTTAACCAAGCTCCACCTTCCA 1561  
 OY 1438 AAGTCTCTGAGACCAAGTGTGAACATTTGGCTGTGAAGACGGTCAACATCATGGAAG 1497  
 DB 1562 AAGGACCTACTGTGCGCAAAAAGAGGAAAAAGAGAGCTGTCTTAAGTGGGACC 1621  
 OY 1498 AGATTCGCAAGAGTGAAGAAAGGTATCATCTGCAATACATCATCTTTACCAAGCTG 1557  
 DB 1622 AACTTCTCTGTGATGTTTACAGATGATTTATCAGAAATTAATATATATTTATGAACCA 1681  
 OY 1558 AAGTGTGAAGAAAGATTTCTCAAGACAGTCAATTCAGCATTTTCAGTACGCGCTGAGT 1617  
 DB 1682 TCATTTGGAATGAAGATGCTGTGATGTGATTTCTTCCACACAGAAATATACATTTGTCT 1741  
 OY 1618 CCCGTAAGCAAGAAAGCTTTACATTTGTCAGTCAATGCGCAACAGCAAGTCTGGGGAA 1677  
 DB 1742 CTTTGACTAGTGAACATTTGTCATGTGTACATGTGAGCAATGGCAATACAGATTAAGTGGGA 1801  
 OY 1678 CCAAGGAGCAGCAGATTAATTTCAAGACATGTCTATGAGTGTCTTGAATATTCCTCA 1737  
 DB 1802 AGGATGTGCAAGATTCATCTTTTACACCCCAAGTTGCTCAAGAGAAATTTGAAGCCA 1861  
 OY 1738 TAACTCTCTGATTTGTGGAGGCTTCTTATTTCTATATTCCTGACAGTGCATATAGTCT 1797

DB 1862 TAGTCGTGCTGTTGCTTAGCATTTCCATAGACAACTCTTCGGAGTGTGTTCTGCT 1921  
 OY 1798 TCAAAAAACCAACAAATTTGATCTATGTGTGGCCACCGCTTCCCAACCTCTGAAA 1857  
 DB 1922 TTAATTAAGCGAGACCTTAATTAATAACATCTGCGCTAATGTTTCCAGATCTTTCAAGA 1981  
 OY 1858 GTAGTATAGCCACATGG 1874  
 DB 1982 GTCATATTTGCCCACTGG 1998

RESULT 9  
 us-09-312-611-5  
 ; Sequence 5, Application US/09312611  
 ; Patent No. 6380160  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHARKEY, ANDREW  
 ; APPLICANT: SMITH, STEPHEN K.  
 ; APPLICANT: DELLOW, KIMBERLEY A.  
 ; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
 ; STREET: 1100 NEW YORK AVENUE  
 ; CITY: WASHINGTON  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/312.611  
 ; FILING DATE: 17-MAY-1999  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: ESMOND, ROBERT W.  
 ; REGISTRATION NUMBER: 32,893  
 ; REFERENCE/DOCKET NUMBER: 0623.0530002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)371-2600  
 ; TELEFAX: (202)371-2540  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2754 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..2754  
 ; us-09-312-611-5

Query Match 4.0%; Score 96.6; DB 4; Length 2754;  
 Best Local Similarity 44.6%; Pred. No. 8.1e-20;  
 Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;

QY 724 CGTCAACCTGACGGGCTGCAGCCTTTTACAGAAATGTCATAGCTCTGCGATGCGG 783  
 DB 848 CATTCACTGTCACAGACCTTAACCTTTTACGAATATGTTTGGATTCGCTATGA 907  
 OY 784 TCAAGAGTCAAG---TTCTGAGTGTGAGTGCACCAAGAAAATGGAAATGACTGAG 840  
 DB 908 AGGAAGATGTGAAGGATACGTGAGTGTGAGTGAAGAGCAAGTGGATCCACTATG 967  
 OY 841 AAGAAGTCCATGT---GGCCTGGAAGTGTGAGAGTCTGGAACCAAGCTGAGCGGATG 897  
 DB 968 AAGATAGACCATTAAGACACAGTTTCTGTATTAATAATGATTCATCCATFCTCAAG 1027

QY 898 GAAGAGGCCAGTGGCTTTGATGGAAGAGGAGAGGAGCCCACTCTAGAGAAA 957  
DB 1028 GCTACAGAACTGTACAACTCGTGTGGAAGACATTCGCCCTTTGAAACCAATGGAATA 1087  
QY 958 CACTTGGCTACACATATGTACTATCAGAAAGCACACTTAACCTCAGAAACAATGA 1017  
DB 1088 TCTTGATTAAGAGTGCATCTCACAGATGGAATGCAATTTACAAATTAACACAGTTA 1147  
QY 1018 ACATTAACACAGAGCTTGAAGTGCATCTGGAGGAGAGGAGCTTTGGTGTATGA 1077  
DB 1148 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATCGCTATGTACCAACCTTAA 1201  
QY 1078 TTTCTTAATATCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGATTCACCTATTCAAG 1137  
DB 1202 CAGTAAGAAATCTTGTGGCAATTCAGATGCAGCTGTTTAACTAATCCCTCGTGTACT 1261  
QY 1138 AAAATATCTTCACTGCTTGAAGTGCATGACAGGCTGCTGTGAGAGACCACTAGTGG 1197  
DB 1262 TTCAAGCTACTACCCCTGTATGATCTTAAAGCATTCGCCCAAGATTAACATGCTTGGG 1321  
QY 1198 TGAAGTGCAAAAGCTCTGCTAGACGTGAACACTGTGATGATGAATGGTTCCGGATG 1257  
DB 1322 TGGATGACACTACTCCAAAGGAATCTGAAGAAATATATCTTGAAGTGTCTGTAT 1381  
QY 1258 TGAAGTGAAGCCCAACCCCTTCTGGAATCTGTCTCAGGCGCAGAACTGGAGCA 1317  
DB 1382 CAGATTAAGACCCCTGTATCAGACAGCTGGCAAGAAAGATGATGATGATGATGATG 1441  
QY 1318 TCCAGCAAGATTAATTAACCTTCTGTGTCTATACATCTCTGTGTATCCATGTTC 1377  
DB 1442 ATTTAAGGGGAACTTGAAGCAAGCAATCTTATGATTAACAGTTACTCCATATATG 1501  
QY 1378 ATGACAAAGTTGGGAGGAGCAATCTCAATCCAGCTTATGCCAAAGAGGCTTCATCAG 1437  
DB 1502 CTGATGAGACCAAGAGCCCTTAATCCATTAAGGCATACCTTAACAGAGCTCACCTTCA 1561  
QY 1438 AAGTCTGAGACCAAGGTGAGAACATTTGGCTGAAGACGCTCAGATCATGGAAG 1497  
DB 1562 AAGACCTACTGTGCGCAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1621  
QY 1498 AGATTTCCAAAGTGAAGAGGATTCATCTGCACACTACACATCTTTTACCAAGTGT 1557  
DB 1622 AACTTCTGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1681  
QY 1558 AAGTGAAGAAAGATTTCTCAAGACAGTCAATTCAGATCTTCCAGTACGCTGAGT 1617  
DB 1682 TCATTTGAAGATGAAGTGTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1741  
QY 1618 CCTGAAGACGAAGACCTTTACATTTGTCAGTGTGATGAGGAGGAGGAGGAGGAG 1677  
DB 1742 CTGTGACTAGTGAACATTTGATGATGATGATGATGATGATGATGATGATGATG 1801  
QY 1678 CCAAGGAGGAGGAGGAGGATTTCAAGACATTTGATGATGATGATGATGATGATG 1737  
DB 1802 AGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1861  
QY 1738 TAACTTCTGATGTGTGAGGAGGCTTTTATTTCAATTAATGATGATGATGATGATG 1797  
DB 1862 TAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1921  
QY 1798 TCAAAAAACCAACAAATTTGATGATGATGATGATGATGATGATGATGATGATG 1857  
DB 1922 TTAATTAAGGAGGAGGATTTAAAGAACATCTGAGGCTTAATGATGATGATGATG 1981  
QY 1858 GTAGTATAGCCACATGG 1874  
DB 1982 GTCAATTTGCCAGTGG 1998

RESULT 10  
US-08-795-473B-4  
Sequence 4, Application US/08795473B  
Patent No. 6217858

GENERAL INFORMATION:  
APPLICANT: Galun, Eithan  
APPLICANT: Nahot, Orit  
APPLICANT: Blum, Herbert E.  
TITLE OF INVENTION: A Pharmaceutical Composition for Treating  
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Davidson, Davidson and Kappel, LLC  
STREET: 1140 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS EDITOR  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795.473B  
FILING DATE: 11-FEB-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Davidson, Clifford M.  
REGISTRATION NUMBER: 32,728  
REFERENCE/DOCKET NUMBER: 963.1007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)-997-1028  
TELEFAX: (212)-997-1037  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-08-795-473B-4  
Query Match 4.0%; Score 96.6; DB 3; Length 3085;  
Best Local Similarity 44.6%; Pred. No. 8.7e-20;  
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;  
QY 724 GGTACAACTCAGCGGCTGCGAGCTTTTACAGATATGATGATGATGATGATGATG 783  
DB 1103 CATTCACGTGTCAGACACTTAACCTTTACAGATATGATGATGATGATGATGATG 1162  
QY 784 TCAAGGATCAAG---TTCTGAGTACTGTGAGGAGGAGGAGGAGGAGGAGGAGG 840  
DB 1163 AGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1222  
QY 841 AAGAAGCTCCATGT---GGCTGGAAGTGTGAGAGTCTTGAACCAAGCTGAGCGGATG 897  
DB 1223 AAGATAGACCTCTTAAGGACCAAGTTTGTGTATTAATATGATGATGATGATGATG 1282  
QY 898 GAAGAGGCCAGTGGCTTTTATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 957  
DB 1283 GCTACAGAACTGTCAACTCGTGTGAAAGACATTTGCTTTTGAAGCCAAATGAAAA 1342  
QY 958 CACTTGGCTACACATATGTACTATCCAGAAACCAACACTTAACCTCAGAAACAATGA 1017  
DB 1343 TCTTGATTAAGAGTGCATCTCACAGATGGAATGCAATTTAAATTAACACAGTTA 1402  
QY 1018 ACATTAACACAGAGCTTGAAGTGCATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1077  
DB 1403 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATGATGATGATGATGATG 1456  
QY 1078 TTTCTTAATATCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCAGATTTCAAG 1137  
DB 1457 CAGTAAGAAATCTTGTGGCAATTCAGATGATGATGATGATGATGATGATGATGATG 1516  
QY 1138 AAAATATCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197  
DB 1517 TTCAAGCTACTACCCCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1576

QY 1198 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1257  
1198 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1257  
DB 1577 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1636  
1577 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1636  
QY 1258 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1317  
1258 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1317  
DB 1637 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1636  
1637 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1636  
QY 1318 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1377  
1318 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1377  
DB 1697 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1756  
1697 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1756  
QY 1378 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1437  
1378 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1437  
DB 1757 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1816  
1757 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1816  
QY 1438 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1497  
1438 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1497  
DB 1817 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1876  
1817 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1876  
QY 1498 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1557  
1498 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1557  
DB 1877 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1936  
1877 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1936  
QY 1558 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1617  
1558 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1617  
DB 1937 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1996  
1937 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1996  
QY 1618 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1677  
1618 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1677  
DB 1997 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2056  
1997 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2056  
QY 1678 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1737  
1678 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1737  
DB 2057 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2116  
2057 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2116  
QY 1738 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1797  
1738 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1797  
DB 2117 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2176  
2117 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2176  
QY 1798 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1857  
1798 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1857  
DB 2177 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2236  
2177 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2236  
QY 1858 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1874  
1858 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1874  
DB 2237 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2253  
2237 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 2253

RESULT 11  
US-09-439-856-4  
Sequence 4, Application US/09439856  
Patent No. 6410009  
GENERAL INFORMATION:  
APPLICANT: Galun, Eithan  
APPLICANT: Nahot, Orit  
APPLICANT: Blum, Herbert E.  
TITLE OF INVENTION: A Pharmaceutical Composition for Treating  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Davidson, Davidson and Kappel, LLC  
STREET: 1140 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS-DOS EDITOR

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/439,856  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/795,473  
FILING DATE: 11-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Davidson, Clifford M.  
REGISTRATION NUMBER: 32,728  
REFERENCE/DOCKET NUMBER: 963,1007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)-997-1037  
TELEFAX: (212)-997-1037  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3085 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-09-439-856-4  
Query Match 4.0%; Score 96.6; DB 4; Length 3085;  
Best Local Similarity 44.6%; Pred. No. 8.7e-20;  
Matches 516; Conservative 0; Mismatches 629; Indels 12; Gaps 3;  
QY 724 CGTACACCTGACGAGGCTGACGCTTTTACAGATATGTCATGCTGCGATGCGG 783  
724 CGTACACCTGACGAGGCTGACGCTTTTACAGATATGTCATGCTGCGATGCGG 783  
DB 1103 CATTGCTGCTCAAGACCTTAAACCTTTTACAGATATGTTAGATTCGTGTATGA 1162  
1103 CATTGCTGCTCAAGACCTTAAACCTTTTACAGATATGTTAGATTCGTGTATGA 1162  
QY 784 TCAAGAGTCAAG---TTGAGAGTACAGGACCAAGAAATGAGATGACTGAG 840  
784 TCAAGAGTCAAG---TTGAGAGTACAGGACCAAGAAATGAGATGACTGAG 840  
DB 1163 AGGAAGATGTAAGAGATACAGAGTACAGTACAGTGAAGAAAGCAAGTGCATCATG 1222  
1163 AGGAAGATGTAAGAGATACAGAGTACAGTACAGTGAAGAAAGCAAGTGCATCATG 1222  
QY 841 AAGAGCTCATGT---GGCTGAGACTGAGAGATCTGGAACACAGCTGAGCGGATG 897  
841 AAGAGCTCATGT---GGCTGAGACTGAGAGATCTGGAACACAGCTGAGCGGATG 897  
DB 1223 AAGATAGACCATTAAGACCAAGTTTCTGTATTAAGATGATCCATCCATCTCAAG 1282  
1223 AAGATAGACCATTAAGACCAAGTTTCTGTATTAAGATGATCCATCCATCTCAAG 1282  
QY 898 GAAAGAGCGAGTGGGTGTTATGGAAGAGCAAGAGAGAGCCGCTAGAGAAA 957  
898 GAAAGAGCGAGTGGGTGTTATGGAAGAGCAAGAGAGAGCCGCTAGAGAAA 957  
DB 1283 GCTACAGAGCTGACACTGCTGTGGAAGACATTCCTCTTTGAGACCAATGAGAAA 1342  
1283 GCTACAGAGCTGACACTGCTGTGGAAGACATTCCTCTTTGAGACCAATGAGAAA 1342  
QY 958 CACTTGCTACACATATGACTATCCAGAAAGCAACACTAACCTCAGAAACATGA 1017  
958 CACTTGCTACACATATGACTATCCAGAAAGCAACACTAACCTCAGAAACATGA 1017  
DB 1343 TCTTGATATGAGAGTGCCTCTCAGAGATGGAATCATCTTACAAATATACACAGTTA 1402  
1343 TCTTGATATGAGAGTGCCTCTCAGAGATGGAATCATCTTACAAATATACACAGTTA 1402  
QY 1018 ACAGTACTAACAGAGCTTGAAGTCACTGAGAGCGAGAGCTTTTGGTGTATGA 1077  
1018 ACAGTACTAACAGAGCTTGAAGTCACTGAGAGCGAGAGCTTTTGGTGTATGA 1077  
DB 1403 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATCGCTATCTACCAACCCYAA 1456  
1403 ATGCCACAAACTGA-----CAGTAATCTCACAAATGATCGCTATCTACCAACCCYAA 1456  
QY 1078 TTTCTATATCTCTTGGAAGTCTCCAGTGGCCACCCCTGAGATTCACATTCAGAG 1137  
1078 TTTCTATATCTCTTGGAAGTCTCCAGTGGCCACCCCTGAGATTCACATTCAGAG 1137  
DB 1457 CAGTAAAGATCTTGTGGCAAAATGAGTGAAGCTGTTTAACTATCTCTGCTGACT 1516  
1457 CAGTAAAGATCTTGTGGCAAAATGAGTGAAGCTGTTTAACTATCTCTGCTGACT 1516  
QY 1138 AAAATCATTTGAGTCAATGAGTCACTGAGGCTGCTGCTGAGAGCAGCTAGTG 1197  
1138 AAAATCATTTGAGTCAATGAGTCACTGAGGCTGCTGCTGAGAGCAGCTAGTG 1197  
DB 1517 TTCAAGTACTACACCTGCTATGATCTTAAAGATCTTCCCAAGATTAACATGCTTGGG 1576  
1517 TTCAAGTACTACACCTGCTATGATCTTAAAGATCTTCCCAAGATTAACATGCTTGGG 1576  
QY 1198 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1257  
1198 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1257  
DB 1577 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1636  
1577 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1636  
QY 1258 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1317  
1258 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1317  
DB 1637 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1696  
1637 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1696  
QY 1318 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1377  
1318 TGAAGTGCAGAACGCTCTGCTCTAGACGTGAACACTTGATGATGAATGTTCCGATG 1377  
DB 1697 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1756  
1697 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1756  
QY 1757 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1816  
1757 TGAATGAGTACTCTCCAGGAAATCTGTAAAGAAATATATCTGAGGGGTGTGTAT 1816

1438 AAGTCTGAGACCAAGGTGAGACATTTGGCGTGAGACGTCACATCATGTGAAG 1497  
1817 AAGGACCTACTGTTGCGACAAAAAAGTAGGAAAAAGAACGCTCTTAGAGTGGACC 1876  
1498 AGATTCCCAAGAGTGAAGAAAGGTATCATCTGCACTACACATCTTTTACCAAGCTG 1557  
1877 AACTTCCTGTTGATGATTCAGATGATTTATCAGAAATTTATCTATTTTATAGACCA 1936  
1558 AAGGTGAAAAGATTTCTTCAAGACATTCACAGATCTTGGAGTGGCCGAGT 1617  
1937 TCATTGAAATGAATCTGCTGTAATGATGATCTTCCACACAGAAATATCATTTGCT 1996  
1618 CCCTGAAAGAAAGACCTCTTACATTTTCAAGTATGATGATGATGATGATGATGAT 1677  
1997 CTTTACATGATGACATTTGATGATGATGATGATGATGATGATGATGATGATGAT 2056  
1678 CCACGGGACGACATTAATTTCAAGACATTTGATGATGATGATGATGATGATGAT 1737  
2057 AGGATGCTCAGAAATTCATCTTTACTACCCCAAGTCTTCAAGAGAAATTTGAAGCA 2116  
1728 TAACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1797  
2117 TAGTCGCTGCTGTTGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 2176  
1798 TCAGAAAGACCAACAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1857  
2177 TTAATGAAGGAGACCTAATTAAGAAACATCTGCTTATGATGATGATGATGATGATGAT 2236  
1858 GTAGATATGACCATG 1874  
2237 GTCAATATGCGCCAGTGG 2253

## RESULT 12

US-08-825-558-3  
Sequence 3, Application US/08825558  
Patent No. 5965724

## GENERAL INFORMATION:

APPLICANT: SHARKEY, ANDREW  
APPLICANT: SMITH, STEPHEN K.  
APPLICANT: DELLOW, KIMBERLEY A.  
TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA

ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/825.558  
FILING DATE: 19-MAR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.  
REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0623,0530001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2600

TELEFAX: (202)371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1977 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1974  
US-08-825-558-3

Query Match 3.2%; Score 76.4; DB 2; Length 1977;  
Best Local Similarity 44.5%; Pred. No. 1.6e-13;  
Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

724 CGTACACCTACGGGCTGACGCTTTTACAGATATGATGATGATGATGATGATGAT 783  
848 CATTCACTCCCAAGACCTTAACCTTTTACAGATATGATGATGATGATGATGATGAT 907  
784 TCAGGAGTCAAG---TTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 840  
908 AGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967  
841 AAGAAGTCCATGT---GGCTGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 897  
968 AAGATGACATCTTAACGACCAAGTTTCTGATATAAATAGATCCATCCATCTCAAG 1027  
898 GAGACGCGCAGTGGCTTTTATGAGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 957  
1028 GCTACAGAACTGTACACCTGCTGTGAGAGAGATTCCTCTTTGGAAGCCATGGA 1087  
958 CACTGCTTACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017  
1088 TCTTGATTTATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1147  
1018 ACATCTATACAGACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1077  
1148 ATGCCACAA-----AATGACAGTAATCTACAAATGATGATGATGATGATGATGAT 1201  
1078 TTTCTTAATATTTCTTGGGAAAGTCCAGTGGCCACCTGAGATTTCCACTATTCAG 1137  
1202 CAGTAAAGAAATCTTGTGCAAAATCAGATGAGAGCTGTTTAACTATCCCTGCTGACT 1261  
1138 AAAATCATTTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1197  
1262 TTCAAGCTACTACCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321  
1198 TGAAGTGCAAGCTCTGCTTGAAGTGAACACTTGGATGATGATGATGATGATGATGAT 1257  
1322 TGAATGACATCTCAAGGAGAACTGTAAGAAATATATCTGAGTGTGATGAT 1381  
1258 TGAATGACACCCACACCTCTTCTGAGATGATGATGATGATGATGATGATGATGATGAT 1317  
1382 CAGATAAAGCACCTGTATCAAGACAGTGGCAAGAGATGATGATGATGATGATGATGAT 1441  
1318 TCAGCAGATTAATTAACCTTTTCTGCTTATGATGATGATGATGATGATGATGATGAT 1377  
1442 ATTTAAGAGGAGACTTACAGAGCAATGCTATTTGATTAAGATTTCTCCAGTATGAT 1501  
1378 ATGACAAAGTTGGCGAGGCAATTTCCATCCAGCTTATGCCAAGAGGCTTCCATCAG 1437  
1502 CTGATGACACGAGAGCCCTGAATCCATAAGGATACCTTAACCAAGCTCCACCTCCA 1561  
1438 AAGTCTGACACCAAGTGGAGAAATTTGGCGTGAACAGGTGACGATCAGATCAGTGAAG 1497  
1562 AAGGACCTACTGTTGCGCAAAAAAAGTAGGAAAAAGGAGGCTCTTAGAGTGGGCC 1621  
1498 AGATTCACAGAGTGAAGAAAGGTATCATCTGCAATCAACATCTTTTACCAAGCTG 1557  
1622 AACTTCCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1681  
1558 AAGGTGAAAAGATTTCTTCAAGACAGTCAATTCAGCATCTTCCAGTACGCGCTGAGT 1617  
1682 TCATTGAAATGAATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1741  
1618 CCCTGAAAGCAAGACCTTTTACATTTTCAAGTGTGATGATGATGATGATGATGATGAT 1677  
1742 CTTGACTAGTGAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1801



QY 1678 CCAAGGAGACCATTAATTTCAGAC 1705  
| | | | | | | | | | | | | | | | | |  
Db 1802 AGGATGGTCCAGATTTCATTCTAC 1829

## RESULT 13

US-09-312-611-3  
Sequence 3, Application US/09312611  
Patent No. 6380160

## GENERAL INFORMATION:

APPLICANT: SHARKEY, ANDREW  
APPLICANT: SMITH, STEPHEN K.  
APPLICANT: DELLOW, KIMBERLEY A.  
TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA

ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/312,611  
FILING DATE: 17-MAY-1999  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0623-0530002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2540  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1977 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1974  
US-09-312-611-3

Query Match 3.2%; Score 76.4; DB 4; Length 1977;  
Best Local Similarity 44.5%; Pred. No. 1.6e-13;  
Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

QY 724 CGTACACCTCAGCGGCTCAGCCCTTTACAGAAATGTCATGCTCTGGAGTGGCGG 783  
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Db 848 CATTCAGCTGCCAAGACTTAACCTTTTACAGAAATGTCATGCTCTGGAGTGGCGG 907  
| | | | | | | | | | | | | | | | | |  
QY 784 TCAAGAGTCAAG--TTCTGAGTGTGAGGACCAAGAAAAAATGGGAATGACTGAG 840  
| | | | | | | | | | | | | | | | | |  
Db 908 AGGAAGATGTAGGATGACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 967  
| | | | | | | | | | | | | | | | | |  
QY 841 AAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 897  
| | | | | | | | | | | | | | | | | |  
Db 968 AAGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1027  
| | | | | | | | | | | | | | | | | |  
QY 898 GAAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 957  
| | | | | | | | | | | | | | | | | |  
Db 1028 GCTACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1087  
| | | | | | | | | | | | | | | | | |  
QY 958 CACTTGGCTACCAATATGCTATCTATCTCAGAAAGCAACACTTACCTCAGAGAAACAATGA 1017  
| | | | | | | | | | | | | | | | | |

Db 1088 TCTTGATATGAAGTACTCTCAGAGATGAAATACATTTACAAATTTACAGATTA 1147  
| | | | | | | | | | | | | | | | | |  
QY 1018 ACCTACTAACAGACACTTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1077  
| | | | | | | | | | | | | | | | | |  
Db 1148 ATGCCACAA-----AACTGACAGTAATCTCAGAAATGCTTACTGACCAACCTTAA 1201  
| | | | | | | | | | | | | | | | | |  
QY 1078 TTTCTTATATCTCTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1137  
| | | | | | | | | | | | | | | | | |  
Db 1202 CAGTAAAGAAATCTTGTGCAAAATCAGATCAGCTGTTTAACTATCTCTGCTGCTGACT 1261  
| | | | | | | | | | | | | | | | | |  
QY 1138 AAAAATCATTTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1197  
| | | | | | | | | | | | | | | | | |  
Db 1262 TTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1321  
| | | | | | | | | | | | | | | | | |  
QY 1198 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1257  
| | | | | | | | | | | | | | | | | |  
Db 1322 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1381  
| | | | | | | | | | | | | | | | | |  
QY 1258 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1317  
| | | | | | | | | | | | | | | | | |  
Db 1382 CAGTAAAGAAATCTTGTGCAAAATCAGATCAGCTGTTTAACTATCTCTGCTGCTGACT 1441  
| | | | | | | | | | | | | | | | | |  
QY 1318 TCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1377  
| | | | | | | | | | | | | | | | | |  
Db 1442 ATTAAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1501  
| | | | | | | | | | | | | | | | | |  
QY 1378 ATGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1437  
| | | | | | | | | | | | | | | | | |  
Db 1502 CTGATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1561  
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QY 1438 AAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1497  
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Db 1562 AAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1621  
| | | | | | | | | | | | | | | | | |  
QY 1498 AGATTTCCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1557  
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Db 1622 AACTTCTGTGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1681  
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QY 1558 AAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1617  
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Db 1682 TCATTGGAATGAAATGCTGTGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1741  
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QY 1618 CCCTGAAAGCAAGACCTTTACATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1677  
| | | | | | | | | | | | | | | | | |  
Db 1742 CTTGACTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1801  
| | | | | | | | | | | | | | | | | |  
QY 1678 CCAAGGAGACCATTAATTTCAGAGC 1705  
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Db 1802 AGGATGGTCCAGATTTCATTCTAC 1829

## RESULT 14

US-09-313-942-25  
Sequence 25, Application US/09313942  
Patent No. 6472179

## GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.  
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
FILE REFERENCE: REG 2003-A  
CURRENT APPLICATION NUMBER: US/09/313,942  
CURRENT FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: 09/313,942  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: 60/101,858  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 25  
LENGTH: 3477  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: CDS  
LOCATION: (1)...(3474)  
US-09-313-942-25

Query Match 3.2%; Score 76.4; DB 4; Length 3477;  
Best Local Similarity 44.5%; Pred. No. 2.3e-13;

Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

QY 724 CGTACAACTTCACGGGCTGCAGCCTTTTACAGATATGTCATAGCTGCTGCGATGCGG 783  
DB 1775 CATTCACTGTCACAGACCTTAACCTTTTACAGATATGTCATAGCTGCTGCGATGCGG 1834  
QY 784 TCAAGAGTCAAG---TTCTGAGTACGCTGAGCCAGAAAATGGGAATGACTGAG 840  
DB 1835 AGGAAGTGTGAAGGATGACTGAGTCACTGAGTGAAGCAAGTGGGATCACTATG 1894  
QY 841 AAGAAGTCCATGT---GGCCTGAGACTGTGAGAGTCCCTAACCAGCTAGGCGATG 897  
DB 1895 AAGATTAGACCATTAAGCCACCAAGTTTGTGTAAATATGATCCATCCATCTCAG 1954  
QY 898 GAAGAAGGCCAGTCCGCTTTGTATGAGAAGCAAGCAAGGAGCCAGCTCTAGAGAAA 957  
DB 1955 GCTACAGACTGTCAACTGCTGTGGAAGACATTCCTCTTTGGAAGCCATGGAAAA 2014  
QY 958 CACTTGGCTACACATATGCTATCCAGAACCAACTACCTACAGAAACATGA 1017  
DB 2015 TCTTGATTTATGAGTACTCTCACAAGATGAATCACAATTTACAAATTCACAGTTA 2074  
QY 1018 ACATCTACACACAGCTTGAATGATCTGAGGAGGAGAGCTTTGGTGTCTATGA 1077  
DB 2075 ATGCCACAA-----AACTGACATTAATCTCACAATATGATCGCTATACCAACCTAA 2128  
QY 1078 TTTCTTAATTTCTTGGGAGTCTCCAGTCCAGCCCTGAGATTCACAGCTATTCAG 1137  
DB 2129 CAGTAAGAATCTTGTGGCAATCAGATGAGCTGTTTATCAATCCCTGCTGACT 2188  
QY 1138 AAAAATATTTCACTGATGAGTCAATGACGCGCTGCTGAGAGACCACTAGTG 1197  
DB 2189 TTCAAGTACTCCCTGTATGATGATCTTAAAGCATTCCTCCCAAGATTAACATGCTTTGGG 2248  
QY 1198 TGAAGTGGCAAGCTGTGCTTAGAGTGAACACTTGGATGATGATGATGCTTCCGATG 1257  
DB 2249 TGGATGAGTACTTCCCAAGGAAATCTTAAGAAATATATCTGAGTGGTGTAT 2308  
QY 1258 TGAAGTGAAGCCACCACTCTTCTGGAATCTGTCTCAGGCCAGCAATCGAGA 1317  
DB 2309 CAGATTAAGCACCTGTATCAGACTGAGCAAAAGAAATGATCCGTCGATGCACT 2368  
QY 1318 TCCAGCAAGATTAATTAACCTTTCTGTGCTATTAACATCTCTGTATCCATGTTGC 1377  
DB 2369 ATTTAAGAGGAACTTGAAGAGAGCAAAATCTTGTATTAAGTTACTCCATATATG 2428  
QY 1378 ATGACAAAGTTGGGAGCATATTCATCCAGGCTTATGCCAAGAAGGCGTTCATCAG 1437  
DB 2429 CTGATGAGACCAAGAGCCCTGAATCCATTAAGGATACCTTTAAACAAGCTCACCTTCCA 2488  
QY 1438 AAGTCTGAGACCAAGGTGAGAAATGCGCTGAAGAGCGTCAAGATCAATGGAAG 1497  
DB 2489 AAGGACCTACTGTCGAGCAAAAAGTAAGGAAAAAGCAAGAGCTGTCTAGAGTGGACC 2548  
QY 1498 AGATTCCCAAGAGTGAAGAAAGGATCATCTCAACTACACATCTTTTACCAACTG 1557  
DB 2549 AACTCTGTTGATGATCAGAAATGATTTTACGAAATTTATATATTTTATGAAACA 2608  
QY 1558 AAGTGGAAAAAGATTTCTCCAGACAGTCAATTCACAGCTTTCAGTACGCGCTGAGAT 1617  
DB 2609 TCATTGGAATGAAGTCTGTGATGATGATTTCTTCCACAGCAATATATCATTTGCTCT 2668  
QY 1618 CCCTGAAGCAAGAACCTCTTACATTTGCAAGGTCATGCGCAGCAGCAAGTCTGGGGAA 1677  
DB 2669 CTTTGACTAGTACACATTTGTACATGTTAGCAATGAGCAGATACAGATGAAGTGGGA 2728  
QY 1678 CCAAGGGACAGCATTAATTTCAAGAC 1705

DB 2729 AGGATGTCAGAAATCACTTTTACTAC 2756

RESULT 15

US-09-313-942-23  
Sequence 23, Application US/09313942  
Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.  
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A  
CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 23  
LENGTH: 3507

TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS

LOCATION: (1)...(3504)  
US-09-313-942-23

Query Match 3.2%; Score 76.4; DB 4; Length 3507;  
Best Local Similarity 44.5%; Pred. No. 2.3e-13;

Matches 440; Conservative 0; Mismatches 536; Indels 12; Gaps 3;

QY 724 CGTACAACTTCACGGGCTGCAGCCTTTTACAGATATGTCATAGCTGCTGCGATGCGG 783  
DB 1805 CATTCACTGTCACAGACCTTAACCTTTTACAGATATGTCATAGCTGCTGCGATGCGG 1864  
QY 784 TCAAGAGTCAAG---TTCTGAGTACGCTGAGCCAGAAAATGGGAATGACTGAG 840  
DB 1865 AGGAAGTGTGAAGGATGACTGAGTCACTGAGTGAAGCAAGCAAGTGGGATCACCTATG 1924  
QY 841 AAGAAGTCCATGT---GGCCTGGAAGTGTGAGAGTCTGGAACCAAGCTGAGCGGATG 897  
DB 1925 AAGATTAGACCATTAAGCAACCAAGTTTGTGTAAATATGATCCATCTCAG 1984  
QY 898 GAAGAAGGCCAGTCCGCTTTGTATGAGAAGCAAGCAAGGAGCCAGCTCTAGAGAAA 957  
DB 1985 GCTACAGACTGTCAACTGCTGTGGAAGCAACATTCCTCTTTGGAAGCCAAATGGA 2044  
QY 958 CACTTGGCTACACATATGCTATCTCAGAAAGCAACACTACCTCAGAAACATGA 1017  
DB 2045 TCTTGATTTTGAAGTACTCTCAGATGGAATGGAATCAATTTTACAAATTTACACACTTA 2104  
QY 1018 AACTTACTTAACAGACCTTGAAGTGCATCTGGAGGCGAGAGCTTTGGGTCTATGA 1077  
DB 2105 ATGCCACAA-----AACTGACATTAATCTCACAATATGATGCTATCTAGCAACCTAA 2158  
QY 1078 TTTCTTAATTTCTTGGGAGTCTCCAGTCCAGGCGACCCGAGAGATTCACGATATCAG 1137  
DB 2159 CAGTAAGAATCTTGTGGCAAAATCAGATCAGCTGTTTAACTATCTCCTGCTGACT 2218  
QY 1138 AAAAATATTTCAAGTCAATGAGTCAATGCAAGGCTCTGTTGCTGAGAGACAGTATGAG 1197  
DB 2219 TTTCAAGTACTCAACCCCTGATATGATTTTAAAGATTTCCCAAGAAATTAACATGTTGGG 2278  
QY 1198 TGAAGTGGCAAGGCTGTCTGATGAGCTGGAACACTTGGATGATGAATGATGCTTCCGATG 1257  
DB 2279 TGGATGAGTACTTCCAAAGGAAATCTGTAAGAAATATATATCTGAGTGTGTAT 2338  
QY 1258 TGAAGTGAAGCCACCACTTCTCTGGAATCTGTCTCAGGCCAGCAACTGAGCA 1317  
DB 2339 CAGATTAAGCAACCTGTATCAGACACTGGAAGCAAGAAATGATGATCCGTCATCGACCT 2398

OY	1318	CCGAGCAAGATTAATAAACCCTTCGAGCTCTTAACATCTCTGTGATGCATGTTGTC	1377
Db	2359	ATTTAAGAGGGAACTTAGCAGAGAGCAAAATGCTTTTGATACAGTTACTCCATATATG	2458
OY	1378	ATGACAAAGTTGGCGAGCATTTCCATCCAGGCTTATGCCMAAGAGCGCTTCCATCAG	1437
Db	2459	CTGATGAGCACCAGSAAAGCCCTGATTCATCAATGAAGCATACCTTAAMCAAGCTCCACCTTCA	2518
OY	1438	AAGTCTCTGAGACCAGSTGAGAAACATTTGCGGTGAAGAGCGTACAGTCATGGAAG	1497
Db	2519	AAGGACCTCAGTGTTCGGCAAAAAAGTAGGGAAGAAAGAAAGCTGCTTTAAGTGGACCC	2578
OY	1498	AGATTCCCAAGAGTGAAGAAAGGTTATCTGCTCAACTACACCATGTTTATACCAAGCTG	1557
Db	2579	AACCTTCCTGTGATGTTTCAGATGATGATTTATCAAAATTAATACATATATTTATAGAACCA	2638
OY	1558	AAGGTGAAAGATTTCCCAAGACAGTCAATTCAGATCTTTCAGTACCGCTGGAGT	1617
Db	2639	TCATTTGGAAATGAAACTGCTGTGATGATGGATTTCTTCCACACAGAAATATACATTTGTCT	2698
OY	1618	CCCTGAAACGAAAGACCTTTACATTTGTCAGGTCATGCGCCAGCACCAAGTCTGGGGGA	1677
Db	2699	CTTTGACTAGTGAACACATTTGACATGTGACCAATGCGACGATCACAGATGAAGTGGGA	2758
OY	1678	CCAAGCGGACACGACATAAATTTCAAGAC	1705
Db	2759	AGGATGGTCCGAATTCACTTTTACTAC	2786

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Search completed: August 4, 2003, 20:13:45
Job time : 145 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 20:00:56 ; Search time 492 Seconds  
(without alignments)  
10071.804 Million cell updates/sec

Title: US-09-892-949-1  
Perfect score: 2402  
Sequence: 1 ggcacgaggtgtgtgtgcag.....atgagaccctgcggccctca 2402

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
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15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2258.6	94.0	2480	11	US-09-892-949-1
3	2225.6	92.7	2238	11	US-09-892-949-1
4	2075	86.4	2529	11	US-09-892-949-1
5	1947	81.1	2119	14	US-10-006-265-16
6	1945.4	81.0	2903	11	US-09-892-949-1
7	1932.8	80.5	2196	14	US-10-006-265-1
8	1592.2	66.1	2295	11	US-09-892-949-1
9	1586.8	65.3	2445	14	US-10-227-884-91
10	1568.4	65.3	2445	14	US-10-230-163-91
11	1568.4	65.3	2445	14	US-10-230-338-91
12	1568.4	65.3	2445	14	US-10-218-631-91
13	1568.4	65.3	2445	14	US-10-230-414-91
14	1568.4	65.3	2445	14	US-10-216-159A-91
15	1568.4	65.3	2445	14	US-10-218-649-91
16	1568.4	65.3	2445	14	US-10-218-649-91

17	1568.4	65.3	2445	14	US-10-227-873-91	Sequence 91, Appl
18	1568.4	65.3	2445	14	US-10-227-883-91	Sequence 91, Appl
19	1568.4	65.3	2445	14	US-10-219-076-91	Sequence 91, Appl
20	1568.4	65.3	2445	14	US-10-230-434-91	Sequence 91, Appl
21	1568.4	65.3	2445	14	US-10-219-003-91	Sequence 91, Appl
22	1568.4	65.3	2445	14	US-10-219-075-91	Sequence 91, Appl
23	1568.4	65.3	2445	14	US-10-219-464-91	Sequence 91, Appl
24	1568.4	65.3	2445	14	US-10-219-466-91	Sequence 91, Appl
25	1568.4	65.3	2445	14	US-10-219-479-91	Sequence 91, Appl
26	1568.4	65.3	2445	14	US-10-219-481-91	Sequence 91, Appl
27	1568.4	65.3	2445	14	US-10-230-260-91	Sequence 91, Appl
28	1568.4	65.3	2445	14	US-10-232-231-91	Sequence 91, Appl
29	1568.4	65.3	2445	14	US-10-232-233-91	Sequence 91, Appl
30	1568.4	65.3	2445	14	US-10-216-165-91	Sequence 91, Appl
31	1568.4	65.3	2445	14	US-10-218-956-91	Sequence 91, Appl
32	1568.4	65.3	2445	14	US-10-219-468-91	Sequence 91, Appl
33	1568.4	65.3	2445	14	US-10-219-478-91	Sequence 91, Appl
34	1568.4	65.3	2445	14	US-10-219-536-91	Sequence 91, Appl
35	1568.4	65.3	2445	14	US-10-233-205-91	Sequence 91, Appl
36	1568.4	65.3	2445	14	US-10-219-072-91	Sequence 91, Appl
37	1568.4	65.3	2445	14	US-10-219-470-91	Sequence 91, Appl
38	1568.4	65.3	2445	14	US-10-219-474-91	Sequence 91, Appl
39	1568.4	65.3	2445	14	US-10-219-524-91	Sequence 91, Appl
40	1568.4	65.3	2445	14	US-10-219-528-91	Sequence 91, Appl
41	1568.4	65.3	2445	14	US-10-227-880-91	Sequence 91, Appl
42	1568.4	65.3	2445	14	US-10-227-881-91	Sequence 91, Appl
43	1568.4	65.3	2445	14	US-10-227-882-91	Sequence 91, Appl
44	1568.4	65.3	2445	14	US-10-230-436-91	Sequence 91, Appl
45	1568.4	65.3	2445	14	US-10-232-223-91	Sequence 91, Appl

## ALIGNMENTS

RESULT 1  
US-09-892-949-1  
Sequence 1, Application US/09892949  
Publication No. US2003096339A1  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Presnell, Scott R.  
APPLICANT: Gao, Zeren  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Kujiper, Joseph L.  
APPLICANT: Maurer, Mark F.  
TITLE OR INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
FILE REFERENCE: 00-42  
CURRENT APPLICATION NUMBER: US/09/892,949  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: US 60/214,282  
PRIOR FILING DATE: 2000-06-26  
PRIOR APPLICATION NUMBER: US 60/214,955  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/267,963  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 2402  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (171)...(2366)  
US-09-892-949-1

Query Match 100.0%; Score 2402; DB 11; Length 2402;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGCACGAGGTGTGTGTGATGAAATTAGACAGGACGAGTGTACCTTGTTC 60

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Db	61	CAACCTCAGCTGGGAATGTGCATCAGGCAACTCAAGTTTTTTCACACGGCATGTGTCGTG	120
QY	121	AATGTCGGAAAAACATTTCTCTCTCCCGACGCTTCAATGTGTTAACTGGGGATGATGTGGA	180
Db	121	AATGTCGGAAAAACATTTCTCTCTCCCGACGCTTCAATGTGTTAACTGGGGATGATGTGGA	180
QY	181	CCTGGGCACTGTGATGCTCCCCCTCAGTCTGCAAAATTCAGCCTGGCAGCTGCGCAGCTA	240
Db	181	CCTGGGCACTGTGATGCTCCCCCTCAGTCTGCAAAATTCAGCCTGGCAGCTGCGCAGCTA	240
QY	241	AGCCGAGAACATTTTCCGTGTCTACTCTACTATAGGAAAAATTAACCTGCACCTTGGAGTC	300
Db	241	AGCCGAGAACATTTTCCGTGTCTACTCTACTATAGGAAAAATTAACCTGCACCTTGGAGTC	300
QY	301	CAGGAAAGAAAACGATTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAA	360
Db	301	CAGGAAAGAAAACGATTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAA	360
QY	361	AACATGATTAATTGTACAACCAATAGTTCTACAGTGAAGAAATCGTCTTCCTTTT	420
Db	361	AACATGATTAATTGTACAACCAATAGTTCTACAGTGAAGAAATCGTCTTCCTTTT	420
QY	421	TCCCTCCAAAGAAATACGATCCAGATTAATTTAACATTGAGGTGGAACCTGAAAATGGAG	480
Db	421	TCCCTCCAAAGAAATACGATCCAGATTAATTTAACATTGAGGTGGAACCTGAAAATGGAG	480
QY	481	ATGCTGTAAATTAATCTATATGACATAGTGGAGATTAGAGAACATAGCGAAAACCTGAGC	540
Db	481	ATGCTGTAAATTAATCTATATGACATAGTGGAGATTAGAGAACATAGCGAAAACCTGAGC	540
QY	541	CACCTAACAATTTCCGCTGGAACCAAGTTTTGGCATAAACGATGATTCAAATTTGAT	600
Db	541	CACCTAACAATTTCCGCTGGAACCAAGTTTTGGCATAAACGATGATTCAAATTTGAT	600
QY	601	GGATTAAGCCCTGAGTGTGGCGCCTGTTTATCTGATTTAAATATACACTTCGATTCAGAGA	660
Db	601	GGATTAAGCCCTGAGTGTGGCGCCTGTTTATCTGATTTAAATATACACTTCGATTCAGAGA	660
QY	661	CAGTAAACAGTACACAGCTGTGATGGAAGTCAACTTCGTAAGAACCGTAAGGATAAAAAC	720
Db	661	CAGTAAACAGTACACAGCTGTGATGGAAGTCAACTTCGTAAGAACCGTAAGGATAAAAAC	720
QY	721	AAAGCTACAACTCAGCGGGCTGCAGCCTTTTACGAAATATGTCACTACCTCGCATGTG	780
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Db	781	CGGTCAAGAGACTCAAAGTTCTGAGATGACTGGAGCCAAAGAAAAATGGGAATGACTGAG	840
QY	841	AAGAAAGCTCCATGTGGCCTTGGAACTGTGTGAAGATCTTGAACCAAGCTGAGCGGATGGAA	900
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QY	901	GAAAGCCAGTCCGCTGTTTATGGAAGAGGAAGAGGAGCCCACTTACAGAAACATGAAAC	960
Db	901	GAAAGCCAGTCCGCTGTTTATGGAAGAGGAAGAGGAGCCCACTTACAGAAACATGAAAC	960
QY	961	TTGGCTACACATATGATTAATCCAGAAACCAACACTTAACCTACAGAAAACATGAAACA	1020
Db	961	TTGGCTACACATATGATTAATCCAGAAACCAACACTTAACCTACAGAAAACATGAAACA	1020
QY	1021	CTACTAACACAGCTTGAATCACTCTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTT	1080
Db	1021	CTACTAACACAGCTTGAATCACTCTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTT	1080
QY	1081	CTTAAATATTTCTTGGGAAGTCTCAGAGGCGACCCCTAGAGATTCAGCTTTTCAAGAAA	1140
Db	1081	CTTAAATATTTCTTGGGAAGTCTCAGAGGCGACCCCTAGAGATTCAGCTTTTCAAGAAA	1140

QY	1144	AATTCATTTCAGTGCATTTAGAGTGCATCCAGGCGCTGCCTGCTGAGGACACAGCTATGTTGTGA	1200
Db	1141	AATTCATTTCAGTGCATTTAGAGTGCATCCAGGCGCTGCCTGCTGAGGACACAGCTATGTTGTGA	1200
QY	1201	ACTGGCAAGCTCTGCTTAGACGTACACTTGGATGATGTAATGGTTTCCGAGTGTGG	1260
Db	1201	ACTGGCAAGCTCTGCTTAGACGTACACTTGGATGATGTAATGGTTTCCGAGTGTGG	1260
QY	1261	ACTCAGAGCCACACACCTTTTCCCTGGGAATCTGTGCTCAGGCCACAGACTGAGCATCC	1320
Db	1261	ACTCAGAGCCACACACCTTTTCCCTGGGAATCTGTGCTCAGGCCACAGACTGAGCATCC	1320
QY	1321	ACCAAGATTAATTAATAACCTTCTGCTGCTATACATCTCTGTGTAATCCAAATTTTGATC	1380
Db	1321	ACCAAGATTAATTAATAACCTTCTGCTGCTATACATCTCTGTGTAATCCAAATTTTGATC	1380
QY	1381	ACAAAGTTGGCGACGCTATTTCCATCTCAGGCTTATGCCAAGAGAGCGTTCCATCGAAG	1440
Db	1381	ACAAAGTTGGCGACGCTATTTCCATCTCAGGCTTATGCCAAGAGAGCGTTCCATCGAAG	1440
QY	1441	GTCCGAGACCCAAAGGTGGAGAACATTTGGGTGAGAGCGGTGCAGATCACATGGAAGAAGA	1500
Db	1441	GTCCGAGACCCAAAGGTGGAGAACATTTGGGTGAGAGCGGTGCAGATCACATGGAAGAAGA	1500
QY	1501	TTCCCAAGATGAGAGAAAGGGTATCATCTGCACATACACCATCTTTTACCAAGCTGAAG	1560
Db	1501	TTCCCAAGATGAGAGAAAGGGTATCATCTGCACATACACCATCTTTTACCAAGCTGAAG	1560
QY	1561	GTGGAAAAAGATTTCTCCAGACAGTCATTTCCAGCTATTCGACATTCGACATGACGCTGAGTCCC	1620
Db	1561	GTGGAAAAAGATTTCTCCAGACAGTCATTTCCAGCTATTCGACATTCGACATGACGCTGAGTCCC	1620
QY	1621	TGAAACGAAAGACCTTCTACATTTGTTCAGGTATGCGCCAGCACACAGTGTGGGGGAGACA	1680
Db	1621	TGAAACGAAAGACCTTCTACATTTGTTCAGGTATGCGCCAGCACACAGTGTGGGGGAGACA	1680
QY	1681	ACGGGACCAGCATTAATTTCAAGACATGTCTCATTCAGTGTCTTTGAGATTATCTCATTA	1740
Db	1681	ACGGGACCAGCATTAATTTCAAGACATGTCTCATTCAGTGTCTTTGAGATTATCTCATTA	1740
QY	1741	CTTCTCTGATTTGGTGGAGGCTTCTTATATCTCATTTCTCGACAGAGGCAATAGTCTCA	1800
Db	1741	CTTCTCTGATTTGGTGGAGGCTTCTTATATCTCATTTCTCATTTCTCGACAGAGGCAATAGTCTCA	1800
QY	1801	AAAAACCCACAATTTGACTCATCTGTGTGTGGCCACCGTTCGCCAACCTCTGCTGAAGAAT	1860
Db	1801	AAAAACCCACAATTTGACTCATCTGTGTGTGGCCACCGTTCGCCAACCTCTGCTGAAGAAT	1860
QY	1861	GTATAGCCACATGGGATGGATGAGATGATTTCAAGGATTAAGTTAAACGTAAGGAGGTCTGATG	1920
Db	1861	GTATAGCCACATGGGATGGATGAGATGATTTCAAGGATTAAGTTAAACGTAAGGAGGTCTGATG	1920
QY	1921	ACTCTGTGAACACAGAGAAGAGATCTTAAACCAATGTTTCCACCCCGACAGTGCAMATTGG	1980
Db	1921	ACTCTGTGAACACAGAGAAGAGATCTTAAACCAATGTTTCCACCCCGACAGTGCAMATTGG	1980
QY	1981	TGATTGACAAGTGTGGTGTGGAACCTTTGGGAATGTTCTGCAAAATTTTTCACAGATGAAG	2040
Db	1981	TGATTGACAAGTGTGGTGTGGAACCTTTGGGAATGTTCTGCAAAATTTTTCACAGATGAAG	2040
QY	2041	CCAGAACGGGTGAGAAAAACAATTTAGAGAGGGAAAAAGAAATGGGTATGTGACCTGCCCC	2100
Db	2041	CCAGAACGGGTGAGAAAAACAATTTAGAGAGGGAAAAAGAAATGGGTATGTGACCTGCCCC	2100
QY	2101	TCAGGCTGATTTGCCCTGGGGAAAAAGTTTGAAGAGCTCCCAATTTTCACTCGAGATTC	2160
Db	2101	TCAGGCTGATTTGCCCTGGGGAAAAAGTTTGAAGAGCTCCCAATTTTCACTCGAGATTC	2160
QY	2161	CGCCCGAAGAAATCCCAATACCTACGTTTGAGGATGATCCAGAGGGGACCGCCCGAAGACCA	2220
Db	2161	CGCCCGAAGAAATCCCAATACCTACGTTTGAGGATGATCCAGAGGGGACCGCCCGAAGACCA	2220
QY	2221	AAGACACACTTCTCTTTCTGGTCAAAAGTTTATGACCAAGATCATCTGTGTGAGAAGAG	2280

Db 2221 AAAGAGAGCTTCTCTTCTGCTCAAGTTAGTACAGATCTGTGTGAGAGAG 2280  
QY 2281 CCCCAATCCATATTGAAATAATTCAGTGCAGCCAGGGAAATTTCTGTCTGAAAAAC 2340  
Db 2281 CCCCAATCCATATTGAAATAATTCAGTGCAGCCAGGGAAATTTCTGTCTGAAAAAC 2340  
QY 2341 TTCCAGAGCAGCAGCAGGAGAGAGTCTAAATGAGACATAGCATGAGACCCCTGGGCGCT 2400  
Db 2341 TTCCAGAGCAGCAGCAGGAGAGAGTCTAAATGAGACATAGCATGAGACCCCTGGGCGCT 2400  
QY 2401 CA 2402  
Db 2401 CA 2402  
RESULT 2  
US-09-972-708-3  
; Sequence 3, Application US/09972708  
; Publication No. US20030059871A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Cosman, David J.  
; APPLICANT: Mosley, Bruce A.  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Dubose, Robert F.  
; APPLICANT: Willey, Steven R.  
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
; FILE REFERENCE: 3160-B  
; CURRENT APPLICATION NUMBER: US/09/972.708  
; NUMBER OF FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2480  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-972-708-3  
Query Match 94.0%; Score 2258.6; DB 11; Length 2480;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2261; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 138 CTCTCTCCCGAGCCTTCATGTTAACTGGGATGATGTGACCTGGCAGCTGTGATG 197  
Db 138 CTCTCTCCCGAGCCTTCATGTTAACTGGGATGATGTGACCTGGCAGCTGTGATG 197  
QY 198 CTCTCTCTCTGCAAAATTCAGCTGCGAGCTCTGCCAGCTAAAGCTTGAACATTTCC 257  
Db 198 CTCTCTCTCTGCAAAATTCAGCTGCGAGCTCTGCCAGCTAAAGCTTGAACATTTCC 257  
QY 258 TGTGTCTACTACTATAGGAAAAATTTAACTGCAGCTGAGTCCAGGAAAGGAAACAGT 317  
Db 258 TGTGTCTACTACTATAGGAAAAATTTAACTGCAGCTGAGTCCAGGAAAGGAAACAGT 317  
QY 318 TATACCCAGTACAGAGTTAAGAGAACTTACGCTTTTGAGAAAAACATGATTAATTGACA 377  
Db 318 TATACCCAGTACAGAGTTAAGAGAACTTACGCTTTTGAGAAAAACATGATTAATTGACA 377  
QY 378 ACCAATAGTTCTACAAATGAAAAATCGTCTTCTTTTCTTCCCAAGAAATACG 437  
Db 378 ACCAATAGTTCTACAAATGAAAAATCGTCTTCTTTTCTTCCCAAGAAATACG 437  
QY 438 ATCCAGATATATATATACATTTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497  
Db 438 ATCCAGATATATATATACATTTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497  
QY 498 CATATGACATACAGGAGATTAAGAGAACATGACGAAAACTGAACCACTAAGATTTTCGGT 557  
Db 498 CATATGACATACAGGAGATTAAGAGAACATGACGAAAACTGAACCACTAAGATTTTCGGT 557  
QY 558 GTGAACCACTTTTGGGATCAAAAGCATGATTAATTTGAATGATTAAGGCTGAGTTG 617  
Db 558 GTGAACCACTTTTGGGATCAAAAGCATGATTAATTTGAATGATTAAGGCTGAGTTG 617

Db 558 GTGAACCACTTTTGGGATCAAAAGCATGATTAATTTGAATGATTAAGGCTGAGTTG 617  
QY 618 GCGCTGTTCATCTGATTTAAATACACTTCGATTCAGGACAGTCAACAGTACAGC 677  
Db 618 GCGCTGTTCATCTGATTTAAATACACTTCGATTCAGGACAGTCAACAGTACAGC 677  
QY 678 TGTATGAGAGTCACTTCGCTAAGAACCTTAAGATTAAGCAAAACGTAACCTTCACG 737  
Db 678 TGTATGAGAGTCACTTCGCTAAGAACCTTAAGATTAAGCAAAACGTAACCTTCACG 737  
QY 738 GGGCTGACGCTTTTACAGAAATATGATAGCTGTGAGTGTGGCTCAAGAGTCAAG 797  
Db 738 GGGCTGACGCTTTTACAGAAATATGATAGCTGTGAGTGTGGCTCAAGAGTCAAG 797  
QY 798 TTCTGAGTACAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 857  
Db 798 TTCTGAGTACAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 857  
QY 858 CTGGAAGTGTGAGAGTCTGAAAACAGCTGAGGCGGAGTGAAGAGGAGGAGGAGGAGGAG 917  
Db 858 CTGGAAGTGTGAGAGTCTGAAAACAGCTGAGGCGGAGTGAAGAGGAGGAGGAGGAGGAG 917  
QY 918 TTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 977  
Db 918 TTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 977  
QY 978 TACTATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1037  
Db 978 TACTATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1037  
QY 1038 GAAGTGCATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1097  
Db 1038 GAAGTGCATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1097  
QY 1098 AAGTCTCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1157  
Db 1098 AAGTCTCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1157  
QY 1158 GAGGTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1217  
Db 1158 GAGGTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1217  
QY 1218 CTAGACGTGAACACTTGGATGATTAATGATGTTCCGAGTGTGACAGCAGGAGGAGGAGGAG 1277  
Db 1218 CTAGACGTGAACACTTGGATGATTAATGATGTTCCGAGTGTGACAGCAGGAGGAGGAGGAG 1277  
QY 1278 CTTTCTGAGGATCTGTCTCAGGCGCAGCACTGACAGTCCAGCAAGATTAATTAA 1337  
Db 1278 CTTTCTGAGGATCTGTCTCAGGCGCAGCACTGACAGTCCAGCAAGATTAATTAA 1337  
QY 1338 CCTTCTGAGGATCTGTCTCAGGCGCAGCACTGACAGTCCAGCAAGATTAATTAA 1397  
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Db 1398 TATTCATCCAGGCTTATGCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1457  
QY 1458 GAGAACATTTGGCGTGAAGAGGAGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1517  
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QY 1518 AAGGATATCATCTGCACTACACCATCTTTTACCAAGTGAAGTGAAGGAGGAGGAGGAGGAG 1577  
Db 1518 AAGGATATCATCTGCACTACACCATCTTTTACCAAGTGAAGTGAAGGAGGAGGAGGAGGAG 1577  
QY 1578 AAGACATCAATTCAGCATCTTGCAGTACGCGCTGAGGAGTCCCTGAAACGAAAGACCTCT 1637  
Db 1578 AAGACATCAATTCAGCATCTTGCAGTACGCGCTGAGGAGTCCCTGAAACGAAAGACCTCT 1637  
QY 1638 TACATTTGTCAGGTCATAGGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1697  
Db 1638 TACATTTGTCAGGTCATAGGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1697

QY	1698	TTCAAGACATGTGTAATAGAGTGTCTTTAGAGTAAATATCCCATAAACTTCTCTGATGTGGA	1757
Db	1698	TTCAAGACATGTGTAATAGAGTGTCTTTAGAGTAAATATCCCATAAACTTCTCTGATGTGGA	1757
QY	1758	GGCCCTTCTTATTCATATATTCCTGCACAGTGCATATGTGTCACAAAAACCCAAACAAATG	1817
Db	1758	GGCCCTTCTTATTCATATATTCCTGCACAGTGCATATGTGTCACAAAAACCCAAACAAATG	1817
QY	1818	ACTATCTGTGTGGCCCCACCGTCCCAACCTGCTGAAAGTAGATATGCCATATGGCAT	1877
Db	1818	ACTATCTGTGTGGCCCCACCGTCCCAACCTGCTGAAAGTAGATATGCCATATGGCAT	1877
QY	1878	GGAGATGATTTCAAGGATTAACCTGAAGAGTGTGATGACTCTGTGAACACAGAA	1937
Db	1878	GGAGATGATTTCAAGGATTAACCTGAAGAGTGTGATGACTCTGTGAACACAGAA	1937
QY	1938	GACAGGATCTTAAACCAATGTTCCACCCCACTGACAAAGTGTGATTTGACAAATGGTG	1997
Db	1938	GACAGGATCTTAAACCAATGTTCCACCCCACTGACAAAGTGTGATTTGACAAATGGTG	1997
QY	1998	GTGAACCTTTGGGAATGCTCTCAAGAAATTTTACAGATGAAGCCAGAACGGGTAGGAA	2057
Db	1998	GTGAACCTTTGGGAATGCTCTCAAGAAATTTTACAGATGAAGCCAGAACGGGTAGGAA	2057
QY	2058	AACAAATTTAGAGGGGAAAGAAATGGTATGTGACCTGCCCTTCAGGCTGATTTGCC	2117
Db	2058	AACAAATTTAGAGGGGAAAGAAATGGTATGTGACCTGCCCTTCAGGCTGATTTGCC	2117
QY	2118	CTGGGGAAAGATTTTGAAGAGCTCCCAATTCACCTGAGATTTCCGCCCCAGAAATCCCA	2177
Db	2118	CTGGGGAAAGATTTTGAAGAGCTCCCAATTCACCTGAGATTTCCGCCCCAGAAATCCCA	2177
QY	2178	TACCTAGCTTGAGAGATGCCAGAGGGAGCCGCCAGAGCCAAAGACACAGCTTCTCTT	2237
Db	2178	TACCTAGCTTGAGAGATGCCAGAGGGAGCCGCCAGAGCCAAAGACACAGCTTCTCTT	2237
QY	2238	TCTGGTCAAAATTTAGTACCAAGATCATCTGTGTGAGGAAGAGGCCCAAAATCATATTTG	2297
Db	2238	TCTGGTCAAAATTTAGTACCAAGATCATCTGTGTGAGGAAGAGGCCCAAAATCATATTTG	2297
QY	2298	AAAAATTCAGTACAGCCAGGGAATTTCTGTGTCGAAAAAATCTCCAGACACACCAAG	2357
Db	2298	AAAAATTCAGTACAGCCAGGGAATTTCTGTGTCGAAAAAATCTCCAGACACACCAAG	2357
QY	2358	GGAGAAGCTTAAATGCGACCATAGCATAGAACCTCTGGGGGCTCA	2402
Db	2358	GGAGAAGCTTAAATGCGACCATAGCATAGAACCTCTGGGGGCTCA	2402

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US-09-972-708-5
RESULT 3
Sequence 5, Application US/09972708
Publication No. US20030059871A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRL AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 2238
TYPE: DNA
ORGANISM: Homo sapiens
US-09-972-708-5

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Query Match	Similarity	92.7%	Score	2225.6	DB	11	Length	2238	
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Db	7	CTCTCTCCCAACCTTCATGTGTAACTGGGGATGATGTGACCTGGGCACTGTGATG	66						
OY	198	CTCCCTCACTCTGCAAAATTCAGCCTGGACCTTGCCAGCTAAGCCTGAGAACATTTCC	257						
Db	67	CTCCCTCACTCTGCAAAATTCAGCCTGGACCTTGCCAGCTAAGCCTGAGAACATTTCC	126						
OY	258	TGTGTCTACTCTATAGAGAAAAATTAACCTGCACCTGTGAGCCAGAGAAACCACTG	317						
Db	127	TGTGTCTACTCTATAGAGAAAAATTAACCTGCACCTGTGAGCCAGAGAAACCACTG	186						
OY	318	TATACCAAGTACACAGTTAAGAGACTTACGCTTTTGGAGAAAAACATGATTAATGTACA	377						
Db	187	TATACCAAGTACACAGTTAAGAGACTTACGCTTTTGGAGAAAAACATGATTAATGTACA	246						
OY	378	ACCAATAGTCTACAGATGAAAAATCGTCTTCGTCCTTTTTCCTTCCAAAGATTAACG	437						
Db	247	ACCAATAGTCTACAGATGAAAAATCGTCTTCGTCCTTTTTCCTTCCAAAGATTAACG	306						
OY	438	ATCCAGATTAATTATACCATTTGAGTGGAGAGCTGAAATGGAGATGGTGTATTAATCT	497						
Db	307	ATCCAGATTAATTATACCATTTGAGTGGAGAGCTGAAATGGAGATGGTGTATTAATCT	366						
OY	498	CATATGACATCTAGAGATTTAGAGAACATTAAGGAAACAGAACCCACTTAAGTTTCCGT	557						
Db	367	CATATGACATCTAGAGATTTAGAGAACATTAAGGAAACAGAACCCACTTAAGTTTCCGT	426						
OY	558	GTGAACACAGTTTGGGCATCAACGAATGATTCAAATTTGAATGAATGAAGCTGAGTTG	617						
Db	427	GTGAACACAGTTTGGGCATCAACGAATGATTCAAATTTGAATGAATGAAGCTGAGTTG	486						
OY	618	GCGCTGTTTCATCTGCATTTAAATATACACACTTCGATTCAGAGACGTAAACAGTACCAAG	677						
Db	487	GCGCTGTTTCATCTGCATTTAAATATACACACTTCGATTCAGAGACGTAAACAGTACCAAG	546						
OY	678	TGATGAGAAAGTCAACTTCGCTAGAACCGTAAAGATTAATAAACCAAGCTACACCTCCAG	737						
Db	547	TGATGAGAAAGTCAACTTCGCTAGAACCGTAAAGATTAATAAACCAAGCTACACCTCCAG	606						
OY	738	GGGCTGCAGCCTTTTACAGAAATATGTCACTAGCTGCGATGTGCGGTCAAGAGTCAAG	797						
Db	607	GGGCTGCAGCCTTTTACAGAAATATGTCACTAGCTGCGATGTGCGGTCAAGAGTCAAG	666						
OY	798	TTTCGGAATGACTGGAGGCCAAGAAAAATTTGGGAATGACTGAGAGAAAGCTTCCATGTGCG	857						
Db	667	TTTCGGAATGACTGGAGGCCAAGAAAAATTTGGGAATGACTGAGAGAAAGCTTCCATGTGCG	726						
OY	858	CTGGAACGTGGAGAGCTCTGAAACACAGCTAGGGGGATGGAAGAGGCCAGTGGGGTTG	917						
Db	727	CTGGAACGTGGAGAGCTCTGAAACACAGCTAGGGGGATGGAAGAGGCCAGTGGGGTTG	786						
OY	918	TTATGGAAGAGGCAAGAGAGGCCCAAGTCTAGAGAAACACTTGGCTACAACTATATGG	977						
Db	787	TTATGGAAGAGGCAAGAGAGGCCCAAGTCTAGAGAAACACTTGGCTACAACTATATGG	846						
OY	978	TACTATCCAGAAAGCAACACTTACCTCACAAACAAATGAACACTTACACAGCAGTT	1037						
Db	847	TACTATCCAGAAAGCAACACTTACCTCACAAACAAATGAACACTTACACAGCAGTT	906						
OY	1038	GAAGTGCATCTGGGAGGGGAGAGGCTTTTGGGTGTCATGATTTCTTAATTTCTCTTGGG	1097						
Db	907	GAAGTGCATCTGGGAGGGGAGAGGCTTTTGGGTGTCATGATTTCTTAATTTCTCTTGGG	966						
OY	1098	AAGTCTCCAGTGGCCACCCCTGAGGATTCACACTTTCGAAGAAAAATCATTTTCAGTGCATT	1157						
Db	967	AAGTCTCCAGTGGCCACCCCTGAGGATTCACACTTTCGAAGAAAAATCATTTTCAGTGCATT	1026						
OY	1158	GAGGTGATGACGGCCTGCGTTGCTGAGAGACCAAGCTAGTGGTGAAGTGGCAAAAGCTTGCT	1217						



Db	1027	GAGGTCAATGCAGGCGTCGCTGGTTCGTAAGSACCAGCTAGTGGTGAAGTGGCAAAAGCCCTGCT	1111
QY	1218	CTAGACGTGAACACTTGGATGATTGAATGGTTTCCGATGTGGACTAGAGCCACACACC	1277
Db	1087	CTAAGACGTGAACACTTGGATGATTGAATGGTTTCCGATGTGGACTAGAGCCACACACC	1146
QY	1278	CTTTCCTGGGGAATCTGTGTCTCAGGCCACGAACGTGAGCATCCGACGAAGATTAATTTAAA	1337
Db	1147	CTTTCCTGGGGAATCTGTGTCTCAGGCCACGAACGTGAGCATCCGACGAAGATTAATTTAAA	1206
QY	1338	CCTTTCTGGTGCATTAACATCTCTGTGTATCCAAATGTTGCATGACAAAGTTGGCGAGCA	1397
Db	1207	CCTTTCTGGTGCATTAACATCTCTGTGTATCCAAATGTTGCATGACAAAGTTGGCGAGCA	1286
QY	1398	TATTCATCCAGCGCTTATGCCAAGAAGCGCTTCATATCAGAAGTCTGAGACCAAGGTG	1457
Db	1267	TATTCATCCAGCGCTTATGCCAAGAAGCGCTTCATATCAGAAGTCTGAGACCAAGGTG	1326
QY	1458	GAGAACATTTGGCGCTGGAAGAGCGTTCAGCATCATGAAAGAGATTCACAGTGAAGAGA	1517
Db	1327	GAGAACATTTGGCGCTGGAAGAGCGTTCAGCATCATGAAAGAGATTCACAGTGAAGAGA	1386
QY	1518	AAGGATTCATCTGCAACTACACCATCTTTTACCAGCTGAGSTGGAAAAAGATTCTCC	1577
Db	1387	AAGGATTCATCTGCAACTACACCATCTTTTACCAGCTGAGSTGGAAAAAGATTCTCTCC	1446
QY	1578	AAGACGTCATTCACGATCTTCAGTACAGCGCGTGGAGTCCCGAAACGAAACACGCT	1637
Db	1447	AAGACGTCATTCACGATCTTCAGTACAGCGCGTGGAGTCCCGAAACGAAACACGCT	1506
QY	1638	TACATTTGTTCAGTATGCGCCAGCAGCAGTGTGGGGAAACCAAGGGACCGACATTAAT	1697
Db	1507	TACATTTGTTCAGTATGCGCCAGCAGCAGTGTGGGGAAACCAAGGGACCGACATTAAT	1566
QY	1698	TTCAAGACATTTGTCATTCAGTGTCTTGAATTTTCCATTAATCTCTGTATGTGGTGA	1757
Db	1567	TTCAAGACATTTGTCATTCAGTGTCTTGAATTTTCCATTAATCTCTGTATGTGGTGA	1626
QY	1758	GGCCTTTCTTATTCATTAATCTTACAGAGTGGCATATGGTCTCAAAAAACCAACAATTTG	1817
Db	1627	GGCCTTTCTTATTCATTAATCTTACAGAGTGGCATATGGTCTCAAAAAACCAACAATTTG	1686
QY	1818	ACTATCTGTGTGGCCACCCTTCCACACCCTGCTGAAGTAGTATAGCCATATGGCAT	1877
Db	1687	ACTATCTGTGTGGCCACCCTTCCACACCCTGCTGAAGTAGTATAGCCATATGGCAT	1746
QY	1878	GGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGTGTGATGCTGTGAACAACAGAA	1937
Db	1747	GGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGTGTGATGCTGTGAACAACAGAA	1806
QY	1938	GACAGATCTTAAAAACATGTTTCCACCCCGAGTACAAAGTTGGTATTGACAAAGTTGGTG	1997
Db	1807	GACAGATCTTAAAAACATGTTTCCACCCCGAGTACAAAGTTGGTATTGACAAAGTTGGTG	1866
QY	1998	GTTGAACCTTTGGGATGTTCTGCAAGAAATTTTCCAGATGTAAGCCAGAAAGGGTCAAGAA	2057
Db	1867	GTTGAACCTTTGGGATGTTCTGCAAGAAATTTTCCAGATGTAAGCCAGAAAGGGTCAAGAA	1928
QY	2058	AACAATTTAGAGAGGGGAAAAAAGATGGGTATGTGACCTGCCCTTCAGGCTCGATTTGTCC	2117
Db	1927	AACAATTTAGAGAGGGGAAAAAAGATGGGTATGTGACCTGCCCTTCAGGCTCGATTTGTCC	1986
QY	2118	CTGGGGAAAAAGTTTGAAGAGCTCCCACTTTCACCTGAGATTCGCGCCACGAAAAATCCCA	2177
Db	1987	CTGGGGAAAAAGTTTGAAGAGCTCCCACTTTCACCTGAGATTCGCGCCACGAAAAATCCCA	2048
QY	2178	TACCTAGCTTGAGAGATCCAGAGGGGACCGCCACGAAAGCCAAAGACACTTCTCTTT	2237
Db	2047	TACCTAGCTTGAGAGATCCAGAGGGGACCGCCACGAAAGCCAAAGACACTTCTCTTT	2106
QY	2238	TCTGTGCAAAATTAGTACAGATCTCTGTGAGGAAGAGCCCAATTCATATTTG	2297

Db	2107	TCGTGTCGAAGTTAGTACACGATCATTCTGTGTGAGGAAGAGGACCCCAAAATTCATATTTTG	2166
OY	2298	AAAAATTCAGTGACAGCCAGGGAATTTCTTGTCTGTGAAAAAACTTCAGACACACCAAG	2357
Db	2167	AAAAATTCAGTAGAGCAGCCAGGGAATTTCTTGTGTGAAAAAACTTCAGACACCAAG	2226
OY	2358	GGAGAGCTCTAA	2369
Db	2227	GGAGAGCTCTAA	2238
RESULT 4			
US-09-892-949-45			
Sequence 45, Application US/09892949			
Publication NO. US20030096339A1			
GENERAL INFORMATION:			
APPLICANT: Sprecher, Cindy A.			
APPLICANT: Presnell, Scott R.			
APPLICANT: Gao, Zeren			
APPLICANT: Whitmore, Theodore E.			
APPLICANT: Kujiper, Joseph L.			
APPLICANT: Maurer, Mark F.			
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17			
FILE REFERENCE: 00-42			
CURRENT APPLICATION NUMBER: US/09/892, 949			
CURRENT FILING DATE: 2001-06-26			
PRIOR APPLICATION NUMBER: US 60/214, 282			
PRIOR FILING DATE: 2000-06-26			
PRIOR APPLICATION NUMBER: US 60/214, 955			
PRIOR FILING DATE: 2000-06-29			
PRIOR APPLICATION NUMBER: US 60/267, 963			
PRIOR FILING DATE: 2001-08-02			
NUMBER OF SEQ ID NOS: 93			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 45			
LENGTH: 2529			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (162)...(2108)			
US-09-892-949-45			
Query Match	86.4%	Score 2075;	DB 11: Length 2529;
Best Local Similarity	100.0%	Pred. No. 0;	
Matches 2075;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	10	TGTTGTGTCGATATGAAAAATGACACAGSAGGAGCAATGTGCAGCTTTCCACTCAGC	69
Db	1	TGTTGTGTCGATATGAAAAATGACACAGSAGGAGCAATGTGCAGCTTTCCACTCAGC	60
OY	70	TGGGAAGTGTGCATCAGGCACTCAAGTTTTCACACAGGCATGTGTCTGTGAATGTCCGC	129
Db	61	TGGGAAGTGTGCATCAGGCACTCAAGTTTTCACACAGGCATGTGTCTGTGAATGTCCGC	120
OY	130	AAAAATTTCTCTTCCCGCAGCCTTCATGTGTTAACTGGGATATATGTGGACCTGGGCAC	189
Db	121	AAAAATTTCTCTTCCCGCAGCCTTCATGTGTTAACTGGGATATATGTGGACCTGGGCAC	180
OY	190	TGTGTGATGCTCCCTCAGCTGTGCAAAATTCAGCCTGGAGCTCTGCACACTAAAGCTTGAA	249
Db	181	TGTGTGATGCTCCCTCAGCTGTGCAAAATTCAGCCTGGAGCTCTGCACACTAAAGCTTGAA	240
OY	250	ACATTTCCCTGTGTCTACTACTATATAGAAAAAATTTAACTGCACATTGAGTCCAGGAAGG	309
Db	241	ACATTTCCCTGTGTCTACTACTATATAGAAAAAATTTAACTGCACATTGAGTCCAGGAAGG	300
OY	310	AAACCAAGTTATACCAAGTACACAGTTAGAGAACTTACGTTTGGAAAAAACAATGATA	369
Db	301	AAACCAAGTTATACCAAGTACACAGTTAGAGAACTTACGTTTGGAAAAAACAATGATA	360
OY	370	ATTGTACACCAATAGTTCTCAAGATGAAAAATCGTCTTGCTGCTTTTTCCTTCACA	429

361 ATGTACACCAATAGTTCTACAMGTGAAAAATCGTCTTGCTCTTTTCTTCCAA 420  
430 GAATTAAGCATCCAGATATATTATACATTTGAGTGGAGCTGAAATGAGATGTAA 489  
421 GAATTAAGCATCCAGATATATTATACATTTGAGTGGAGCTGAAATGAGATGTAA 480  
430 TTAATATCATATGACATAGTGAATAGAGAACATAGCGAAAACTGACCACTAGA 549  
481 TTAATATCATATGACATAGTGAATAGAGAACATAGCGAAAACTGACCACTAGA 540  
550 TTTTCCGCTGAACCACTTTTGGGATCAACGAATATTCATTAATGATGATAAGC 609  
541 TTTTCCGCTGAACCACTTTTGGGATCAACGAATATTCATTAATGATGATAAGC 600  
610 CTGAGTTGGCCCTTTCATCTGATTTAAATACACATTCGATTCAGAGACAGTACA 669  
601 CTGAGTTGGCCCTTTCATCTGATTTAAATACACATTCGATTCAGAGACAGTACA 660  
670 GTACAGCTGATGGAAGTCAACTTCGCTAAGAACCCGTAGAGATTAACCAACGTACA 729  
661 GTACAGCTGATGGAAGTCAACTTCGCTAAGAACCCGTAGAGATTAACCAACGTACA 720  
730 ACCTCAGCGGGCTGACGCTTTTACAGAAATATGTCATAGCTTCGATGCGGTCAAG 789  
721 ACCTCAGCGGGCTGACGCTTTTACAGAAATATGTCATAGCTTCGATGCGGTCAAG 780  
790 AGTCAAAGTTCGAGTACTGAGAGCCAAAGAAAAATGGGAATGACTAGGAAAGAGCTC 849  
781 AGTCAAAGTTCGAGTACTGAGAGCCAAAGAAAAATGGGAATGACTAGGAAAGAGCTC 840  
850 CATGTGGCTGGAACCTGTGAGAGTCTGAAACCAAGCTGAGCGGATGGAAGAGCCAG 909  
841 CATGTGGCTGGAACCTGTGAGAGTCTGAAACCAAGCTGAGCGGATGGAAGAGCCAG 900  
910 TGGGTTGTATNGAAG 969  
901 TGGGTTGTATNGAAG 960  
970 ACATATGCTACTATCCAGAAAGCAACACTAACCTCAGAAAAATGAACTACTAAC 1029  
961 ACATATGCTACTATCCAGAAAGCAACACTAACCTCAGAAAAATGAACTACTAAC 1020  
1030 AGCAGCTTGAACCTGATCTGGGAGGCGAGAGCTTTGGGTCTATGATTTCTTAAAT 1089  
1021 AGCAGCTTGAACCTGATCTGGGAGGCGAGAGCTTTGGGTCTATGATTTCTTAAAT 1080  
1090 CTCTGGGAAGTCTCCAGTGGCCAGCCCTGAGAGATTCGAGTATTCAGAAAAATCATTC 1149  
1081 CTCTGGGAAGTCTCCAGTGGCCAGCCCTGAGAGATTCGAGTATTCAGAAAAATCATTC 1140  
1150 AGTGCATTTGAGTATGAGAGGCTGCTGCTGAGAGACAGCTAGTGTGAAGTGGCAAA 1209  
1141 AGTGCATTTGAGTATGAGAGGCTGCTGCTGAGAGACAGCTAGTGTGAAGTGGCAAA 1200  
1210 GCTTGTCTTAGAGCTGAACTTTGATGATGATTAATGATTTCCGATGTGACATCAGAGC 1269  
1201 GCTTGTCTTAGAGCTGAACTTTGATGATGATTAATGATTTCCGATGTGACATCAGAGC 1260  
1270 CCACACACCTTCTCGTGGGAATCTGCTGCTCAGGCGCAGCACTGACATCCAGAGATA 1329  
1261 CCACACACCTTCTCGTGGGAATCTGCTGCTCAGGCGCAGCACTGACATCCAGAGATA 1320  
1330 AATTAAAACTTTCTGCTGATTAACATCTCTGTATCCATGATGATGATGATGATGATG 1389  
1321 AATTAAAACTTTCTGCTGATTAACATCTCTGTATCCATGATGATGATGATGATGATG 1380  
1390 GCGAGCCATATTCATCCAGGCTTATGCGCAAGAGGCTTCATCAGAGAGTCTCTGAGA 1449  
1381 GCGAGCCATATTCATCCAGGCTTATGCGCAAGAGGCTTCATCAGAGAGTCTCTGAGA 1440  
1450 CCAAGGTGAGAAACATTTGGCTGAAAGAGGCTCAGATACATGGAAGAGATTCACAGA 1509  
1441 CCAAGGTGAGAAACATTTGGCTGAAAGAGGCTCAGATACATGGAAGAGATTCACAGA 1500

1510 GTGAGAGAAAGGCTATCATCTGCACTACACATCTTTTACCAAGCTGAGGAGAAAG 1569  
1501 GTGAGAGAAAGGCTATCATCTGCACTACACATCTTTTACCAAGCTGAGGAGAAAG 1560  
1570 GATTCTCCAGACACTGATTCACATCTTGCACTAGCGGCTGAGTCCCTGAAACGAA 1629  
1561 GATTCTCCAGACACTGATTCACATCTTGCACTAGCGGCTGAGTCCCTGAAACGAA 1620  
1630 AGACCTTTACATTTTTCAGGTCATGCGCAGCAGCAGAGTGTGGGGAACCAACGGACCA 1689  
1621 AGACCTTTACATTTTTCAGGTCATGCGCAGCAGCAGAGTGTGGGGAACCAACGGACCA 1680  
1690 GCATTAATTTTCAAGACATTTGTCATGTCAGTGTGTTGAGATTAATCTCATACCTCTGTA 1749  
1681 GCATTAATTTTCAAGACATTTGTCATGTCAGTGTGTTGAGATTAATCTCATACCTCTGTA 1740  
1750 TTGTTGAGAGCCCTTCTTATTCATTAATCTGACATGAGTGGCATATGTTCTCAAAAACCCA 1809  
1741 TTGTTGAGAGCCCTTCTTATTCATTAATCTGACATGAGTGGCATATGTTCTCAAAAACCCA 1800  
1810 ACAATTTACATCATCTGTGTTGGCCACCCTTCCCAACCTGCTGAAAGTATGATGACA 1869  
1801 ACAATTTACATCATCTGTGTTGGCCACCCTTCCCAACCTGCTGAAAGTATGATGACA 1860  
1870 CATGCGATGAGATGATTTTCAAGATTAAGCTAAACCTGAGAGAGTCTGATGACTGTTGTA 1929  
1861 CATGCGATGAGATGATTTTCAAGATTAAGCTAAACCTGAGAGAGTCTGATGACTGTTGTA 1920  
1930 ACACAGAGAGAGATCTTAAACCATGTTCCACCCCAAGTACAGTGTGATGATGACA 1989  
1921 ACACAGAGAGAGATCTTAAACCATGTTCCACCCCAAGTACAGTGTGATGATGACA 1980  
1990 AGTTGCTGTGATCTTGGGATGTTTTCGAAAGATTTTTCAGATGATGATGATGATGATG 2049  
1981 AGTTGCTGTGATCTTGGGATGTTTTCGAAAGATTTTTCAGATGATGATGATGATGATG 2040  
2050 GTACGAGAAACATTTTACGAGGCGGAAAGATGGG 2084  
2041 GTACGAGAAACATTTTACGAGGCGGAAAGATGGG 2075

RESULT 5  
US-10-006-265-16  
: Sequence 16, Application US/10006265  
: Publication No. US20030125520A1  
: GENERAL INFORMATION:  
: APPLICANT: Maeda, Masatsugu  
: TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10  
: FILE REFERENCE: 06501-096001  
: CURRENT APPLICATION NUMBER: US/10-006-265  
: PRIOR FILING DATE: 2003-01-06  
: PRIOR APPLICATION NUMBER: PCT/JP00/03556  
: PRIOR FILING DATE: 2000-06-01  
: PRIOR APPLICATION NUMBER: JP 11/155797  
: PRIOR FILING DATE: 1999-06-02  
: PRIOR APPLICATION NUMBER: JP 11/217797  
: PRIOR FILING DATE: 1999-07-30  
: NUMBER OF SEQ ID NOS: 40  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 16  
: LENGTH: 2119  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (11)...(1996)  
US-10-006-265-16

Query Match 81.1%; Score 1947; DB 14; Length 2119;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	138	CTCTCTCCCAAGCCTTATGtGTTAACCTGGGGATGATGTGGACCTGGGCACtGTGATG	197
Db	17	CTCTCTCCCAAGCCTTATGtGTTAACCTGGGGATGATGTGGACCTGGGCACtGTGATG	76
OY	198	CTCCCTCACtCTCAAAATTGAGCGCTGGACACTGTGCAGCTTAAGCCtGAGACATTTTCC	257
Db	77	CTCCCTCACtCTCAAAATTGAGCGCTGGACACTGTGCAGCTTAAGCCtGAGACATTTTCC	136
OY	258	TGTGTCTACTACTATAGAAAAATTTAACCTGCACCTTGGAGTCCAGGAAGGAACCAgT	317
Db	137	TGTGTCTACTACTATAGAAAAATTTAACCTGCACCTTGGAGTCCAGGAAGGAACCAgT	196
OY	318	TATACCCAGTTCACAGTAAAGAAAGCTTACGCTTTTGGAGAAAAACAATGATTAATTGACA	377
Db	197	TATACCCAGTTCACAGTAAAGAAAGCTTACGCTTTTGGAGAAAAACAATGATTAATTGACA	256
OY	378	ACCAATAGTCTACAGTGAAGAAATGtGTCTGtGTCTTTTTCCTTCCAAGATAAGC	437
Db	257	ACCAATAGTCTACAGTGAAGAAATGtGTCTGtGTCTTTTTCCTTCCAAGATAAGC	316
OY	438	ATCCAGATTAATTATACCATTGAGGTGGAAAGCTGAAGATGGGTATTAATATCT	497
Db	317	ATCCAGATTAATTATACCATTGAGGTGGAAAGCTGAAGATGGGTATTAATATATCT	376
OY	498	CATATGACATCTGAGATTTAGAAACATACGAAAACTGAACCAACCTAAAGTTTTCGT	557
Db	377	CATATGACATCTGAGATTTAGAAACATACGAAAACTGAACCAACCTAAAGTTTTCGT	436
OY	558	GTGAACACAGTTTGGGCATCAAAACGAATGATTTCAATGATGATTAAGCCtGAGTtTG	617
Db	437	GTGAACACAGTTTGGGCATCAAAACGAATGATTTCAATGATGATTAAGCCtGAGTtTG	496
OY	618	GCGCCTGTTTATGTGATTTAAATTAACACATTCGTGATTCAGACAGTCACAGTACCAgC	677
Db	497	GCGCCTGTTTATGTGATTTAAATTAACACATTCGTGATTCAGACAGTCACAGTACCAgC	556
OY	678	TGATTTGAAGTCAACTTCGCTTAAGAACCCTTAAGATTAAAAACCAACGTACACCTCAGC	737
Db	557	TGATTTGAAGTCAACTTCGCTTAAGAACCCTTAAGATTAAAAACCAACGTACACCTCAGC	616
OY	738	GGCGTCGACGCTTTTACGAATATGTATCTCTGCGATTTGGGGTCAAGAGTCACAAG	797
Db	617	GGCGTCGACGCTTTTACGAATATGTATCTCTGCGATTTGGGGTCAAGAGTCACAAG	676
OY	798	TTCTGGAAGTGAAGTGAAGCAAAAAATGGAATGACTGAGGAAGAAAGCTCtATGtGGC	857
Db	677	TTCTGGAAGTGAAGTGAAGCAAAAAATGGAATGACTGAGGAAGAAAGCTCtATGtGGC	736
OY	858	CTGGAACGTGGAGAGTCTGAAACCGAGCTGAGCGGATGGAAGAAGGCCAGTGGGTG	917
Db	737	CTGGAACGTGGAGAGTCTGAAACCGAGCTGAGCGGATGGAAGAAGGCCAGTGGGTG	796
OY	918	TTATGGAAGAAGGAGAGAGACCCCAgTCTCTAGAGAAACAATCTGGCTAACACATATAGG	977
Db	797	TTATGGAAGAAGGAGAGAGACCCCAgTCTCTAGAGAAACAATCTGGCTAACACATATAGG	856
OY	978	TACTATTCAGAAAGCACACTTAACCTCAGAGAAACAATGAACACTACTTAACCGAGCTT	1037
Db	857	TACTATTCAGAAAGCACACTTAACCTCAGAGAAACAATGAACACTACTTAACCGAGCTT	916
OY	1038	GAACTGCATCTGGGGAGGAGAGGCTTTTGGGTGCTATGATTTCTTAAATTCCTTGGG	1097
Db	917	GAACTGCATCTGGGGAGGAGAGGCTTTTGGGTGCTATGATTTCTTAAATTCCTTGGG	976
OY	1098	AAGTCTCCAGTGGCCACCCTGAGATTCACGCTATTCAAGAAAAATCATTTTCAGTCAAT	1157
Db	977	AAGTCTCCAGTGGCCACCCTGAGATTCACGCTATTCAAGAAAAATCATTTTCAGTCAAT	1036
OY	1158	GAGGTCAATGACAGGCTCGCTGTCTGAGAGACCAAGTACGTGTGAAGTGGCAAAAGCTCTCT	1217
Db	1037	GAGGTCAATGACAGGCTCGCTGTCTGAGAGACCAAGTACGTGTGAAGTGGCAAAAGCTCTCT	1096

QY	1218	CTAGACGTGAACACTTGATGATATTTGAATGGTTTCCGGATGTGGACTAGAGCCACCACC	1277
Db	1097	CTAGACGTGAACACTTGATGATATTTGAATGGTTTCCGGATGTGGACTAGAGCCACCACC	1156
QY	1278	CTTTCCTGGGATCTGTGTCTCCAGGCCACGAACCTGGAGCATCCGCAAGATTAATTTAAA	1337
Db	1157	CTTTCCTGGGATCTGTGTCTCCAGGCCACGAACCTGGAGCATCCGCAAGATTAATTTAAA	1216
QY	1338	CCYTTCTGGTCTATTAACATCTGTGTATCCAAATGTTGCATGACAAAGTTGGCGAGCCA	1397
Db	1217	CCYTTCTGGTCTATTAACATCTGTGTATCCAAATGTTGCATGACAAAGTTGGCGAGCCA	1276
QY	1398	TATTCCATCCAGGGCTTATGCCAAGAAGGGCTTCATCAGAAAGGTCCCGAGCCAGAGTG	1457
Db	1277	TATTCCATCCAGGGCTTATGCCAAGAAGGGCTTCATCAGAAAGGTCCCGAGCCAGAGTG	1336
QY	1458	GAGAACATTGGCGTGGAAGACGGTACGCATGCATGGAAGAAGATTCCCAAGATGAGAGA	1517
Db	1337	GAGAACATTGGCGTGGAAGACGGTACGCATGCATGGAAGAAGATTCCCAAGATGAGAGA	1396
QY	1518	AAGGTTATCATCTGCAACTACACCATCTTTACCACGTGAAGGTGGAAGAAAGATTTCTCC	1577
Db	1337	AAGGTTATCATCTGCAACTACACCATCTTTACCACGTGAAGGTGGAAGAAAGATTTCTCC	1456
QY	1578	AAGAGTCATATTCGACGATCTTTCAGTACGAGCGGCTGGAGTCCCTGAAACGAAACCTCT	1637
Db	1457	AAGAGTCATATTCGACGATCTTTCAGTACGAGCGGCTGGAGTCCCTGAAACGAAACCTCT	1516
QY	1638	TACATTTGTCAGGTATCGGCCACGACACGATGCTGGGGAAACCAAGGGACCAGCATTAAT	1697
Db	1517	TACATTTGTCAGGTATCGGCCACGACACGATGCTGGGGAAACCAAGGGACCAGCATTAAT	1576
QY	1698	TTCAAGACATTTGTCATTCAGTGTCTTTAGATTTATCCCATTAACCTTCCTGATTTGGGGA	1757
Db	1577	TTCAAGACATTTGTCATTCAGTGTCTTTAGATTTATCCCATTAACCTTCCTGATTTGGGGA	1636
QY	1758	GGCCTTTCTTATTCATTTATCTGACAGCTGCGATATGGTCTCAAAAAACCACAAATTG	1817
Db	1637	GGCCTTTCTTATTCATTTATCTGACAGCTGCGATATGGTCTCAAAAAACCACAAATTG	1696
QY	1818	ACTCATCTGTGTGGCCCCAGCGTTGCCAACGCTGCTGAAATAGTATATAGCCATGGCAT	1877
Db	1697	ACTCATCTGTGTGGCCCCAGCGTTGCCAACGCTGCTGAAATAGTATATAGCCATGGCAT	1756
QY	1878	GGAGATGATTTCAAGGATTAAGCTTAAGGAGTCTGATGACTCTGTGTAACACAGAA	1937
Db	1757	GGAGATGATTTCAAGGATTAAGCTTAAGGAGTCTGATGACTCTGTGTAACACAGAA	1816
QY	1938	GACAGATCTTAAAAACCATGTTTCCACCCCGCAGTGCACAAGTTGGTGATTTGACAACTGGTG	1997
Db	1817	GACAGATCTTAAAAACCATGTTTCCACCCCGCAGTGCACAAGTTGGTGATTTGACAACTGGTG	1876
QY	1998	GTAAGCTTTGGAAATGTTCTCAGAGAAATTTTCACAGATGAAAGCAGAGAGGGTACAGAA	2057
Db	1877	GTAAGCTTTGGAAATGTTCTCAGAGAAATTTTCACAGATGAAAGCAGAGAGGGTACAGAA	1936
QY	2058	AACAATTTAGAGGGGAAAAAGATGGG 2084	
Db	1937	AACAATTTAGAGGGGAAAAAGATGGG 1963	

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RESULT 6
US-09-892-949-53
; Sequence 53, Application US/098922949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kiljiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17

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FILE REFERENCE: 00-42  
CURRENT APPLICATION NUMBER: US/09/892,949  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: US 60/214,282  
PRIOR FILING DATE: 2000-06-26  
PRIOR APPLICATION NUMBER: US 60/214,955  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/267,963  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 53  
LENGTH: 2903  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (497)...(2482)  
US-09-892-949-53

Query Match Best Local Similarity 81.0%; Score 1945.4; DB 11; Length 2903;  
Matches 1946; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

138 CTCCTCCCGCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCCTGTGATG 197  
138 CTCCTCCCGCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCCTGTGATG 197  
503 CTCCTCCCGCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCCTGTGATG 562  
198 CTCCTCCCGCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCCTGTGATG 257  
563 CTCCTCCCGCAGCCTTCATGTGTTAACCTGGGATGATGTGACCTGGGCCTGTGATG 622  
258 TGTGTCTACTACTATAGAGAAAATTTAACTGCACTTGAGTCCAGGAAAGAAACAGT 317  
623 TGTGTCTACTACTATAGAGAAAATTTAACTGCACTTGAGTCCAGGAAAGAAACAGT 682  
318 TATATCCAGTACAGCAGTTAAGAGACTTACGCTTTGGAGAAAACATGATTAATTGACA 377  
683 TATATCCAGTACAGCAGTTAAGAGACTTACGCTTTGGAGAAAACATGATTAATTGACA 742  
378 ACCAATGATCTACAGTGAAGAAATCGTGGCTGCTTTTCCCTCCAGAAATAGC 437  
743 ACCAATGATCTACAGTGAAGAAATCGTGGCTGCTTTTCCCTCCAGAAATAGC 802  
438 ATCCAGATATATTTACCATTTGAGTGAAGCTGAAGTGAAGTGAATTAATTAATCT 497  
803 ATCCAGATATATTTACCATTTGAGTGAAGCTGAAGTGAAGTGAATTAATTAATCT 862  
498 CATATGACATATCTGAGATTAAGAGACATAGCGAAACCTGAACCCCTAAGATTTCCT 557  
863 CATATGACATATCTGAGATTAAGAGACATAGCGAAACCTGAACCCCTAAGATTTCCT 922  
558 GTGAACACAGTTTGGGATCAAAAGCATGTTCAATTTGAATGATTAAGCCGATG 617  
923 GTGAACACAGTTTGGGATCAAAAGCATGTTCAATTTGAATGATTAAGCCGATG 982  
618 GCGGCTTTTCATCTGATTTAAATATACACATTCGATTCAGGACATCAACAGTACAGC 677  
983 GCGGCTTTTCATCTGATTTAAATATACACATTCGATTCAGGACATCAACAGTACAGC 1042  
678 TGGATGGAAGTCAACTTCGCTAAGAACCTGAAGATTAAGCAACCAACCTGACG 737  
1043 TGGATGGAAGTCAACTTCGCTAAGAACCTGAAGATTAAGCAACCAACCTGACG 1102  
738 GGGCTGAGCCTTTTACAGATATATGATAGCTGTGATGATGGGTCAGAGGATCAAG 797  
1103 GGGCTGAGCCTTTTACAGATATATGATAGCTGTGATGATGGGTCAGAGGATCAAG 1162  
798 TTTTGGAGTACTGAGACCAAGAAAATGGAATGATGAGGAAAGAGCTCCATGTGGC 857  
1163 TTTTGGAGTACTGAGACCAAGAAAATGGAATGATGAGGAAAGAGCTCCATGTGGC 1222  
858 CTGGAAGTGTGAGAGTCTTGAAACCAAGTGAAGCGGATGGAAGAACGCAAGTGGGTTG 917

1223 CTGGAAGTGTGAGAGTCTTGAAACCAAGTGAAGCGGATGGAAGAACGCAAGTGGGTTG 1282  
918 TTATGGAAGAAAGCAAGAGAGCCCGAGCTCTAGAGAAAACACTTGGCTACACATATGG 977  
1283 TTATGGAAGAAAGCAAGAGAGCCCGAGCTCTAGAGAAAACACTTGGCTACACATATGG 1342  
978 TACTATCCAGAAACCACTAATCTCAGAAACATGAACTACTAATACACAGCAGCTT 1037  
1343 TACTATCCAGAAACCACTAATCTCAGAAACATGAACTACTAATACACAGCAGCTT 1402  
1038 GAATGATCTGTGGAGGCGAGAGCTTTGGGTGTCTATGATTTCTTAAATTCCTTGGG 1097  
1403 GAATGATCTGTGGAGGCGAGAGCTTTGGGTGTCTATGATTTCTTAAATTCCTTGGG 1462  
1098 AAGTCTCAGTGGGACCCCTGAGATTTCCAGCTATTTCAAGAAAATATCTAGTGCATT 1157  
1463 AAGTCTCAGTGGGACCCCTGAGATTTCCAGCTATTTCAAGAAAATATCTAGTGCATT 1522  
1158 GAGGTCAATGAGGCGCTGTTGCTGAGAGACAGCTAGTGGTGAAGTGCAGAAAGCTGTGCT 1217  
1523 GAGGTCAATGAGGCGCTGTTGCTGAGAGACAGCTAGTGGTGAAGTGCAGAAAGCTGTGCT 1582  
1218 CTAGACGTGAACACTTGGATGATTAATGCTTCCGATGTGACATGAGCCGACACC 1277  
1583 CTAGACGTGAACACTTGGATGATTAATGCTTCCGATGTGACATGAGCCGACACC 1642  
1278 CTTTCCCTGGGAATCTGTGTCTCAGGCCACCAACCTGAGACATCCAGAAAGTAAATTTAAA 1337  
1643 CTTTCCCTGGGAATCTGTGTCTCAGGCCACCAACCTGAGACATCCAGAAAGTAAATTTAAA 1702  
1338 CTTTCTGTGTCTATACATCTCTGTATTCATCAATTTGATGACAAAGTTGGGAGCCA 1397  
1703 CTTTCTGTGTCTATACATCTCTGTATTCATCAATTTGATGACAAAGTTGGGAGCCA 1762  
1398 TATTCATCCAGGCTTATGCCAAAGAGCGCTTCATAGAGTCTGTGAGACAGTG 1457  
1763 TATTCATCCAGGCTTATGCCAAAGAGCGCTTCATAGAGTCTGTGAGACAGTG 1822  
1458 GAGAACATTTGGCGGAGAGCGGTGAGATCATAGGAAAGAGATTTCCAGAGTGAAGA 1517  
1823 GAGAACATTTGGCGGAGAGCGGTGAGATCATAGGAAAGAGATTTCCAGAGTGAAGA 1882  
1518 AAGGATATCATCTGCAACTACACCATTTTACCAAGCTGAAGTGGAAAAGATTCTCC 1577  
1883 AAGGATATCATCTGCAACTACACCATTTTACCAAGCTGAAGTGGAAAAGATTCTCC 1942  
1578 AAGCACTCAATTCACACATCTTGCACTACGGCTGAGTCCCTGAAGCAAGACCTCT 1637  
1943 AAGCACTCAATTCACACATCTTGCACTACGGCTGAGTCCCTGAAGCAAGACCTCT 2002  
1638 TACATGTTGAGGTCATGAGGCGAGCAGCAGTGGTGGGGAACCAAGGAGACCATTAAT 1697  
2003 TACATGTTGAGGTCATGAGGCGAGCAGCAGTGGTGGGGAACCAAGGAGACCATTAAT 2062  
1698 TTCAAGACATTTGATTCAGTCACTGCTTGAAGATTAATCCATTAATCTCTGATTTGTGA 1757  
2063 TTCAAGACATTTGATTCAGTCACTGCTTGAAGATTAATCCATTAATCTCTGATTTGTGA 2122  
1758 GGCCTTTTATTCATATTTATCTGACAGTGGCATATGCTCAAAAAACCAACAAATTG 1817  
2123 GGCCTTTTATTCATATTTATCTGACAGTGGCATATGCTCAAAAAACCAACAAATTG 2182  
1818 ACTCATCTGTGTGGGCGCCAGCTTCCCAACCCGCTGAAGTGTATAGCCACATGGCAT 1877  
2183 ACTCATCTGTGTGGGCGCCAGCTTCCCAACCCGCTGAAGTGTATAGCCACATGGCAT 2242  
1878 GGAAGATATTTCAAGATTAAGCTTAACCTGAAGAGTCTGATGATCTGTGAACACAGAA 1937  
2243 GGAAGATATTTCAAGATTAAGCTTAACCTGAAGAGTCTGATGATCTGTGAACACAGAA 2302  
1938 GACAGATCTTTAAACCATTTCCACCCCAAGTGAAGTTGGTGTGAAGTTGGTG 1997

Db	2303	GACAGATCTTAAACCATGTCACCCCGAGTACAGATTGTGATTCAGCACTGGTG	2362	Db	949	GTGAACCACTTTTGGGCATCAAAAGATATTCAAATTGAATGATTAAGCCTGAGTTG	1008
Qy	1998	GTGAACCTTTGGGATGTTCTGCAGAAATTTTCACAGTGAAGCCAGAGGGTCAGGAA	2057	Qy	618	GGGCTGTTTATCTGATTTTAAATPACACTTCTGATTCAGGACAGTCAACAGTACAGC	677
Db	2363	GTGAACCTTTGGGATGTTCTGCAGAAATTTTCACAGTGAAGCCAGAGGGTCAGGAA	2422	Db	1009	GGGCTGTTTATCTGATTTTAAATPACACTTCTGATTCAGGACAGTCAACAGTACAGC	1068
Qy	2058	AACAATTTAGAGGGGAGAAAGATGGG	2084	Qy	678	TGATGAGACATCACTTCGCTAAGAACGTTAAGATTAATAACCAAGCTACACCTCAGC	737
Db	2423	AACAATTTAGAGGGGAGAAAGATGGG	2449	Db	1069	TGATGAGACATCACTTCGCTAAGAACGTTAAGATTAATAACCAAGCTACACCTCAGC	1128
RESULT 7							
US-10-006-265-1							
: Sequence 1, Application US/10006265							
: Publication No. US20030125520A1							
: GENERAL INFORMATION:							
: APPLICANT: Maeda, Masatsugu							
: TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10							
: FILE REFERENCE: 06501-096001							
: CURRENT APPLICATION NUMBER: US/10/006,265							
: PRIOR FILING DATE: 2003-01-06							
: PRIOR APPLICATION NUMBER: PCT/JP00/03556							
: PRIOR FILING DATE: 2000-06-01							
: PRIOR APPLICATION NUMBER: JP 11/155797							
: PRIOR FILING DATE: 1999-06-02							
: PRIOR APPLICATION NUMBER: JP 11/217797							
: PRIOR FILING DATE: 1999-07-30							
: NUMBER OF SEQ ID NOS: 40							
: SOFTWARE: FastSeq for Windows Version 4.0							
: SEQ ID NO 1							
: LENGTH: 2969							
: TYPE: DNA							
: ORGANISM: Homo sapiens							
: FEATURE:							
: NAME/KEY: CDS							
: LOCATION: (523)...(2478)							
US-10-006-265-1							
Query March 80.5%: Score 1932.8; DB 14; Length 2969;							
Best Local Similarity 99.8%: Pred. No. 0;							
Matches 1945; Conservative 0; Mismatches 2; Indels 1; Gaps 1;							
Qy	138	CTCTCTCCCGACGCTTCATGTGTTACCTGGGATGATGTGACCTGGGCACTGTGATG	197	Qy	1218	CTAGACGTGAACACTTGGATGATTAATGATTTCCGGATGTGAGCTCAGACCCACACG	1277
Db	529	CTCTCTCCCGACGCTTCATGTGTTACCTGGGATGATGTGACCTGGGCACTGTGATG	588	Db	1609	CTAGACGTGAACACTTGGATGATTAATGATTTCCGGATGTGAGCTCAGACCCACACG	1668
Qy	198	CTCCCTCTCTCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCCTGAGACATTTCC	257	Qy	1278	CTTTCCTGGGAATCTGTCTCAGGCCACGACATGAGATCCAGCAAGATTAATAA	1337
Db	589	CTCCCTCTCTCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCCTGAGACATTTCC	648	Db	1669	CTTTCCTGGGAATCTGTCTCAGGCCACGACATGAGATCCAGCAAGATTAATAA	1728
Qy	258	TGTCCTACTCTATAGSAAATTTAACTGCACTTGAGTCCAGAGAAAGAAACAGT	317	Qy	1338	CCTTCTGCTGCTATTAACATCTCTGTGTATCCAGTGTGCAATGAAAGTTGGGAGGCA	1397
Db	649	TGTCCTACTCTATAGSAAATTTAACTGCACTTGAGTCCAGAGAAAGAAACAGT	708	Db	1729	CCTTCTGCTGCTATTAACATCTCTGTGTATCCAGTGTGCAATGAAAGTTGGGAGGCA	1788
Qy	318	TATACCCAGTACAGATTAAGAGAACTTACCTTTTGAGAGAAAAACATGATTAATTGCA	377	Qy	1398	TATTCATCCAGGCTTATGCCAAGAAAGGCTTCCATCAGAAAGTCTCGAAGCAAGGTG	1457
Db	709	TATACCCAGTACAGATTAAGAGAACTTACCTTTTGAGAGAAAAACATGATTAATTGCA	768	Db	1789	TATTCATCCAGGCTTATGCCAAGAAAGGCTTCCATCAGAAAGTCTCGAAGCAAGGTG	1848
Qy	378	ACCAATAGTCTACAGTGAAGTAAATCGTCTCTCTTTTTCCTTCCAAAGATAAG	437	Qy	1458	GAGAACATTTGGCGGTGAAGCGGTCCAGATCAATGAGAAAGATTTCCCAAGATGAGAG	1517
Db	769	ACCAATAGTCTACAGTGAAGTAAATCGTCTCTCTTTTTCCTTCCAAAGATAAG	828	Db	1849	GAGAACATTTGGCGGTGAAGCGGTCCAGATCAATGAGAAAGATTTCCCAAGATGAGAG	1908
Qy	438	ATCCAGATTAATTAACATGAGGTGAAGCTGAAATGAGATGGTGAATTAATCT	497	Qy	1518	AAGGTATCATCTGCAATCAACATCTTTTAACCAAGCTGAAGGTGAAGAAAGANTCTCC	1577
Db	829	ATCCAGATTAATTAACATGAGGTGAAGCTGAAATGAGATGGTGAATTAATCT	888	Db	1909	AAGGTATCATCTGCAATCAACATCTTTTAACCAAGCTGAAGGTGAAGAAAGANTCTCC	1968
Qy	498	CATATGACATCTAGAGATTAAGAGAACTAGCAAAACCTGAACCACTAAGATTTCCGT	557	Qy	1578	AAGACATCAATTCAGCATCTTTCAGTACGCGCTGAGTCCCTGAAACGAAACCTCT	1637
Db	889	CATATGACATCTAGAGATTAAGAGAACTAGCAAAACCTGAACCACTAAGATTTCCGT	948	Db	1969	AAGACATCAATTCAGCATCTTTCAGTACGCGCTGAGTCCCTGAAACGAAACCTCT	2028
Qy	558	GTGAACCACTTTTGGGCATCAAAAGATGATTCAAATTTGAATGATTAAGCCTGAGTTG	617	Qy	1638	TACATGTTTCAGGTGATGAGCCACGACAGTGTCTGGGGAGAACCAACGGGACCATTAAT	1697
Db				Db	2029	TACATGTTTCAGGTGATGAGCCACGACAGTGTCTGGGGAGAACCAACGGGACCATTAAT	2088

OY	1698	TTCAAGACATGTGCTATTAGTGTCTTTAGATTAATTCATTAACCTTCTGTATTGGTGA	1751
Db	2089	TTCAAGACATGTGCTATTAGTGTCTTTAGATTAATTCATTAACCTTCTGTATTGGTGA	2148
OY	1758	GCCCTTCCTTATTCATTCATTCCTGACATGGGCAATGGTCTCAAAAAAACCACAATTG	1817
Db	2149	GCCCTTCCTTATTCATTCATTCCTGACATGGGCAATGGTCTCAAAAAAACCACAATTG	2208
OY	1818	ACTCATCTGTGTGGCCACCCTTCCCAACCTGCTGAAGTAGATTAAGCCATGGCAT	1877
Db	2209	ACTCATCTGTGTGGCCACCCTTCCCAACCTGCTGAAGTAGATTAAGCCATGGCAT	2268
OY	1878	GGAGATGATTTTCAAGGATTAAGCTTAACCTGAAGGAGTCTGATGACTGTGTAACACAGAA	1937
Db	2269	GGAGATGATTTTCAAGGATTAAGCTTAACCTGAAGGAGTCTGATGACTGTGTAACACAGAA	2328
OY	1938	GACAGGATCTTAANAACCATGTTTCCACCCCGGTACACAGTTGGTGATTTGACAGTTGGTG	1997
Db	2339	GACAGGATCTTAANAACCATGTTTCCACCCCGGTACACAGTTGGTGATTTGACAGTTGGTG	2388
OY	1998	GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTCCACATGTAAGCCAGACGGGTCAAGG -A	2056
Db	2389	GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTCCACATGTAAGCCAGACGGGTCAAGAA	2448
OY	2057	AAACAATTTAGAGGGGAAAAAAGATGGG	2084
Db	2449	AAACAATTTAGAGGGGAAAAAAGATGGG	2476

```

RESULT 8
US-09-892-949-4
Sequence 4, Application US/09892949
Publication No. US2003096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.
APPLICANT: Kulpfer, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIORITY APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 2196
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate polynucleotide sequence of SEQ ID NO:2.
NAME/KEY: misc.feature
LOCATION: (1)...(2196)
OTHER INFORMATION: n = A,T,C or G
US-09-892-949-4

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Query Match	66.3%;	Score 1592.2;	DB 11;	Length 2196;
Best Local Similarity	58.8%;	Pred. No. 0;		
Matches 1291;	Conservative 530;	Mismatches 374;	Indels 0;	Gaps 0;

QY 171 ATGATGTGACCTGGGCACCTGTGATGCTCCCTCACTGTGCAATTGACGTGGCAGCT 230  
||||| ||||| :| ||||| || :| ||||| :||| :| |||  
Db 1 ATGATGTGACCTGGGCATTTGATGTGCTTCCNNSTNTTGYARTTWTYSNYTNGCGNCN 60  
QY 231 CTGCGAGCTAAGCTGAGACACATTTCCGTGTCTACACACTATAGAGAAAATTTTAACTGC 290

[illegible]

Db	1141	TGACCNTHCARCARGAAYARVTNAACNMTTGTGGYTAAYAAATHMSNGTAAACN	1200
QY	1371	ATGTTGCATGACAAAGTTGGCGAGCCATATTCATCCAGCCTTATGCCAAAGGCGTT	1430
Db	1201	ATGTTTCAAYAAAFRTGNGNGARCGTAAVWSNTHCARCNPATYGCNARAGGNGTN	1260
QY	1431	CCATCAACAAGTCTGTGAGCCAAAGGTGGACAACCTTTGGCTGAAAGAGGTCAGATACA	1490
Db	1261	CCMNSNARGNCCNGARACNAAAGTGGARAAVTHGNGSTNAARACNGTNACATACN	1320
QY	1491	TGCAAAAGATATTCOCAGAGTGGAGAGAAAGGGTTCATCTGCAACTCACCATCTTTAC	1550
Db	1321	TGGAARARARATHCCNAARMSGARMGAARGNATHHTHTGYAATYTAACNATHTTAY	1380
QY	1551	CAAGCTGAAGGTGAAAAAGGATTTCTCCAGACAGTCAATTCACGACATCTTGAGTACGC	1610
Db	1381	CARCCNARGNGNGNARCGNTTYSNAARCNCTNAAYMSWSNATHYNCARTAYG	1440
QY	1611	CTGAGATCCCTGGAACGAAGACCTCTTACATGTTTGTAGTCACTGGCCAGCACAGTCT	1670
Db	1441	YTNARMSNTTNAARMGNARACMSNTAAVHTGNCARGTNAAGCNSACMSWSG	1500
QY	1671	GGGGGAACCAAGGAGGACACCATCAATTAATTTCCAGCATTCGATTCAGTCTTTGAGAT	1730
Db	1501	GGNGNACNAAYGNCNMSNATHAATTTAAARCNATNSNTTYSNGTNTTYYGARATH	1560
QY	1731	ATCCTCAATCTTCTGATTTGGTGAAGGCTTCTTATTCATTAATCCTGACAGTGGCA	1790
Db	1561	ATHYTNTATHACMSNTYNTATHGGNGGCGNTYTNTATHYNTATHYNTACNGTNGCN	1620
QY	1791	TATGCTGTCAAAAAACCCAAATATTCATCTGTGTGTGGCCACCCTTCCCAACCT	1850
Db	1621	TATGNTTNAARARCCNAAVAAATYTNACCAVATNTGYGGCCNACNGNCCAAACCN	1680
QY	1851	GCTCAAGATGATATGACCATGTGCGATGAGATGATTTCAAGGATTAAGCTAAACCTGA	1910
Db	1681	GCNARMSNMSNATHGCMACNTGCCAAGNGATYATTTAARGAAYARVTAAYTNAAR	1740
QY	1911	GAGTCTGATGACTGTGGAACACAGAAGACAGATCTTAAACCATGTTCCACCCAGT	1970
Db	1741	GARMSNCAAYGWSNGTNAAYACNGAGAVMGNTHTYNAARCCNTGYWSNACNCNWSN	1800
QY	1971	GACAAGTTGGGATGTGCAAGTGTGCTGTGAACCTTTGGGATGTTCTGCAAGAAATTTTC	2030
Db	1801	GAYARVTNGTNATHGAYAAAYTNGTGNATNAAYTTYGNAAYGTNYNCARGARATHTY	1860
QY	2031	ACAGATGAAGCGCAAGGCTGACGAAGAAACAATTTAGAGGGGAAAGATGGGTATGTG	2090
Db	1861	ACNAYARGRCNMGNACNGNCARGARAAVTAAYTTGNGNGNKGARAPAAAGTATAGTN	1920
QY	2091	ACCTGCCCTTACAGCCTGATTTGTCCTCCCTGGGGAAGATTTTGAGGAGCTCCAGTTTCA	2150
Db	1921	ACNTGYCCNTTMYMNCNGAYTGYCYNTINGNNAARMSNTTYGARGARVYTMCCGTMWSN	1980
QY	2151	CCTAGATTCGGCCCAAGAAATCCCAATACCTACGTTCCAGAGTCCAGAGGGGACCCGC	2210
Db	1981	CCNBARPTHCCNCNMNNAARMSNCARTAYTTNGMNSNMGNATGCCNGARGCAACNMGN	2040
QY	2211	CCAGAAGCGAAAGAGCTCTCTCTTTCTGCGTCAAAAGTTAGTACAGATCACTGTGT	2270
Db	2041	CCNGARCNARNGARCARVNTYNTTWTWSNGNCARMSNTTNGNCCNGAAYVNTGY	2100
QY	2271	GAGGAAGAGAGCCCAATTCATATTTTGAAGAAATTCAGTGACAGCCAGAGAAATTTCTGTG	2330
Db	2101	GARGARGNGNCCNNAAYCCNTAYTTNAARAAYWSNCTNACNCGNMGNARATYYTNGTN	2160
QY	2331	TCTTAAAAAATCTCCAGAGCACACCAAGGAGAGCT 2365	
Db	2161	WSNGARARAYTNCNCGARCAVACNAAGNGANGRGT 2195	

	Sequence 68, Application US/098929949
	Publication No. US20030096339A1
	GENERAL INFORMATION:
	APPLICANT: Sprecher, Cindy A.
	APPLICANT: Presnell, Scott R.
	APPLICANT: Gao, Zeren
	APPLICANT: Whitmore, Theodore E.
	APPLICANT: Kullper, Joseph L.
	TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTORL7
	FILE REFERENCE: 00-42
	CURRENT APPLICATION NUMBER: US/09/892,949
	CURRENT FILING DATE: 2001-06-26
	PRIOR APPLICATION NUMBER: US 60/214,282
	PRIOR FILING DATE: 2000-06-26
	PRIOR APPLICATION NUMBER: US 60/214,955
	PRIOR FILING DATE: 2000-06-29
	PRIOR APPLICATION NUMBER: US 60/267,963
	PRIOR FILING DATE: 2001-08-02
	NUMBER OF SEQ ID NOS: 93
	SOFTWARE: FastSeq for Windows Version 3.0
	SEQ ID NO 68
	LENGTH: 2295
	TYPE: DNA
	ORGANISM: Artificial Sequence
	FEATURE:
	OTHER INFORMATION: Polynucleotide encoding human zcytorl7-Fc4 fusion
	NAME/KEY: CDS
	LOCATION: (1)...(2295)
	US-09-892-949-68
Query Match	66.1%, Score 1586.8; DB 11; Length 2295;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1588; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	138 CTCCTCCCGCAGCTTCATGTGTTAACTGGGGGATGATGTGACTTGCGCATGTGATG 197
DB	7 CTCCTCCCGCAGCTTCATGTGTTAACTGGGGGATGATGTGACTTGCGCATGTGATG 66
OY	198 CTCCCCTCACCTCGCAAAATTACGCTGCAGCTCGCCAGCTTAACCTGAGAACATTTCC 257
DB	67 CTCCTTCACCTCGCAAAATTACGCTGCAGCTCGCCAGCTTAACCTGAGAACATTTCC 126
OY	258 TGTGCTACTACTATAGAAAAAATTTAACTGCACTTGSAGTCCAGAAAAGGAACAAGT 317
DB	127 TGTGCTACTACTATAGAAAAAATTTAACTGCACTTGSAGTCCAGAAAAGGAACAAGT 186
OY	318 TATACCAGTACACAGTTAAGAAGAACTTACGCTTTTGGAGAAAAACATGATATTGTACA 377
DB	187 TATACCAGTACACAGTTAAGAAGAACTTACGCTTTTGGAGAAAAACATGATATTGTACA 246
OY	378 ACCATAATGTTACACAGTGAAGAAATGSGCTTCGCTGCTTTTTCCTCCAGAAATPACG 437
DB	247 ACCATAATGTTACACAGTGAAGAAATGSGCTTCGCTGCTTTTTCCTCCAGAAATPACG 306
OY	438 ATCCAGATAATTATACCATTTAGAGTGGAGCTGAAAATGAGATGATTAATTAAATCT 497
DB	307 ATCCAGATAATTATACCATTTAGAGTGGAGCTGAAAATGAGATGATTAATTAAATCT 366
OY	498 CATATGACATCTGAGAGATTAGAGAACATPAGGAAAACAGCAACACCTTAGATTTTTCCG 557
DB	367 CATATGACATCTGAGAGATTAGAGAACATPAGGAAAACAGCAACACCTTAGATTTTTCCG 426
OY	558 GTGAACACAGTTTGGGCAATCAAAGAAATGATCAAAATGAAATGATTAAGCTCAGATTG 617
DB	427 GTGAACACAGTTTGGGCAATCAAAGAAATGATCAAAATGAAATGATTAAGCTCAGATTG 486
OY	618 GCGCCGTTTCATCGATTAAAAATACACACTTCGATTCAGAGACAGTCAACAGTACCAAGC 677
DB	487 GCGCCGTTTCATCGATTAAAAATACACACTTCGATTCAGAGACAGTCAACAGTACCAAGC 546
OY	678 TGATGAGAGTCACTTGCGTAAAGACCGTAAAGATTAANAACCAACGTAACAACCTCACG 737



Db 547 TGGATGGAAGTCACTTCGCTAAGAACCGTAAGATAAAACCAAGCTACACCTCAGC 606  
Qy 738 GGGCTGCGACCTTTTACAGAAATATGTCACTAGCTGCGATGTGGCGTCAAGAGTCAAG 797  
Db 607 GGGCTGCGACCTTTTACAGAAATATGTCACTAGCTGCGATGTGGCGTCAAGAGTCAAG 666  
Qy 798 TTCTGAGAGTGAAGTGAAGCAAGAAATGGGAATGACTGAGGAAGAAAGCTCATGTGGC 857  
Db 667 TTCTGAGAGTGAAGTGAAGCAAGAAATGGGAATGACTGAGGAAGAAAGCTCATGTGGC 726  
Qy 858 CTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 917  
Db 727 CTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 786  
Qy 918 TTATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 977  
Db 787 TTATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 846  
Qy 978 TACTATCCAGAAACAACTAATCTCAGAGAAACATGAACACTACTAACACAGCCTT 1037  
Db 847 TACTATCCAGAAACAACTAATCTCAGAGAAACATGAACACTACTAACACAGCCTT 906  
Qy 1038 GAATGATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1097  
Db 907 GAATGATCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 966  
Qy 1098 AAGTCTCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1157  
Db 967 AAGTCTCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1026  
Qy 1158 GAGGTCATGACAGGCGCTGCTGCTGAGAGACAGCTAGTGTGAAGTGGCAAGCTGCT 1217  
Db 1027 GAGGTCATGACAGGCGCTGCTGCTGAGAGACAGCTAGTGTGAAGTGGCAAGCTGCT 1086  
Qy 1218 CTACAGCTGAACATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1277  
Db 1087 CTACAGCTGAACATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146  
Qy 1278 CTTTCCTGGAATCTGTGTCTCAGGCGACGAACTGAGAGATCGAGAAATTAATTAATA 1337  
Db 1147 CTTTCCTGGAATCTGTGTCTCAGGCGACGAACTGAGAGATCGAGAAATTAATTAATA 1206  
Qy 1338 CTTTCCTGGAATCTGTGTCTCAGGCGACGAACTGAGAGATCGAGAAATTAATTAATA 1397  
Db 1207 CTTTCCTGGAATCTGTGTCTCAGGCGACGAACTGAGAGATCGAGAAATTAATTAATA 1266  
Qy 1398 TATTCATCCAGGCTTATGCAAAAGAGGCTTCATCAGAAAGTCTCGAGACCAAGTGTG 1457  
Db 1267 TATTCATCCAGGCTTATGCAAAAGAGGCTTCATCAGAAAGTCTCGAGACCAAGTGTG 1326  
Qy 1458 GAGAACATTTGGCGTGAAGAGCGTCAAGATCATGAGAAAGATTTCCCAAGAGTGAAGA 1517  
Db 1327 GAGAACATTTGGCGTGAAGAGCGTCAAGATCATGAGAAAGATTTCCCAAGAGTGAAGA 1386  
Qy 1518 AAGGCTATCATCTGCAACTACACCATCTTTTACCAGCTGAAGTGAAGTGAAGTGAAGT 1577  
Db 1387 AAGGCTATCATCTGCAACTACACCATCTTTTACCAGCTGAAGTGAAGTGAAGTGAAGT 1446  
Qy 1578 AAGGCTATCATCTGCAACTACACCATCTTTTACCAGCTGAAGTGAAGTGAAGTGAAGT 1637  
Db 1447 AAGGCTATCATCTGCAACTACACCATCTTTTACCAGCTGAAGTGAAGTGAAGTGAAGT 1506  
Qy 1638 TACATTTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1697  
Db 1507 TACATTTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1566  
Qy 1698 TTCAAGATTTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1727  
Db 1567 TTCAAGATTTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1566

RESULT 10  
US-10-227-884-91

Sequence 91, Application US/10227884  
Publication No. US20030027988A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C79  
CURRENT APPLICATION NUMBER: US/10/227,884  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089905  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090651  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/095302  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095318  
PRIOR FILING DATE: 1998-08-04



PRIOR APPLICATION NUMBER:	60/093519
PRIOR FILING DATE:	1998-08-10
PRIOR APPLICATION NUMBER:	60/096146
PRIOR FILING DATE:	1998-08-11
PRIOR APPLICATION NUMBER:	60/096791
PRIOR FILING DATE:	1998-08-17
PRIOR APPLICATION NUMBER:	60/097966
PRIOR FILING DATE:	1998-08-26
PRIOR APPLICATION NUMBER:	60/098544
PRIOR FILING DATE:	1998-08-31
PRIOR APPLICATION NUMBER:	60/099566
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099558
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/099803
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099811
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099812
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099816
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/100038
PRIOR FILING DATE:	1998-09-11
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PRIOR FILING DATE:	1998-09-16
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PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1998-09-17
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PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101738
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101741
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101766
PRIOR FILING DATE:	1998-09-25
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PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101922
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/106178
PRIOR FILING DATE:	1998-10-28
PRIOR APPLICATION NUMBER:	60/106248
PRIOR FILING DATE:	1998-10-29
PRIOR APPLICATION NUMBER:	60/106464
PRIOR FILING DATE:	1998-10-30
PRIOR APPLICATION NUMBER:	60/106905
PRIOR FILING DATE:	1998-11-03
PRIOR APPLICATION NUMBER:	60/108787
PRIOR FILING DATE:	1998-11-17
PRIOR APPLICATION NUMBER:	60/108801
PRIOR FILING DATE:	1998-11-17
PRIOR APPLICATION NUMBER:	60/108849
PRIOR FILING DATE:	1998-11-18
PRIOR APPLICATION NUMBER:	60/112422
PRIOR FILING DATE:	1998-12-15
PRIOR APPLICATION NUMBER:	60/113266
PRIOR FILING DATE:	1998-12-22
PRIOR APPLICATION NUMBER:	60/113605
PRIOR FILING DATE:	1998-12-23
PRIOR APPLICATION NUMBER:	60/113621
PRIOR FILING DATE:	1998-12-23
PRIOR APPLICATION NUMBER:	60/115558
PRIOR FILING DATE:	1999-01-12
PRIOR APPLICATION NUMBER:	60/115565
PRIOR FILING DATE:	1999-01-12
PRIOR APPLICATION NUMBER:	60/115733
PRIOR FILING DATE:	1999-01-12
PRIOR APPLICATION NUMBER:	60/115733

1	PRIOR FILING DATE: 1999-01-12
2	PRIOR APPLICATION NUMBER: 60/119549
3	PRIOR FILING DATE: 1999-02-10
4	PRIOR APPLICATION NUMBER: 60/123618
5	PRIOR FILING DATE: 1999-03-10
6	PRIOR APPLICATION NUMBER: 60/125259
7	PRIOR FILING DATE: 1999-03-19
8	PRIOR APPLICATION NUMBER: 60/125775
9	PRIOR FILING DATE: 1999-03-23
10	PRIOR APPLICATION NUMBER: 60/126773
11	PRIOR FILING DATE: 1999-03-29
12	PRIOR APPLICATION NUMBER: 60/127867
13	PRIOR FILING DATE: 1999-04-05
14	PRIOR APPLICATION NUMBER: 60/130232
15	PRIOR FILING DATE: 1999-04-21
16	PRIOR APPLICATION NUMBER: 60/131022
17	PRIOR FILING DATE: 1999-04-26
18	PRIOR APPLICATION NUMBER: 60/131270
19	PRIOR FILING DATE: 1999-04-27
20	PRIOR APPLICATION NUMBER: 60/131291
21	PRIOR FILING DATE: 1999-04-27
22	PRIOR APPLICATION NUMBER: 60/131445
23	PRIOR FILING DATE: 1999-04-28
24	PRIOR APPLICATION NUMBER: 60/134287
25	PRIOR FILING DATE: 1999-05-14
26	PRIOR APPLICATION NUMBER: 60/140650
27	PRIOR FILING DATE: 1999-06-22
28	PRIOR APPLICATION NUMBER: 60/140723
29	PRIOR FILING DATE: 1999-06-22
30	PRIOR APPLICATION NUMBER: 60/141037
31	PRIOR FILING DATE: 1999-06-23
32	PRIOR APPLICATION NUMBER: 60/144758
33	PRIOR FILING DATE: 1999-07-20
34	PRIOR APPLICATION NUMBER: 60/145698
35	PRIOR FILING DATE: 1999-07-26
36	PRIOR APPLICATION NUMBER: 60/146222
37	PRIOR FILING DATE: 1999-07-28
38	PRIOR APPLICATION NUMBER: 60/146953
39	PRIOR FILING DATE: 1999-08-03
40	PRIOR APPLICATION NUMBER: 60/149320
41	PRIOR FILING DATE: 1999-08-17
42	PRIOR APPLICATION NUMBER: 60/149638
43	PRIOR FILING DATE: 1999-08-17
44	PRIOR APPLICATION NUMBER: 60/151733
45	PRIOR FILING DATE: 1999-08-31
46	PRIOR APPLICATION NUMBER: 60/164418
47	PRIOR FILING DATE: 1999-11-09
48	PRIOR APPLICATION NUMBER: 60/166361
49	PRIOR FILING DATE: 1999-11-16
50	PRIOR APPLICATION NUMBER: 60/169445
51	PRIOR FILING DATE: 1999-12-07
52	PRIOR APPLICATION NUMBER: 60/169495
53	PRIOR FILING DATE: 1999-12-07
54	PRIOR APPLICATION NUMBER: 60/169835

	Query Match	Best Local Similarity	Score 1568.4	DB 14	Length 2445
	Matches 1575	Conservative 0	Pred. No. 0	Mismatches 11	Indels 0
QY	4	ACGAGGTGTGTGTCAGATGAAAAATTAGACAGGAGGACAGAGTGTAGCTTGTTCAC	63		
	11				
Db	122	AAGCAGTGTGTGTSCAGATGATAAAATTGACAGGAGGACAGAGTGTAGCTTGTTCAC	181		
QY	64	CTCAGCTGGGAATGTGCATCAGGCAACCTCAAGTTTTTCACCACGGCATGTGCTGTGAAT	123		
Db	182	CTCAGCTGGGAATGTGCATCAGGCAACCTCAAGTTTTTCACCACGGCATGTGCTGTGAAT	241		
QY	124	GTCGGCAAAACATTCTCTCTCCCAAGCCTTATGTGTTAACTGGGGATGGATGTGGACCT	183		
Db	242	GTCGGCAAAACATTCTCTCTCCCAAGCCTTATGTGTTAACTGGGGATGGATGTGGACCT	301		
QY	184	GGGCACTGTGGATGCTCCCTTCACTCTTGCAAAATTGACCTGGACACTTGCAGCTAAGC	243		
	11				

Db 302 GGGCAGTGTGGATGCTCCCTTCACTCTGCAAAATTCAGCCCTGGCAGCTTCCGACGCTAAAC 361  
Qy 244 CTGAGAACATTTCTCTGTCTACTACTATAGAAAAATTTAAACCGCAGCTTGGAGTCCAG 303  
Db 362 CTGAGAACATTTCTCTGTCTACTACTATAGAAAAATTTAAACCGCAGCTTGGAGTCCAG 421  
Qy 304 GAAAGGAACAGATTATACCAAGTACACAGTTTAAAGAGACCTTACGCTTTTGGAGAAAAAC 363  
Db 422 GAAAGGAACAGATTATACCAAGTACACAGTTTAAAGAGACCTTACGCTTTTGGAGAAAAAC 481  
Qy 364 ATGATTAATTGTACAAACCAATAGTTCTACAGTAAATCGTCCGCTCTCTTTTCC 423  
Db 482 ATGATTAATTGTACAAACCAATAGTTCTACAGTAAATCGTCCGCTCTCTTTTCC 541  
Qy 424 TTCCAGAAATACGATCCAGATTAATTAATACATTTGAGTGAAGCTGAAATGAGAGATG 483  
Db 542 TTCCAGAAATACGATCCAGATTAATTAATACATTTGAGTGAAGCTGAAATGAGAGATG 601  
Qy 484 GTGTAATTAATTCATATATGACATATGAGATTAAGAGACATAGCAAAAACGTAACAC 543  
Db 602 GTGTAATTAATTCATATATGACATATGAGATTAAGAGACATAGCAAAAACGTAACAC 661  
Qy 544 CTAGATTTTCCGTTGTGAACAGTTTGGCATCAACGAATGATTAATTAATGAATGA 603  
Db 662 CTAGATTTTCCGTTGTGAACAGTTTGGCATCAACGAATGATTAATTAATGAATGA 721  
Qy 604 TAAAGCCTGAGTGGCGCTGTTTCATCTGATTTAAATATACACATTCGATTCAGACAG 663  
Db 722 TAAAGCCTGAGTGGCGCTGTTTCATCTGATTTAAATATACACATTCGATTCAGACAG 781  
Qy 664 TCAACAGTACAGCTGATGAGTGAAGTCAACTTCGCTAAGAACCGTAAGATTAACCAAA 723  
Db 782 TCAACAGTACAGCTGATGAGTGAAGTCAACTTCGCTAAGAACCGTAAGATTAACCAAA 841  
Qy 724 CGTCAACCTCAGCGGGGCTGAGGCTTTTACAGAAATATGATATGCTGTGGAGTGGG 783  
Db 842 CGTCAACCTCAGCGGGGCTGAGGCTTTTACAGAAATATGATATGCTGTGGAGTGGG 901  
Qy 784 TCAAGAGATCAAAATTTCTGAGTACTGAGACCAAGAAAAATGGAATGACTAGAGAG 843  
Db 902 TCAAGAGATCAAAATTTCTGAGTACTGAGACCAAGAAAAATGGAATGACTAGAGAG 961  
Qy 844 AAGCTCATGTGGCGCTGGAAGTGTGGAGAGTCTGAAACCAAGCTGAGCGGATGGAAGAA 903  
Db 962 AAGCTCATGTGGCGCTGGAAGTGTGGAGAGTCTGAAACCAAGCTGAGCGGATGGAAGAA 1021  
Qy 904 GGGCAGTGGGCTTGTATGGAAGAGCAAGAGAGCCCGCTGAGAGAAAAACACTG 963  
Db 1022 GGGCAGTGGGCTTGTATGGAAGAGCAAGAGAGCCCGCTGAGAGAAAAACACTG 1081  
Qy 964 GCTACACATATGTGTAATTCAGAAAGCAACACTAACCTCAGAAAAACATGAACACTA 1023  
Db 1082 GCTACACATATGTGTAATTCAGAAAGCAACACTAACCTCAGAAAAACATGAACACTA 1141  
Qy 1024 CTAAACGACAGCTTGAAGTCTGGAGGCGAGAGCTTTTGGGTGTATGATTTCTT 1083  
Db 1142 CTAAACGACAGCTTGAAGTCTGGAGGCGAGAGCTTTTGGGTGTATGATTTCTT 1201  
Qy 1084 ATAAATTTCTTGGGAAGTCTCAGTGGGCAACCTGAGAGATTCAGACTATTCAGAAAAAT 1143  
Db 1202 ATAAATTTCTTGGGAAGTCTCAGTGGGCAACCTGAGAGATTCAGACTATTCAGAAAAAT 1261  
Qy 1144 CATTTAGTGCATTTGAGTCTGAGGCGCTGCTTGTGAGAGACACAGTATGTTGTAAGT 1203  
Db 1262 CATTTAGTGCATTTGAGTCTGAGGCGCTGCTTGTGAGAGACACAGTATGTTGTAAGT 1321  
Qy 1204 GGCAGAGCTGCTCTGAGAGTGAACCTTGGATGATTAATGATGTTTCCGAGTGGAGT 1263  
Db 1322 GGCAGAGCTGCTCTGAGAGTGAACCTTGGATGATTAATGATGTTTCCGAGTGGAGT 1381  
Qy 1264 CAGAGCCACACACCTTTCGAGGAATCTGATGCTCAGGCGACAGAACTGAGCATTCAGC 1323  
Db 1382 CAGAGCCACACACCTTTCGAGGAATCTGATGCTCAGGCGACAGAACTGAGCATTCAGC 1441

Qy 1324 AAGATTAATTAACCTTTCTGTGCTCTATTAACATCTCTGTGATCCATGTTGCATGACA 1383  
Db 1442 AAGATTAATTAACCTTTCTGTGCTCTATTAACATCTCTGTGATCCATGTTGCATGACA 1501  
Qy 1384 AAGTTGGGAGCCATATTCATCCAGGCTTATGCCAAAGAGGCGTTCCATCAGAGCTC 1443  
Db 1502 AAGTTGGGAGCCATATTCATCCAGGCTTATGCCAAAGAGGCGTTCCATCAGAGCTC 1561  
Qy 1444 CTGAGACCAAGGTGAGAACATTTGGCGTGAAGACGCTACGATCAGATGGAAGATTC 1503  
Db 1562 CTGAGACCAAGGTGAGAACATTTGGCGTGAAGACGCTACGATCAGATGGAAGATTC 1621  
Qy 1504 CCAAGAGTGAAGAGGATTCATCTGCAACTACACCATCTTTTACCAAGCTGAAGTGC 1563  
Db 1622 CCAAGAGTGAAGAGGATTCATCTGCAACTACACCATCTTTTACCAAGCTGAAGTGC 1681  
Qy 1564 GAAAGGATTTCTCCAGACAGTCAAT 1589  
Db 1682 GAAAGGATTTCTCCAGACAGTCAAT 1707

RESULT 11  
US-10-230-163-91  
; Sequence 91, Application US/10230163  
; Publication No. US20030036635A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C96  
; CURRENT APPLICATION NUMBER: US/10/230.163  
; CURRENT FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13



;; PRIOR APPLICATION NUMBER: 60/169445  
;; PRIOR FILING DATE: 1999-12-07  
;; PRIOR APPLICATION NUMBER: 60/169495  
;; PRIOR FILING DATE: 1999-12-07  
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.3%; Score 1568.4; DB 14; Length 2445;

Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1575; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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OY 4 ACGAGCTGTGTGAGTATGATAAATTTAGACAGGAGGAGGTGATGAGTGTTCAC 63
DB 122 AAGCATGTGTGTGAGATGATAAATTTAGACAGGAGGAGGTGATGAGTGTTCAC 181
OY 64 CTCAGCTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 123
DB 182 CTCAGCTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
OY 124 GTCCGCAAAACATTTCTCTCTCCAGCCCTTACATGTGTTAACCTGGGATGTGACCT 183
DB 242 GTCCGCAAAACATTTCTCTCTCCAGCCCTTACATGTGTTAACCTGGGATGTGACCT 301
OY 184 GGGGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
DB 302 GGGGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
OY 244 CTGAGAACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303
DB 362 CTGAGAACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 421
OY 304 GAAAGGAAACAGTTATATCCAGTACAGTACAGTACAGTACAGTACAGTACAG 363
DB 422 GAAAGGAAACAGTTATATCCAGTACAGTACAGTACAGTACAGTACAGTACAG 481
OY 364 ATGATTAATTTGACAAACATGTTCTACAGTGAATTCGTTCTGCTCTCTCTCTCC 423
DB 482 ATGATTAATTTGACAAACATGTTCTACAGTGAATTCGTTCTGCTCTCTCTCTCC 541
OY 424 TTCCAGATATAGATCCAGATATATATATATATATATATATATATATATATAT 483
DB 542 TTCCAGATATAGATCCAGATATATATATATATATATATATATATATATATAT 601
OY 484 GTGTAATTAATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 543
DB 602 GTGTAATTAATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 661
OY 544 CTAGATTTTCCGCTGTAACAGTTTGGGATCAAAAGATGTTCAATTTGAATGA 603
DB 662 CTAGATTTTCCGCTGTAACAGTTTGGGATCAAAAGATGTTCAATTTGAATGA 721
OY 604 TAAAGCCTGATGAGGCGCTGTTTCACTGATTTAAATATACACTTCGATTCAGACAG 663
DB 722 TAAAGCCTGATGAGGCGCTGTTTCACTGATTTAAATATACACTTCGATTCAGACAG 781
OY 664 TCAACAGTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
DB 782 TCAACAGTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 841
OY 724 CGTCAACCTCAGCGGGGCTGAGCCTTTTACAGATATGATATGCTGCTGAGATGAGG 783
DB 842 CGTCAACCTCAGCGGGGCTGAGCCTTTTACAGATATGATATGCTGCTGAGATGAGG 901
OY 784 TCAAGGAGTCAAAAGTTCTGAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 843
DB 902 TCAAGGAGTCAAAAGTTCTGAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 961
OY 844 AAGTCCATGTGCGCTGGAAGTGTGAGAGTCTGGAACAGCTGAGGCGGATGGAAGAA 903
DB 962 AAGTCCATGTGCGCTGGAAGTGTGAGAGTCTGGAACAGCTGAGGCGGATGGAAGAA 1021
OY 904 GGGCAGTGGGCTGTTATGGAAGGCAAGAGAGGCGGCTGCTGAGAGAAACACTTG 963
DB 1022 GGGCAGTGGGCTGTTATGGAAGGCAAGAGAGGCGGCTGCTGAGAGAAACACTTG 1081
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OY 964 GCTACACATATGCTACTATCCAGAAAGCAACACTTAACCTCAGAGAAACATGAACACTA 1023
DB 1082 GCTACACATATGCTACTATCCAGAAAGCAACACTTAACCTCAGAGAAACATGAACACTA 1141
OY 1024 CTAAACAGCAGCTTGAACTGATGATGAGGAGGAGAGGCTTTTGGTGTCTATGATTTCTT 1083
DB 1142 CTAAACAGCAGCTTGAACTGATGATGAGGAGGAGAGGCTTTTGGTGTCTATGATTTCTT 1201
OY 1084 ATATTTCTTTGGGAAGTCTCCAGTGGGCGACCTTGAGATTCAGACTTTTAAAGAAAT 1143
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OY 1144 CATTTCAGTATGAGTGTGATGAGGCGCTGTTGCTGAGAGACAGCTAGTGGTGAAGT 1203
DB 1262 CATTTCAGTATGAGTGTGATGAGGCGCTGTTGCTGAGAGACAGCTAGTGGTGAAGT 1321
OY 1204 GGCAGAGCTGCTCTAGACGTGAACACTTGGATGATTTGAATGGTTCCGATGTGACT 1263
DB 1322 GGCAGAGCTGCTCTAGACGTGAACACTTGGATGATTTGAATGGTTCCGATGTGACT 1381
OY 1264 CAGAGCCAGCAGCTTTCTGAGGATCTGTCTCAGGCGCAGAGACCTGAGATCCAGC 1323
DB 1382 CAGAGCCAGCAGCTTTCTGAGGATCTGTCTCAGGCGCAGAGACCTGAGATCCAGC 1441
OY 1324 AAGATTAATTTAAACCTTTCTGCTGCTATTAACATCTCTGTATGCCAATGTTGATGACA 1383
DB 1442 AAGATTAATTTAAACCTTTCTGCTGCTATTAACATCTCTGTATGCCAATGTTGATGACA 1501
OY 1384 AAGTTGGGAGCATATTTCCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAGGTC 1443
DB 1502 AAGTTGGGAGCATATTTCCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAGGTC 1561
OY 1444 CTGAGACCAAGTGGAGAACATTTGGCGTGAAGAGCGTCCAGATCATAGGAAGATTC 1503
DB 1562 CTGAGACCAAGTGGAGAACATTTGGCGTGAAGAGCGTCCAGATCATAGGAAGATTC 1621
OY 1504 CCAAGAGTGAAGAAAGGATTCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTG 1563
DB 1622 CCAAGAGTGAAGAAAGGATTCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGTG 1681
OY 1564 GAAAAGATTTCTCAACAGACAGTCAAT 1589
DB 1682 GAAAAGATTTCTGAAGCAGCGCCAT 1707
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RESULT 12  
US-10-230-338-91  
; Sequence 91, Application US/10230338  
; Publication No. US20030044934A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C92  
; CURRENT FILING DATE: US/10/230, 338  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17





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OY      1444  CTGAGACCAAGGTGTGAGACACTTTGGCGTGAAGAGCGTCACATGACATGCAAGAGATTC 1503
Db      1562  CTGAGACCAAGGTGTGAGACACTTTGGCGTGAAGAGCGTCACATGACATGCAAGAGATTC 1621
OY      1504  CCAGAGTGTGAGAGAAAGGATATCATCTGCAACTACACCATCTTTTACCAGCTGAAGGTG 1563
Db      1622  CCAGAGTGTGAGAGAAAGGATATCATCTGCAACTACACCATCTTTTACCAGCTGAAGGTG 1681
OY      1564  GAAAAGATTTCTCCAGACAGCTCAT 1589
Db      1682  GAAAAGATTTCTGTAAAGCAGCCCAT 1707

RESULT 14
US-10-230-414-91
: Sequence 91, Application US/10230414
: Publication No. US20030050448A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Matanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C98
: CURRENT APPLICATION NUMBER: US/10/230.414
: CURRENT FILING DATE: 2002-08-28
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 91
: LENGTH: 2445
: TYPE: DNA
: ORGANISM: Homo Sapien
: FEATURE:
: NAME/KEY: unsize
: LOCATION: 2424
: OTHER INFORMATION: unknown base
US-10-230-414-91

Query Match      65.3%; Score 1568.4; DB 14; Length 2445;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY      4  ACAGAGGTGTGTGTGTCAGATATGAAAAATTGAGACAGAGAGCGAGTGTAGCTTGTCCAC 63
Db      122  AAGGACATGTGTGTGTCAGATATGAAAAATTGAGACAGAGAGCGAGTGTAGCTTGTCCAC 181

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OY	64	CTCAGCGTGGGAATGTCATGAGCACTCAAGTTTTTCAACACAGGCGATGTCGTGGAA	123
Db	182	CTCAGCGTGGGAATGTGCATCAGGCACACTCAAGTTTTTTCACACAGCGATGTCTTGGAA	241
OY	124	GTCCGCAAAACATTTCTCTCTCCCGAGCCTTCATGTGTTAACTCGGGGATGATGTGGACCT	183
Db	242	GTCCGCAAAACATTTCTCTCTCCCGAGCCTTCATGTGTTAACTCGGGGATGATGTGGACCT	301
OY	184	GGGCACTGTGATGCTCCCTCCTCCTCTGCAATTCAGCCTGGCAGCTCTCCACGCTAAGC	243
Db	302	GGGCACTGTGATGCTCCCTCCTCCTCCTCCTGCAATTCAGCCTGGCAGCTCTCCACGCTAAGC	361
OY	244	CTGGAAACATTTCCCTGCTCTACTACTATGTGAAAAATTTAACTCGACTGTGGAGTCCAG	303
Db	362	CTGGAAACATTTCCCTGCTCTACTACTACTATGTGAAAAATTTAACTCGACTGTGGAGTCCAG	421
OY	304	GAAGAAGAACAGTTATATCCAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAAC	363
Db	422	GAAGAAGAACAGTTATATCCAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAAC	481
OY	364	ATGATTAATTGTACACCAATAGTTCTACAAAGTAAAAATCGTCTTGCTCTTTTTC	423
Db	482	ATGATTAATTGTACACCAATAGTTCTACAAAGTAAAAATCGTCTTGCTCTTTTTC	541
OY	424	TTCCAGAAATPACATCCCGATTAATATACATTTGAGTGGAGAGCTGAAAAATGGAGATG	483
Db	542	TTCCAGAAATPACATCCCGATTAATATACATTTGAGTGGAGAGCTGAAAAATGGAGATG	601
OY	484	GTGTAATTTAAATCTCATATGACATACAGGATTTAGAGAAATAGGAAAACTGAACAC	543
Db	602	GTGTAATTTAAATCTCATATGACATACAGGATTTAGAGAAATAGGAAAACTGAACAC	661
OY	544	CTAAGATTTTCCGTGTAAACACAGTTTGGGCATCAACGAATGATTCAATTGAATGGA	603
Db	662	CTAAGATTTTCCGTGTAAACACAGTTTGGGCATCAACGAATGATTCAATTGAATGGA	721
OY	604	TAAAGCCTGAGTTGGGCGCTGTTTCATCATGTAAATTAACACTCGATTCAGAGACAG	663
Db	722	TAAAGCCTGAGTTGGGCGCTGTTTCATCATGTAAATTAACACTCGATTCAGAGACAG	781
OY	664	TCAACAGTACAGCTGATGGAAGTCAACTTCGTTAAGAACCGTAAGATTAATAAACCAAA	723
Db	782	TCAACAGTACAGCTGATGGAAGTCAACTTCGTTAAGAACCGTAAGATTAATAAACCAAA	841
OY	724	CGTCAACCTCAGCGGCGCTGCAGCCTTTTACAGAAATGTGCATATGCTCTGCGATGTGCGG	783
Db	842	CGTCAACCTCAGCGGCGCTGCAGCCTTTTACAGAAATGTGCATATGCTCTGCGATGTGCGG	901
OY	784	TCAAGGAGTCAAAATTTTGGAGTACTGTGAGGCCCAAGAAAAATGGGAATGACTGAGAGAG	843
Db	902	TCAAGGAGTCAAAATTTTGGAGTACTGTGAGGCCCAAGAAAAATGGGAATGACTGAGAGAG	961
OY	844	AAGCTCATGTGGCCTTGGAACTGTGAGAGTCTCTGAAAACAGCTGAGGCGGATGGAGAA	903
Db	962	AAGCTCATGTGGCCTTGGAACTGTGAGAGTCTCTGAAAACAGCTGAGGCGGATGGAGAA	1021
OY	904	GGCCAGTGCCTTTTATGGAAGAAGCAGAGAGAGCCCAAGTCTTAGAGAAAAACACTTG	963
Db	1022	GGCCAGTGCCTTTTATGGAAGAAGCAGAGAGAGCCCAAGTCTTAGAGAAAAACACTTG	1081
OY	964	GCTCAACATTTGTGTACTATCTCAAAAGCAACACTTAATCTCACAGAAACAATGAACTA	1023
Db	1082	GCTCAACATTTGTGTACTATCTCAAAAGCAACACTTAATCTCACAGAAACAATGAACTA	1141
OY	1024	CTAACACGACCTTGAACCTGCATCTGGAGAGCGAGACCTTTTGGTGTCTATGATTTCTT	1083
Db	1142	CTAACACGACCTTGAACCTGCATCTGGAGAGCGAGACCTTTTGGTGTCTATGATTTCTT	1201
OY	1084	ATAATTTCTTTGGGAATGCTTCAGATGGCCACCTGTGAGGATTTCCAGCTATTCAGAAAAAT	1143
Db	1202	ATAATTTCTTTGGGAATGCTTCAGATGGCCACCTGTGAGGATTTCCAGCTATTCAGAAAAAT	1261

OY 1144 CATTTCAGTCATGAGGTCATGACGAGCCTGCTGAGAGCAGCTAGTGTGAAGT 1203  
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DB 1262 CATTTCAGTCATGAGGTCATGACGAGCCTGCTGAGAGCAGCTAGTGTGAAGT 1321  
OY 1204 GGCAAGGTCCTGCTAGAGCTGAACACTTGGATGATGAATGGTTCCGATGTGACT 1263  
|||  
DB 1322 GGCAAGGTCCTGCTAGAGCTGAACACTTGGATGATGAATGGTTCCGATGTGACT 1381  
OY 1264 CAGAGCCACGACCTTCCGAGAGTGTGCTCAGAGCCACGAGACGAGATCCAGC 1323  
|||  
DB 1382 CAGAGCCACGACCTTCCGAGAGTGTGCTCAGAGCCACGAGACGAGATCCAGC 1441  
OY 1324 AAGATAAATTAACCTTCTGCTGCTATACATCTGTGTATCCATGTTGATGACA 1383  
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DB 1442 AAGATAAATTAACCTTCTGCTGCTATACATCTGTGTATCCATGTTGATGACA 1501  
OY 1384 AAGTTGGGAGCCATATTCATCCAGGCTTATGCCAAGAGGCTTCCATCAGAGTTC 1443  
|||  
DB 1502 AAGTTGGGAGCCATATTCATCCAGGCTTATGCCAAGAGGCTTCCATCAGAGTTC 1561  
OY 1444 CTGAGACCAAGTGAGAGACATTTGGCGTGAAGAGGTCAGATCAGATGAAGATTC 1503  
|||  
DB 1562 CTGAGACCAAGTGAGAGACATTTGGCGTGAAGAGGTCAGATCAGATGAAGATTC 1621  
OY 1504 CCAAGAGTGAGAGAGGATTCATCTGCAACTACACCCTTTTACCAAGCTGAAGTGTG 1563  
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DB 1622 CCAAGAGTGAGAGAGGATTCATCTGCAACTACACCCTTTTACCAAGCTGAAGTGTG 1681  
OY 1564 GAAAAGATTTCTCCAAAGCATCAT 1589  
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DB 1682 GAAAAGATTTCTGTAAGCAGCCCAT 1707  
|||

## RESULT 15

US-10-216-159A-91

: Sequence 91, Application US/10216159A  
: Publication No. US20030069397A1

: GENERAL INFORMATION:

: APPLICANT: Baker, Kevin P.

: APPLICANT: Desnoyers, Luc

: APPLICANT: Gerritsen, Mary

: APPLICANT: Goddard, Audrey

: APPLICANT: Godowski, Paul J.

: APPLICANT: Grimaldi, J. Christopher

: APPLICANT: Gurney, Austin L.

: APPLICANT: Smith, Victoria

: APPLICANT: Stephan, Jean-Philippe F.

: APPLICANT: Watanabe, Colin L.

: APPLICANT: Wood, William I.

: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

: FILE REFERENCE: P3530P1C6

: CURRENT APPLICATION NUMBER: US/10/216, 159A

: PRIOR FILING DATE: 2002-08-09

: PRIOR APPLICATION NUMBER: 10/119,480

: PRIOR FILING DATE: 2002-04-09

: PRIOR APPLICATION NUMBER: 60/059113

: PRIOR FILING DATE: 1997-09-17

: PRIOR APPLICATION NUMBER: 60/062287

: PRIOR FILING DATE: 1997-10-17

: PRIOR APPLICATION NUMBER: 60/063549

: PRIOR FILING DATE: 1997-10-28

: PRIOR APPLICATION NUMBER: 60/064103

: PRIOR FILING DATE: 1997-10-31

: PRIOR APPLICATION NUMBER: 60/069873

: PRIOR FILING DATE: 1997-12-17

: PRIOR APPLICATION NUMBER: 60/078910

: PRIOR FILING DATE: 1998-03-20

: PRIOR APPLICATION NUMBER: 60/079294

: PRIOR FILING DATE: 1998-03-25

: PRIOR APPLICATION NUMBER: 60/079656

: PRIOR FILING DATE: 1998-03-26

: PRIOR APPLICATION NUMBER: 60/079728

: \*

: PRIOR FILING DATE: 1998-03-27  
: Remaining Prior Application data removed - See File Wrapper or PALM.  
: NUMBER OF SEQ ID NOS: 246  
: SEQ ID NO 91  
: LENGTH: 2445  
: TYPE: DNA  
: ORGANISM: Homo Sapien  
: FEATURE:  
: NAME/KEY: unsure  
: LOCATION: 2424  
: OTHER INFORMATION: unknown base  
US-10-216-159A-91

Query Match 65.3%; Score 1568.4; DB 14; Length 2445;

Best Local Similarity 99.3%; Pred. No. 0; Mismatches 11; Indels 0; Gaps 0;

Matches 1575; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 4 ACAGGCTGTGTGTCAGATGAAAAATTTGAGACAGAGAGAGAGAGTGTGAGTTCAC 63  
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DB 122 AAGACATGTGTGTCAGATGAAAAATTTGAGACAGAGAGAGAGTGTGAGTTCAC 181  
OY 64 CTCAGCTGGATGTGTCAGAGCACTCAAGTTTTCACACGCGATGTGTGTGAT 123  
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DB 182 CTCAGCTGGATGTGTCAGAGCACTCAAGTTTTCACACGCGATGTGTGTGAT 241  
OY 124 GTCCGCAAAACATTTCTCTCCCGAGCCTCATGTGTAACTGGGGATGTGGAGCT 183  
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DB 242 GTCCGCAAAACATTTCTCTCCCGAGCCTCATGTGTAACTGGGGATGTGGAGCT 301  
OY 184 GGGCAGTGTGATGCTCCCTCAGCTCTGCAAAATTCAGCGTGGAGCTTGCAGCTAAGC 243  
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DB 302 GGGCAGTGTGATGCTCCCTCAGCTCTGCAAAATTCAGCGTGGAGCTTGCAGCTAAGC 361  
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OY 304 GAAAGGAACAGATTAATCCAGTACAGACAGTTAAGAGACATTTAGCGTTTGGAGAAAAAC 363  
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DB 422 GAAAGGAACAGATTAATCCAGTACAGACAGTTAAGAGACATTTAGCGTTTGGAGAAAAAC 481  
OY 364 ATGATTAATTTGACAACCAATAGTTCTACAGAGTGAATCGTCTGCTCTTTTTC 423  
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DB 482 ATGATTAATTTGACAACCAATAGTTCTACAGAGTGAATCGTCTGCTCTTTTTC 541  
OY 424 TTCCAAGATTAAGCATCCCATATATATACCATTTGAGGTGGAAGCTGAATGGAATG 483  
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DB 542 TTCCAAGATTAAGCATCCCATATATATACCATTTGAGGTGGAAGCTGAATGGAATG 601  
OY 484 GTGTAATTAATTCATATGACATACAGAGATTAAGAGACATAGCGAAAACTGAACAC 543  
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DB 602 GTGTAATTAATTCATATGACATACAGAGATTAAGAGACATAGCGAAAACTGAACAC 661  
OY 544 CTAAAGTTTTCGCTGTGAACCAAGTTTGGGCATCAACGAATGATTCATTAATGGA 603  
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DB 662 CTAAAGTTTTCGCTGTGAACCAAGTTTGGGCATCAACGAATGATTCATTAATGGA 721  
OY 604 TAAAGCCTGAGTGGCGCTGTTCACTGATTAATAATACACCTTGATTCAGGACAG 663  
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DB 722 TAAAGCCTGAGTGGCGCTGTTCACTGATTAATAATACACCTTGATTCAGGACAG 781  
OY 664 TCAACAGTACAGCTGATGAGAGTCAACTTCGTTAAGAACCTTAAGATTAATAACCAA 723  
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DB 782 TCAACAGTACAGCTGATGAGAGTCAACTTCGTTAAGAACCTTAAGATTAATAACCAA 841  
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DB 842 CGTACAACTTCAGCGGGCTGAGGCTTTTACAGAAATATGATAGCTTCGAGATGCGG 901  
OY 784 TCAAGGAGTCAAAATTTCTGAGTCACTGAGAGCCCAAGAAAAATGGAATGATCTAGAGAG 843  
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DB 902 TCAAGGAGTCAAAATTTCTGAGTCACTGAGAGCCCAAGAAAAATGGAATGATCTAGAGAG 961  
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OY 844 AAGCTCCATGTGGCCCTGGAACTGTGGAGAGTCTTGAACCAAGCTGAGGGGATGGAGAA 903
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Db 962 AAGCTCCATGTGGCCCTGGAACTGTGGAGAGTCTTGAACCAAGCTGAGGGGATGGAGAA 1021
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OY 904 GGCAGAGCGGCTTTTATGGAAGAAGCAAGAGAGCCGCCAGTCTAGAGAAAACACTTG 963
    |||||||
Db 1022 GGCAGAGCGGCTTTTATGGAAGAAGCAAGAGAGCCGCCAGTCTAGAGAAAACACTTG 1081
    |||||||
OY 964 GCTACACATATGTAGTACTATCCAGAAAGCAACACTTAACCTCAGAGAAACATGAACACTA 1023
    |||||||
Db 1082 GCTACACATATGTAGTACTATCCAGAAAGCAACACTTAACCTCAGAGAAACATGAACACTA 1141
    |||||||
OY 1024 CTAACCAAGCAGCTTGAACCTGCAATCTGGAGGCGAGAGCCTTTGGGTGCTATGATTTCTT 1083
    |||||||
Db 1142 CTAACCAAGCAGCTTGAACCTGCAATCTGGAGGCGAGAGCCTTTGGGTGCTATGATTTCTT 1201
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OY 1084 ATATTTCTCTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCAGACTATTCAGAAAAAT 1143
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Db 1202 ATATTTCTCTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCAGACTATTCAGAAAAAT 1261
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OY 1144 CATTTCAAGTCATGTAGAGTCAATGAGGCGCTGCTGAGAGCAAGCTAGTGGTGAAGT 1203
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Db 1262 CATTTCAAGTCATGTAGAGTCAATGAGGCGCTGCTGAGAGCAAGCTAGTGGTGAAGT 1321
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OY 1204 GGCAAAAGCTGTGCTGTAGACGTGAACACTTGATGATTTGAATGGTTTCCGGATGTGACT 1263
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OY 1384 AAGTTGGGAGCCATATTTCCATCCAGGCTTATGCCAAAGAGCGCTTCCATCAGAAAGTTC 1443
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OY 1444 CTGAGACCAAGGTGGAAGACATTTGGCGTGAAGAGCGGTACAGATCAGTGAAGAGATTTC 1503
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Db 1622 CCAAGAGTGAAGAAAGGTATCATCTGCAACTACACCATCTTTACCAAGCTGAAGGTG 1681
    |||||||
OY 1564 GAAAAGATTTCTCCAGACAGACTCAAT 1589
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Db 1682 GAAAAGATTTCTGTAAGCAGGCCCAT 1707
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Job time : 494 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 20:13:52 ; Search time 4964 Seconds  
(without alignments)  
11760.546 Million cell updates/sec

Title: US-09-892-949-1  
Perfect score: 2402  
Sequence: 1 ggcacgaggtgtgtgtcag.....atgagacctcgggcctca 2402

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rpd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	286.4	11.9	663 10	BB617934 BB617934
3	230.6	9.6	612 29	AG138991 Pan trogl
4	197	8.2	653 13	BU455838 603772418

5	163.8	6.8	459	28	AK022781	AK022781 HS_2180_A
6 <td>155.2 <td>6.5 <td>592 <td>14 <td>CA561173 <td>CA561173 K0283D09-</td> </td></td></td></td></td>	155.2 <td>6.5 <td>592 <td>14 <td>CA561173 <td>CA561173 K0283D09-</td> </td></td></td></td>	6.5 <td>592 <td>14 <td>CA561173 <td>CA561173 K0283D09-</td> </td></td></td>	592 <td>14 <td>CA561173 <td>CA561173 K0283D09-</td> </td></td>	14 <td>CA561173 <td>CA561173 K0283D09-</td> </td>	CA561173 <td>CA561173 K0283D09-</td>	CA561173 K0283D09-
7 <td>149.4 <td>6.2 <td>479 <td>14 <td>CA560924 <td>CA560924 K0279C07-</td> </td></td></td></td></td>	149.4 <td>6.2 <td>479 <td>14 <td>CA560924 <td>CA560924 K0279C07-</td> </td></td></td></td>	6.2 <td>479 <td>14 <td>CA560924 <td>CA560924 K0279C07-</td> </td></td></td>	479 <td>14 <td>CA560924 <td>CA560924 K0279C07-</td> </td></td>	14 <td>CA560924 <td>CA560924 K0279C07-</td> </td>	CA560924 <td>CA560924 K0279C07-</td>	CA560924 K0279C07-
8 <td>134.6 <td>5.6 <td>553 <td>14 <td>CA559889 <td>CA559889 K0266C03-</td> </td></td></td></td></td>	134.6 <td>5.6 <td>553 <td>14 <td>CA559889 <td>CA559889 K0266C03-</td> </td></td></td></td>	5.6 <td>553 <td>14 <td>CA559889 <td>CA559889 K0266C03-</td> </td></td></td>	553 <td>14 <td>CA559889 <td>CA559889 K0266C03-</td> </td></td>	14 <td>CA559889 <td>CA559889 K0266C03-</td> </td>	CA559889 <td>CA559889 K0266C03-</td>	CA559889 K0266C03-
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16 <td>124 <td>5.2 <td>763 <td>13 <td>B0288431 <td>B0288431 603607401</td> </td></td></td></td></td>	124 <td>5.2 <td>763 <td>13 <td>B0288431 <td>B0288431 603607401</td> </td></td></td></td>	5.2 <td>763 <td>13 <td>B0288431 <td>B0288431 603607401</td> </td></td></td>	763 <td>13 <td>B0288431 <td>B0288431 603607401</td> </td></td>	13 <td>B0288431 <td>B0288431 603607401</td> </td>	B0288431 <td>B0288431 603607401</td>	B0288431 603607401
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23 <td>77.4 <td>3.2 <td>625 <td>9 <td>AV359708 <td>AV359708 AV359708</td> </td></td></td></td></td>	77.4 <td>3.2 <td>625 <td>9 <td>AV359708 <td>AV359708 AV359708</td> </td></td></td></td>	3.2 <td>625 <td>9 <td>AV359708 <td>AV359708 AV359708</td> </td></td></td>	625 <td>9 <td>AV359708 <td>AV359708 AV359708</td> </td></td>	9 <td>AV359708 <td>AV359708 AV359708</td> </td>	AV359708 <td>AV359708 AV359708</td>	AV359708 AV359708
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25 <td>76 <td>3.2 <td>2804 <td>11 <td>AK089305 <td>AK089305 Mus muscu</td> </td></td></td></td></td>	76 <td>3.2 <td>2804 <td>11 <td>AK089305 <td>AK089305 Mus muscu</td> </td></td></td></td>	3.2 <td>2804 <td>11 <td>AK089305 <td>AK089305 Mus muscu</td> </td></td></td>	2804 <td>11 <td>AK089305 <td>AK089305 Mus muscu</td> </td></td>	11 <td>AK089305 <td>AK089305 Mus muscu</td> </td>	AK089305 <td>AK089305 Mus muscu</td>	AK089305 Mus muscu
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30 <td>74.4 <td>3.1 <td>522 <td>4 <td>BX528149 <td>BX528149 R2PD Mus</td> </td></td></td></td></td>	74.4 <td>3.1 <td>522 <td>4 <td>BX528149 <td>BX528149 R2PD Mus</td> </td></td></td></td>	3.1 <td>522 <td>4 <td>BX528149 <td>BX528149 R2PD Mus</td> </td></td></td>	522 <td>4 <td>BX528149 <td>BX528149 R2PD Mus</td> </td></td>	4 <td>BX528149 <td>BX528149 R2PD Mus</td> </td>	BX528149 <td>BX528149 R2PD Mus</td>	BX528149 R2PD Mus
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37 <td>62.2 <td>2.6 <td>531 <td>28 <td>BH056800 <td>BH056800 RPCI-24-2</td> </td></td></td></td></td>	62.2 <td>2.6 <td>531 <td>28 <td>BH056800 <td>BH056800 RPCI-24-2</td> </td></td></td></td>	2.6 <td>531 <td>28 <td>BH056800 <td>BH056800 RPCI-24-2</td> </td></td></td>	531 <td>28 <td>BH056800 <td>BH056800 RPCI-24-2</td> </td></td>	28 <td>BH056800 <td>BH056800 RPCI-24-2</td> </td>	BH056800 <td>BH056800 RPCI-24-2</td>	BH056800 RPCI-24-2
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39 <td>61.2 <td>2.5 <td>394 <td>12 <td>B1024387 <td>B1024387 CM3-MT029</td> </td></td></td></td></td>	61.2 <td>2.5 <td>394 <td>12 <td>B1024387 <td>B1024387 CM3-MT029</td> </td></td></td></td>	2.5 <td>394 <td>12 <td>B1024387 <td>B1024387 CM3-MT029</td> </td></td></td>	394 <td>12 <td>B1024387 <td>B1024387 CM3-MT029</td> </td></td>	12 <td>B1024387 <td>B1024387 CM3-MT029</td> </td>	B1024387 <td>B1024387 CM3-MT029</td>	B1024387 CM3-MT029
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## ALIGNMENTS

RESULT 1  
LOCUS AK030512  
DEFINITION Mus musculus adult male pituitary gland cDNA, RIKEN full-length  
full insert sequence.  
ACCESSION AK030512  
VERSION AK030512.1 GI:26326508  
KEYWORDS HTCC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 2049374  
PUBMED 11042159



OY	2088	GTGACGCGCCCTTCAGGCCGATGTGCCCTGGGAAATTTTGTAGGACCTCCAGTT	2147
.Db	860	GTGACCTCCCGTTAGGCCCGAGGCTCCCAAGGAAATTTTAAAGACCCCTCCGTT	919
OY	2148	TCACCTGATGATCCGCCAGAAATTCCTCAATACCTAGCTTGAGATGCCAGAGGGAC	2207
Db	920	TTAATCATGATGCTTCTTGAAAGACTCCACAGCAGCTTCTCAGATATGCGGACGAGCG	979
OY	2208	CGCCAGAGCCAAAGACAGCTTCTCTTTTCTGTGTAAGTTAGTACCGATATCTG	2267
Db	980	TACTCAGAAATGGCGACGACCTTCCTGCTTCCTGTCAGATCCAGGCGTATGCGCTCCC	1039
OY	2268	TGTGAGGAGGAGCCCCCAATCCATATTTGAAATTCATGTGACAGCCAGGAAATTTCTT	2327
Db	1040	CGTGAAGACCCAGCTCAGAAATCCATATTTTGAATTCATGACAAACAGGGAATTTCTT	1099
OY	2328	GTGTCGTGAAAACTTCCAGAGCACACCAAGGAGAAAGTCTAAATGCCACCTATGACATGAG	2387
Db	1100	GTGATGATGAAATATCCAGAGCACAGCAAAAGAAAGTCTAGTGTCTATGTGCATGAA	1159
OY	2388	ACCCTCGGGGCGCTCA 2402	
Db	1160	GTCTCTCAGAAACTGA 1174	

RESULT 2	LOCUS	DEFINITION
BB617934	BB617934	663 bp mRNA linear EST 31-AUG-2001
	BB617934	Riken full-length enriched, adult male pituitary gland Mus musculus cDNA 5330424C19 5', mRNA sequence.

ORGANISM	Mus musculus
SOURCE	Mus musculus (house mouse)
KEYWORDS	EST.
VERSION	BB617934.1
ACCESSION	BB617934
GI	15396442

**REFERENCE**  
**AUTHORS**  
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 663)  
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanaigaki, T., Hara, A.

TITLE	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
JOURNAL	unpublished
COMMENT	Contact: Yoshinide Hayashizaki

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Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
Carninci, P., Shibata, Y., Hayashizaki, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.

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nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001).  
Yamanaka, T., Kiyosawa, H., Kondo, T., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.  
Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct. Funct. Genomics* 2 pre, L72-L76 (2001).  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.  
e mouse tissues.

FEATURES	Location/Qualifiers
source	1. .663

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BASE COUNT
ORIGIN
174 a      161 c      146 g      180 t      2 others
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="5330424C19"
      /sex="male"
      /tissue_type="pituitary gland"
      /dev_stage="adult"
      /lab_host="DH10B"
      /lab_host="DH10B"
      /clone_lib="RIKEN full-length enriched, adult male
      pituitary gland"
      /note="Site.1: Salt; Site.2: BamHI: cDNA library was
      prepared and sequenced in Mouse Genome Encyclopedia
      Project of Genome Exploration Research Group in Riken
      Genomic Sciences Center and Genome Science Laboratory in
      RIKEN. Division of Experimental Animal Research in Riken
      contributed to prepare mouse tissues. 1st strand cDNA was
      primed with a primer [5'
      GAGGAGAGAGAGATCCAGAGGCTCTCTTTTGTTTTNN 3'], cDNA was
      prepared by using trehalose thermo-activated reverse
      transcriptase and subsequently enriched for full-length by
      cap-trapper. cDNA went through one round of normalization
      to Rot = 3.0 and subtraction to Rot = 100.0. Second strand
      cDNA was prepared with the primer adapter of sequence [5'
      GAGGAGAGAGATTCGGATTAAATTAATATCCCCCCCCCCC 3']. cDNA
      was cloned into the XhoI and BamHI sites. Vector: a
      modified pBluescript KS(+) after bulk excision from Lambda
      FLC I. Cloning sites, 5' end: Salt; 3' end: BamHI."

```

	Query Match	11.9%	Score 286.4	DB 10	Length 663
	Best Local Similarity	78.2%	Pred. No. 1.9e-73		
	Matches 355	Conservative 0	Mismatches 98	Indels 1	Gaps 1
QY	1428	GTTCATCAGAGGCTCTGAGACCAAGGTGAGAACATTGGCTGAAGACGGTCAGATC	1487		
Db	209	GCTCCATTAAAGGCTCTGAGACCAAGGTGAGAACATCGGCTGAGACGACGCATC	268		
QY	1488	ACATGGAAGAAGATTCCCAAGAGTGAAGAAAGGATATCATTCTGCAACTACACATCTTT	1547		
Db	269	ACATGGAAGAAGATTCTTAAGAGTCTAGAGATGATTTATCAACAATTAACAGTATTT	328		
QY	1548	TACCAAGCTGAGGTGGAAGAAGATTCTCCAGACAGTCAATTCCAGACTTTCAGATAC	16078		
Db	329	TACCAAGCTGAGGTGGAAGAAGACTCTCCAGAGCTGTAACTCTCATGCCCTGCAGGT	388		
QY	1608	GGCCTGAGTCCCTGGAANAAGAACCTCTTACATTGTTCAAGTCAATGGCCAGCACAGT	1667		
Db	389	GACCTGGAGTCTCTGACACGAAGAACCTCTTATCTGTTGGTTCATAGGCCAGACCGA	448		
QY	1668	GCTGGGGGAACCAACGGGACGACGATAATTCAAGACATGTGATCAGTGCCTTGAG	1727		
Db	449	GCTGGAGGTACCAACGGGCTGAGATTAACATTCAAGACATTGTCAATCAGTGTGAA	508		
QY	1728	ATTATCCCATACCTTCTCTGATTGCTGAGAGCCCTCTTATTCATTATCTGACAGTG	1787		
Db	509	ATTGTCCTTCAACATCTCTGATTGGAGAGGCTTCTTACTTANCATTAANAACAGTG	568		
QY	1788	GCATATGCTCAAAAAAACCACAATTAATCTATCTGTGTGGCCACCCTT-CCCA	1846		
Db	569	ACTTTGGCCCTCAANAAAGCCCAACCGGTTTGACTCCCTGCTTTGCTCGAATGTTCCCA	628		

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OY 1847 CCTGCTGTAAGTACTATAGCCACATGGCATGGA 1880
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DB 629 CCTGCTTAATAATATTTAACCACATGGCTCCGA 662

RESULT 3
AG138991/c 612 bp DNA linear GSS 04-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-153F12.F, genomic survey sequence.
DEFINITION AG138991
ACCESSION AG138991.1 GI:16668669
VERSION GSS.
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Pan troglodytes
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
TITLE Totoki,Y., Matanabe,H. and Sakaki,Y.
JOURNAL BAC end sequences of library PTB
REFERENCE 2 (bases 1 to 612)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
TITLE Totoki,Y., Matanabe,H. and Sakaki,Y.
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Tsukuba-shi, Ibaraki, Japan
(E-mail:chumpes@sc.riken.go.jp, URL:http://hgp.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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location/Qualifiers
source 1..612
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-153F12.F"
/sex="male"
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BASE COUNT 155 a 172 c 120 g 165 t
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Query Match 9.6%; Score 230.6; DB 29; Length 612;
Best Local Similarity 96.1%; Pred. No. 8.4e-57;
Matches 247; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

OY 1886 TTTCAGGATAGCTAAACCTGAAGAGCTGTGACTCTGTGAACAGACAGACAGAT 1945
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 332 TTTCAGGATAGCTAAACCTGAAGAGCTGTGACTCTGTGAACAGACAGACAGAT 274

OY 1946 CTTAAACCATGTTCCACCCAGTGACAGAGTTGGTGAATTCAGCAAGTTGGTGGTGA 2005
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 273 CTTAAACCATGTTCCACCCAGTGACAGAGTTGGTGAATTCAGCAAGTTGGTGGTGA 214

OY 2006 TGGGATGTTCTGCAAGAAATTTTCACAGATGAACCCAGGCGTCAAGAAACAAATTT 2065
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 213 TGGGATGTTCTGCAAGAAATTTTCACAGATGAACCCAGGCGTCAAGAAACAAATTT 154

OY 2066 AGAGGGGAAAGATGGGTATGTGACTGCCCTTCAGGCGTGAATTCCTCCCTGGGAA 2125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 153 AGAGGGGAAAGATGGGTATGTGACTGCCCTTCAGGCGTGAATTCCTCCCTGGGAA 94

OY 2126 AAGTTTGGAGAGCTCC 2142

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DB 93 GAGTTTGGAGAGCTCC 77
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RESULT 4
BU455838 653 bp mRNA linear EST 29-NOV-2002
LOCUS 603772418F1 CSEORBN14 Gallus gallus CDNA clone Chest708c5 5', mRNA
DEFINITION BU455838
ACCESSION BU455838
VERSION BU455838.1 GI:25945149
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
REFERENCE 1 (bases 1 to 653)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
TITLE Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
JOURNAL A Comprehensive Collection of Chicken cDNAs
MEDLINE Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 2235534
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
location/Qualifiers
source 1..653
/mol_type="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="Chest708c5"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEORBN14"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
BASE COUNT 233 a 110 c 134 g 176 t
ORIGIN
Query Match 8.2%; Score 197; DB 13; Length 653;
Best Local Similarity 58.7%; Pred. No. 9.5e-47;
Matches 360; Conservative 0; Mismatches 250; Indels 3; Gaps 1;

OY 1281 TCCTGGGATCTGTCTCTCAGCCGACGACGTTCGACCAAGTATTAATTAACCT 1340
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DB 14 TCATGGCAGTATATATCAAAATTTCAAAAGGAAACTAACAACCTTAATAATTA 73

OY 1341 TTCTGCTTAAACATCTCTGTGATCCATGTTGACGAAAGTGGAGCCATAT 1400
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DB 74 TTGTATGCTCAACATCTCAGTGTATCTTATCTATGAATAATTAAGAGCTCCATAT 133

OY 1401 TCATCCAGGCTTATGCCAAGAGGCGTTCATCAGAGGCTCTGAGACCAAGGTGAG 1460

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Db      134  TCCATACAACTATATCTTCAGAAAAAGACCCTCATCAAGAGCCCTGTGCTGATACGGGT 193
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        Db      194  TTTCAGCAAGAAAATAGATTACAAATTAATGAATGCAATTTCAAGATTAAGAAAT 253
        QY      1521  GGTATCATCTGCACATACACCATCTTTTACCAAGCTGAAGGTGAAGAAAGATCTCCAG 1580
        Db      254  GGCTTTATAGTAGTACATACATATTTTATAAACCTGAAGGTGGAAGAGTTGAATGA 313
        QY      1581  ACAGCAATTCAGCATCTTTGACAGTGGCTGAGTCCCTGGAAGCAAGACCTCTTAC 1640
        Db      314  ACAGTAACTCTGATGTGTACAGTACACACTGAAGCTTACAGGCTAATACACATAC 373
        QY      1641  ATTGTTCAGGTCAATGGCCAGCAGCAGTGTGGGGGAACCAAGGACACATTAATTC 1700
        Db      374  ACTGTCTATATCTGAGCAAGCAAGAGCTGTGGAACCAAGTGAAGCAAAACATTC 433
        QY      1701  AAGACATTTGTCATCAGTGTCTTGAAGATTAATCTCATTAATCTCTGATTTGGAGAG 1760
        Db      434  AACACTTTGAATTCATATAAGAACGTTATTTTCAATGACATGACAGTTGATTTAGC 493
        QY      1761  CTCTTATTTCTCATATATCTGTACAGTGGCATATGCTCAAAAACCAACCAATTTACT 1820
        Db      494  ATGTGTCTCTGTAGAGCCCTTTGGATTAACGTGATTAATGAAGAAAC--ACGTGTTAA 550
        QY      1821  CATCTGTGTGGCCACCGTCCCAACCTGCTGAAGATGTATAGCCATGCGATGA 1880
        Db      551  AAGCTTTGCTGGCGCTGATGACCAATCTTCAGAGAGCGTTGACAGTGGCGCTCTT 610
        QY      1881  GATGATTTCAAG 1893
        Db      611  GATGATCTATGG 623

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RESULT 5
LOCUS   AO022781
DEFINITION HS_2180_A2_B11_MR CIT Approved Human Genomic Sperm Library D Homo
          sapiens genomic clone Plate-2180 Col-22 Row-C, genomic survey
          sequence.
ACCESSION AO022781
VERSION   AO022781
KEYWORDS  GI:3220989
SOURCE    GSS.
ORGANISM  Homo sapiens (human)
REFERENCE
AUTHORS   Hood,L.
          Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
          Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
          Hood,L.
          Sequence-tagged connectors: A sequence approach to mapping and
          scanning the human genome
          Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
          10449764
COMMENT   Contact: Mahairas GG, Wallace JC, Hood L
          High Throughput Sequencing Center
          University of Washington
          401 Queen Anne Avenue North, Seattle, WA 98109, USA
          Tel: (206) 616-3618
          Fax: (206) 616-3887
          Email: jwallace@u.washington.edu
          Sequence Tagged Connector
          Plate: 2180 row: C column: 22
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          High quality sequence stop: 459.
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/sex="male"
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/note="Organ: sperm; Vector: pBeloBac11; BAC Clones in
E-Coli DH10B"
BASE COUNT      132 a      81 c      113 g      130 t      3 others
ORIGIN
Query Match      6.8% Score 163.8; DB 28; Length 459;
Best Local Similarity 98.2% Pred. No. 6e-37;
Matches 165; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      678  TGGTGAAGTCAACTGCTAAGAACCCGTAAGATTAACCAACGTCACACCTACG 737
        208  TAGATGAATCAACTGCTAAGAACCCGTAAGATTAACCAACGTCACACCTACG 267
        Db      738  GGGCTGCAGCCTTTTACAGATATGTCATAGCTCTGCGATGCGGTCAAGAGTCAAG 797
        QY      798  TTCTGAGTACCTGAGCCAAAGAAATGGATGACTGAGAGAA 845
        Db      328  TTCTGAGTACCTGAGCCAAAGAAATGGATGACTGAGAGAA 375
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LOCUS   CA561173
DEFINITION K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
          musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.
ACCESSION CA561173
VERSION   CA561173
KEYWORDS  GI:25105828
SOURCE    EST.
ORGANISM  Mus musculus (house mouse)
REFERENCE
AUTHORS   Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Staag,C.A.,
          Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
          Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
          (Long)
          Unpublished
          Other ESTs: K0283D09-3
          Contact: Dawood B. Dudekula
          Laboratory of Genetics
          National Institute on Aging/National Institutes of Health
          333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
          Email: cdna@sun-grc.nia.nih.gov
          Plate: K0283 row: D column: 09
          Seq primer: M13 Reverse
          High quality sequence stop: 592
          POLYA-No.
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          )"
          /note="Vector: pSPORT1 (Invitrogen); Site:1: SalI; Site:2:
          NotI; Mouse cDNA project by the Laboratory of Genetics,
          National Institute on Aging (NIA), Intramural Research
          Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
          a long-transcript enriched cDNA library (Ref. Genome Res.
          11: 1553-1558 (2001). [PMID: 11544191]). Total RNAs were
          extracted from a pool of 1488 unfertilized eggs.

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Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):  
5'-PGACAGTCTTACATGCGAGCGGCCGCCCCCTTTTTTTTTT-3'),  
treated with T4 DNA polymerase, and purified by  
ethanol-precipitation. The cDNAs were ligated to  
Lone-linker L1-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.5 kb. The library was constructed  
by Yulan Piao (NIA)."

BASE COUNT 156 a 145 c 119 g 172 t  
ORIGIN

Query Match 6.5%; Score 155.2; DB 14; Length 592;  
Best Local Similarity 64.6%; Pred. No. 2.7e-34;  
Matches 257; Conservative 0; Mismatches 123; Indels 18; Gaps 1;

QY 131 AACATTCTCTCTCCAGCCTTATGTTAACTGGGGATGATGGACCTGGCACT 190  
Db 213 AACCTTCATGAAATACAGCCTCTGGGTGAGACGTGAATATGTGACCTGGCACT 272  
QY 191 GTGATGCTCCCTCCACCTGCAATTCAGCTGCGACGCTGCGACAGTCCAGTGA 250  
Db 273 GTGGGCAATCTCTCTCTCTGCAATTCAGCTGCGACGCTGCGACAGTGA 332  
QY 251 CATTCTCTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGTCCAGAGAA 310  
Db 333 CATTCTCTGTCTACTACTATAGAAAAATTTAACTGCACTTGAGTCCAGAGAA 392  
QY 311 AACAGTTATCCAGTACAGATTAAAGAACTTACGCTTTGGAGAAAAACATGAT 370  
Db 393 AACCAATGATACAGTACAGTATGACTTGGACTTACCTATGCA----- 438  
QY 371 TTGATACACCAATGATGTTCTACAGTGAATAATCGTCTGCTTTTCTTCCAG 430  
Db 439 -----AAAAGCAATATAGTGCATGCTACAGAGGCTTCATATTTCTTCCG 494  
QY 431 AATAAGATCCAGATATTAATTAACATTGAGGTGAAAGCTGAAATGAGATGTT 490  
Db 495 TGCATGCCCCCAGACATCTGCACTGTGAAGTACAAAGCTCAAAATGAGATGTA 554  
QY 491 TAAATCTCATATGACATCTGAGATTTAGAACATAG 528  
Db 555 TAAATCTGACATCATATTTGGCAATTAATCTCCATAG 592

RESULT 7 479 bp mRNA linear EST 19-NOV-2002  
CA560924  
LOCUS K0279C07-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus  
DEFINITION musculus cDNA clone NIA:K0279C07 IMAGE:30052254 5', mRNA sequence.  
ACCESSION CA560924  
VERSION CA560924.1 GI:25105579  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 479)  
REFERENCE Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Staeg, C.A.,  
Watt, P., Alba, K., Tanaka, T. and Ko, M.-S.H.  
TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library  
(Long)  
JOURNAL Unpublished  
COMMENT Other ESTs: K0279C07-3  
Contact: Dawood B. Dudekula  
Laboratory of Genetics

National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6620, USA  
Email: cdna@agun.grc.nia.nih.gov  
Plate: K0279 row: C column: 07  
Seq primer: M13 Reverse  
High quality sequence stop: 479  
POLYA=No.

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Source location/Qualifiers  
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/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://agun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). PMID: 11544199). Total RNAs were  
extracted from a pool of 148 unfertilized eggs.  
Double-stranded cDNAs were synthesized with an Oligo(dT)  
primer (Invitrogen):  
5'-PGACTAGTCTTACATGCGAGCGGCCGCCCCCTTTTTTTTTT-3'),  
treated with T4 DNA polymerase, and purified by  
ethanol-precipitation. The cDNAs were ligated to  
Lone-linker L1-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.5 kb. The library was constructed  
by Yulan Piao (NIA)."

BASE COUNT 127 a 117 c 102 g 133 t  
ORIGIN

Query Match 6.2%; Score 149.4; DB 14; Length 479;  
Best Local Similarity 64.8%; Pred. No. 1.2e-37;  
Matches 247; Conservative 0; Mismatches 116; Indels 18; Gaps 1;

QY 148 AGCCTCATGTGTAACTGGGATGATGTGACCTGGGACCTGGATGCTCCCTCAC 207  
Db 117 ATCTCTGGGTGTAAAGCGTGATATGTGAGACTTGGCACTGCTCTTCTCC 176  
QY 208 TCTCAAAATTCAGCTTGGCAGCTTCTGCACTGAGACATTTCTGTCTACT 267  
Db 177 TCTCAAAATTCAGCTTGGCAGCTTCTGCACTGAGACATTTCTGTCTACT 236  
QY 268 ACTATAGAAAATTTAACTGCACTTGGGATGAGAGAAAGCAAGTATACCACT 327  
Db 237 ACTTGCAGAGAAATCTGCTGCACTTGGGATGAGAGAAAGCAAGTATACCACT 296  
QY 328 ACACAGTTAAGAGAACTTACGCTTTTGAGAAAAAATGATTAATGTACAACTAGTT 387  
Db 297 ATATTGTGACTTGTACCTTACCTATGCA-----AAAAGCAATTTATA 338  
QY 388 CTACAGTGAATAATGCTGCTGCTCTTTTCTTCCACAGATTAAGATCCAGATA 447  
Db 339 GTGCAATGCTACAGAGCTTCAATATCTTCTTCCCTGCTGCAATCCCAACACA 398  
QY 448 ATTATACATTGGAGGTGAGAGCTGAATAAGATGATTAATTCATATGACAT 507  
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	OY	508	ACTGAGATTGACAGACATAG	528	
	Dd	459	ATTGCATTATCTCCATAG	479	
RESULT 8					
CAS59989					
LOCUS					
DEFINITION		CAS59989	553 bp	mRNA	linear EST 19-NOV-2002
ACCESSION		K0266C03-5N	NIA Mouse Unfertilized Egg cDNA Library (Long)	Mus	
VERSION		musculus cDNA clone NIA:K0266C03 IMAGE:30051002	5'	mRNA sequence.	
KEYWORDS		CAS59989.1	GI:25104613		
SOURCE		EST.			
ORGANISM		Mus musculus (house mouse)			
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		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE		1 (bases 1 to 553)			
AUTHORS		Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A.,			
		Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.			
TITLE		Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library			
		(long)			
JOURNAL		Unpublished			
COMMENT		Other_ESTS: K0266C03-3			
		Contact: Dawood B. Dudekula			
		Laboratory of Genetics			
		National Institute on Aging/National Institutes of Health			
		333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA			
		Email: cdna@gsun-grc.nia.nih.gov			
		Plate: K0266			
		Seq primer: M13 Reverse			
		High quality sequence stop: 553			
		POLYA-No.			

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QY	191	GTGATGTGTCCTCCCTCAGCTCTGCAATATTCAGCCTTGGCAGCTTGGCAGCTAAGCTTGAGAA	250						
Db	273	GTGGGCAATTCCTCTCCCTCTGCAAAATTCAGCCTTGGCAGCTTGGCAGCTAAGCCAGAGAA	332						
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Db	333	CATTTCCTAGCTCTTTTACTTTCAGACAGAAATCTGACTTGGACCTTGGAGACCGAGAAAGGA	392						
QY	311	AACGAGTTATACCCAGTACACAGATTAAGAGAACTTACGCTTTTGGAGAAAAACATGATAA	370						
Db	393	AACCAATGATACCAAGCTACATTTGAGACTTGTGACTTACCTACCTATATGA-----	438						
QY	371	TTGTACAAACAATAGTTCTTACAGTGAATAATCGTGTCTTGTCTTTTTCCTTCCAG	430						
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Db	495	TGCATATGCCCCAGACACTCTCAGCTGTGGAAGTACAAAGCTCAAAATGAGATGCT	549						
RESULT 9									
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LOCUS									
DEFINITION	CA555774	K0202F08-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus							
ACCESSION	CA555774	musculus cDNA clone NIA:K0202F08 IMAGE:30044899 5', mRNA sequence.							
VERSION	CA555774.1	GI:25100137							
KEYWORDS		EST.							
SOURCE		Mus musculus (house mouse)							
ORGANISM		Mus musculus							
REFERENCE		Mumukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS		Emmaliyola; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.							
TITLE		1 (bases 1 to 546)							
JOURNAL		Piao Y., Karauli G.J., Dudekula D.B., Qian Y., Luo A., Steag, C.A.,							
COMMENT		Martin, P., Albra, K., Tanaka, T. and Ko, M.S.H.							
		Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library							
		(Long)							
		Unpublished							
		Other ESTs: K0202F08-3							
		Contact: Dawood B. Dudekula							
		Laboratory of Genetics							
		National Institute on Aging/National Institutes of Health							
		333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA							
		Email: cdna@nigmsun.grc.nia.nih.gov							
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/home/vecteur.personal/intraorigen/, site\_intraori, site\_2  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA/>). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were

Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen]: 5'-GCAGTACCTTTCAGATCCGACGCGCCGCCCTTTTCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lp-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSP6RT plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Xulan Plao (NIA)."

Query Match	5.5%;	Score 133.2;	DB 14;	Length 546;
Best Local Similarity	64.2%;	Pred. No. 9.4e-28;		
Matches 226;	Conservative 0;	Mismatches 108;	Indels 18;	Gaps 1

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OY      13  AACATTCCTCTCCCCACCACTTCATGTTTAACCTGGGAGTGAATGGAGACTGGGACT 150
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Db      213  AAMCCTTCATGAATTAACAGCCTCTGGGTGTGAGCCTGGAATATGTGGACCTTGGCACT 272
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      191  GTGGATGTCCTCCCTCACTCTGCAAAATACGCTGGCAGCTCTGCCAGCTAAAGCTTGAA 250
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Db      273  GTGGGCAATTCCTCTTCCTGCAAAATACGCTGGCAGCTCTGCCAGCTAAAGCAGGAA 332
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      251  CATTTCTGTGTTACTACTATAGAAAAAATTAACCTGCACCTTGGAGTCCAGGAAGA 310
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Db      333  CATTTCTGTGTTTACTTTGACAGAAATGTGACTTGCACTTGGAGACCAAGAAAGA 392
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY      311  AACCACTTATCCCACTACACAGTTAAGAGAACTTACGCTTTGGAGAAAACATGATA 370
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      393  AACCAATGATACCAAGCTACATTGTGACTTGTGACTTACCTCATATGA----- 438
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OY      371  TTGTACACCAATAGTTCTTCAAGGAAATCGTCTCGCTCTTTTTCCTCCAG 430
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Db      439  ----AAAAGCAATTAATAGTACATGTCTACAGAGGCTTCATATCTTTTCCCGTTCGT 494
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OY      431  AATAAGATCCAGATTAATATACATTGAGTGGAGAACTAAATGAGAT 482
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RESULT	10
LOCUS	B0560019
DEFINITION	B0560019 487 bp mRNA linear EST-20-JUN-2002
ACCESSION	H4061G10-5 NIA Mouse 7.4K cDNA Clone Set musculus cDNA clone
VERSION	H4061G10 5', mRNA sequence.
KEYWORDS	B0560019 B0560019
SOURCE	B0560019.1 GI:21460904 EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Euthyrola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 487) Vanburen,V., Piao,Y., Dudekula,D.B., Qian.Y., Carter,M.G., Martin .P.R., Stagg,C.A., Bassey,U., Alpa,K., Hamdtant,T., Kargul,G.J., Luo,A.G., Keaiso,J., Hide,W. and KO,M.S.H. Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set Genome Res. 12 (12), 1999-2003 (2002)
JOURNAL MEDLINE	22354164
PUBMED	12466305
COMMENT	Other ESTs: H4061G10-3 Contact: Yong Qian Laboratory of Genetics

National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA  
Email: cdn@igsn.grc.nia.nih.gov  
This clone set has been freely distributed to the community. Please  
visit [http://igsn.grc.nia.nih.gov/cdn/NIA\\_74k.html](http://igsn.grc.nia.nih.gov/cdn/NIA_74k.html) for details.  
Plate: H406 Row: G Column: 10  
Seq. primer: -21M13 Reverse  
High quality sequence stop: 487  
POLYA-No.

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	/mol_type="mRNA"
	/strain="C57BL/6"
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	/db_xref="taxon:10090"
	/clone="H4061G10"
	/sex="mixed"
	/dev_stage="mixed"
	/lab_host="DH10B"
	/clone_lib="NIA Mouse 7.4K cDNA Clone Set"
	/note="Vector: pSPOR1; Site1: SalI; Site2: NotI. This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
BASE COUNT	123 a 123 c 98 g 143 t
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	Query Match	5.4%	Score 129	DB 13	Length 487
	Best Local Similarity	71.0%	Pred. No. 1.5e-26		
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QY	131	AAACATTCTCTCTCCACGCTTCATGTGTTAACCTGGGATGATGTGGACTGGGCAC	190		
Db	213	AAACCTCATGAAATATACAGCTCTGGGGTGTAAAGCTGGAAATATGTGGACCTTGGCACT	272		
QY	191	GTGATGTCGCCCTCCTACCTGTCAATTCAGCGCTGGACACTTGGCAGGTAAAGCTTGAA	250		
Db	273	GTGGGCAATTCCTTCTCTCAAAATTCAGCGCTGGCACTCTGGCGAATTAAGCCAGNAA	332		
QY	251	CATTTCCTGTGTCTACTACTATAGGAAAAATTTAACTGCACTTGGAGTCCAGGAAAGA	310		
Db	333	CATTTCCTGTGTCTACTACTGTGACAGAAAACTACTCTGCACTTGGAGAACCCAGGAAAGA	392		
QY	311	AACCAATTATACCCAGTACACAGAGTTAAGAGAACTTACGCTTTGGAGAAAAAACAATGATA	370		
Db	393	AACCAATGATACCCAGTACATTTGTGACTTTGACTTACTCCATATGAGAAAAAACAATTTATAG	452		
QY	371	T 371			
Db	453	T 453			

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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	K0283f09-5N NIA mouse unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone NIA:K0283f09 IMAGE:30052676 5', mRNA sequence.	CA561193									
		CA561193.1	GI:25105848	EST.							
					Mus musculus (house mouse)						
					Mus musculus						
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
					1 (bases 1 to 518)						
					Piao, Y., Karguly, G. J., Dudekula, D. B., Qian, Y., Luo, A., Stagy, C. A., Martin, P., Alba, K., Tanaka, T. and Ko, M. S. H.						
					Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (Long)						
					unpublished						
					Other-ESTs: K0283f09-3						
					Contact: Dawood B. Dudekula						
					Laboratory of Genetics						

National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
Plate: K0283 row: F column: 09  
Seq primer: M13 Reverse  
High quality sequence stop: 518  
POLYA-No.

FEATURES  
source

Location/Qualifiers  
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/clone="NIA:K0283F09 IMAGE:30052676"  
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/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Unfertilized Egg cDNA Library (Long )"  
/note="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGCGAGCGCCGCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker IL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 129 a 134 c 105 g 150 t  
ORIGIN

Query Match 5.4%; Score 129; DB 14; Length 518;  
Best Local Similarity 71.0%; Pred. No. 1.6e-26;  
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

131 AAACATTCTCTCCCGACGCTTTCATGTTAACTGGGATGATGGAGCTGGGCACT 190  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 213 AAACCTCATGAATAAAGAGCCTCTGGGTGTGAAGCGTGAATATGTGGACCTTGGCACT 272  
191 GTGATGCTCCCTCACTCTGCAAAATTCAGCTGGAGCTCTGCCAGCTAAGCTGAGAA 250  
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Db 273 GTGGGCAATTCCTCTCTCTGCAAAATTCAGCTGGAGCTCTGCCAGCTAAGCTGAGAA 332  
251 CATTTCTGTGTCTACTACTATAGGAAATTTAACTGCGACTGGAGTCCAGGAAAGA 310  
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Db 333 CATTTCTGTGTCTACTACTAGGAAATTCAGCTGGAGCTCTGCCAGCTAAGCTGAGAA 392  
311 AACGATTATACCCAGTACAGAGATTAAAGAACTTACGCTTTGGAGAAAACATGATTA 370  
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Db 393 AACCAATGATACAGCTACTATGTGACTTGTACTCTTATGAAAAAACCAATTATAG 452  
371 T 371  
453 T 453

RESULT 12  
CA559290 523 bp mRNA linear EST 19-NOV-2002  
LOCUS CA559290

DEFINITION K0256G09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus  
musculus cDNA clone NIA:K0256G09 IMAGE:30050096 5', mRNA sequence.  
ACCESSION CA559290  
VERSION CA559290.1 GI:25103871  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.  
REFERENCE 1 (bases 1 to 523)  
AUTHORS Piao,Y., Kargul,G.D., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A.,  
Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.  
TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library  
(Long)  
JOURNAL Unpublished  
COMMENT Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
Plate: K0256 row: G column: 09  
Seq primer: M13 Reverse  
High quality sequence stop: 523  
POLYA-No.

FEATURES  
source

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="niaEST:K0256G09-5N"  
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/tissue\_type="unfertilized Egg"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Unfertilized Egg cDNA Library (Long )"  
/note="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGCGAGCGCCGCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker IL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 129 a 134 c 107 g 153 t  
ORIGIN

Query Match 5.4%; Score 129; DB 14; Length 523;  
Best Local Similarity 71.0%; Pred. No. 1.6e-26;  
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

131 AAACATTCTCTCCCGACGCTTTCATGTTAACTGGGATGATGGAGCTGGGCACT 190  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 213 AAACCTCATGAATAAAGAGCCTCTGGGTGTGAAGCGTGAATATGTGGACCTTGGCACT 272  
191 GTGATGCTCCCTCACTCTGCAAAATTCAGCTGGAGCTCTGCCAGCTAAGCTGAGAA 250  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 273 GTGGGCAATTCCTCTCTCTGCAAAATTCAGCTGGAGCTCTGCCAGCTAAGCTGAGAA 332

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Oy      251  CATTTCCGCTGCTACTACTATAGSAAAAATTTAACTCGCACTTGAGATCCAGSAAAGA  310
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Db      333  CATTTCCGCTGCTTTTACTTCGACAGAAATCTGACTTCGATGGAACACGAGAGA  392
Oy      311  AACCAAGTATATCCAGCTACACAGTTAAGAGAACTTACGCTTTTGAGAAAAACATGATA  370
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Db      393  AACCAATATATCCAGCTACATTTGACTTTGACTTCTATGAAAAAGCAATTATAG  452
Oy      371  T 371
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Db      453  T 453

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RESULT	13			
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LOCUS	BZ147466	756 bp	DNA	linear
DEFINITION	CH230-406E16_TJ CHO1-230 Segment 2 <i>Rattus norvegicus</i> genomic clone.			
ACCESSION	CH230-406E16			
VERSION	BZ147466			
KEYWORDS	BZ147466.1	GI:23788403		
SOURCE	GSS			
ORGANISM	<i>Rattus norvegicus</i> (Norway rat)			
	<i>Rattus norvegicus</i>			

REFERENCE	1 (bases 1 to 756)
AUTHORS	Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregregias,E., Overton,L., Russell,D., Chen,D., Riggs,F., deJong,P. and Fraser,C.M.
TITLE	Rat BAC End Sequences From Library CHORI-230 MboI segment
JOURNAL	Unpublished
COMMENT	Other_GSSs: CH230-406E16_TV

Other: GSSS CH230-406E16, TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the rat BAC library CHORI-230  
(<http://www.chori.org/bacpac/rat330.htm>). For BAC library  
availability, please contact Pierlet de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org))  
Clones may be purchased from BACPAC Resources  
(<http://www.chori.org/bacpac/ordering/information.htm>). BAC end  
page: [http://www.tigr.org/tcdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tcdb/bac_ends/rat/bac_end_intro.html)  
Plate: 406 row: E column: 16  
Seq primer: SP6  
Class: BAC ends.

FEATURES	Location/Qualifiers
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/db_xref="taxon:10116"
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/sex="Female"
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CHORI-230 Rat (BN/SSNhsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT      205 a      185 g      202 t
ORIGIN
164 c

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Best Local Similarity	77.98;	Pred. No. 2.8e-26;		
Matches 155;	Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0;

QY	925	AGAA	GCGC	AAGAG	AGAG	CCCC	AGTCC	TAG	AGAAAA	CACTT	GGCT	TACA	CAAT	TATG	TACT	ATC	984
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OY 985 CAGAAAGACACTTAACCTCAGAGAACAATGAAACACTTACCAGAGCTTGAACTGC 1044  
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Db 139 CAGAAAACAGCACTAACCTCACGGGATGAATAACAGCATCCAGCACTATGAACTGC 80  
  
OY 1045 ATCTGGGAGGGGAGAGCGTTTGGGTGTCTATGATTTCCTAATATTCCTTTGGGAAGCTC 1104  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 79 TTCTGTGGGGGCGACAGCGCATGTGTGTGTGACTTTTAACTCTCTTGGCAAGTCC 20  
  
OY 1105 CAGTGGCCCACTTGAAGAT 1123  
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Db 19 AAGAGGCCATACTGAGGAT 1

RESULT	14
BQ938538	BQ938538      924 bp    mRNA               linear   EST_21-AUG-2007 LOCUS AGNCOURT_8931844 NIH_MGC_94 Mus musculus cDNA IMAGE:6466061 DEFINITION 5' , mRNA sequence.
ACCESSION	BQ938538
VERSION	BQ938538.1 GI:22354016
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	1 (bases 1 to 924)
AUTHORS	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

tissue procurement: The Cepro Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution by: Agencourt Bioscience Corporation  
 clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM13969 Row: m Column: 06  
 High quality sequence stop: 636.

FEATURES	Location/Qualifiers
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203 c 233 g 268 t

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BASE COUNT	220 a	203 c	233 g	268 t
ORIGIN				

Query Match	5.38;	Score 126.6;	DB 13;	Length 924;
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QY	1952	ACCATGTGTCACCCCCACAGTGAAGTTGGTCATTGTACACAAGTTGGTGTGAACCTTTGGAA	2011					
Db	715	ACCATGTGTCACCCCCCGGGATC-----TCATTGACACAAGCTGGTAGTGAACCTTTGGAAA	768					

QY	2012	TGTTCTGCAGAAATTTTTCACACATGAAACCACAGCGGTCAAGSAAACATTTTAGGAGC	2071
Db	769	TTTTCTGGAAGTAGTTTTCACACAGGAAGCTGGAAGGGTCACGCGAGCATTTTGGGGAG	828



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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2003, 11:08:21 ; Search time 19 Seconds  
(without alignments)  
1630.081 Million cell updates/sec

Title: US-09-892-949-2

Perfect score: 3908  
Sequence: 1 MMWALMMLPSLCKFSLAA.....VFARFLVSEKLPHTKGEV 732

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfill.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	678.5	17.4	708	1 US-08-308-881-2	Sequence 2, Appli
3	678.5	17.4	708	2 US-09-058-263-2	Sequence 2, Appli
4	678.5	17.4	708	2 US-09-059-099-2	Sequence 2, Appli
5	678.5	17.4	708	3 US-09-058-264-2	Sequence 2, Appli
6	678.5	17.4	708	4 US-09-455-962-2	Sequence 2, Appli
7	678.5	17.4	708	5 PCT-US95-06530-2	Sequence 2, Appli
8	677.5	17.3	918	4 US-08-825-558-6	Sequence 6, Appli
9	677.5	17.3	918	4 US-09-312-611-6	Sequence 6, Appli
10	629	16.1	951	4 US-09-313-942-9	Sequence 9, Appli
11	625	16.0	572	2 US-08-419-652-5	Sequence 5, Appli
12	619	15.8	859	4 US-09-313-942-7	Sequence 7, Appli
13	618	15.8	658	2 US-08-825-558-4	Sequence 4, Appli
14	618	15.8	658	4 US-09-312-611-4	Sequence 26, Appli
15	616	15.8	1158	4 US-09-313-942-26	Sequence 24, Appli
16	616	15.8	1168	4 US-09-313-942-24	Sequence 4, Appli
17	517.5	13.2	836	1 US-07-923-976-4	Patent No. 5422248
18	513.5	13.1	783	6 5422248-2	Sequence 6, Appli
19	508	13.0	602	2 US-08-419-652-6	Sequence 8, Appli
20	506	12.9	863	1 US-07-923-976-8	Sequence 8, Appli
21	471.5	12.1	837	1 US-07-923-976-2	Sequence 5, Appli
22	445	11.4	488	2 US-08-599-455B-5	Sequence 5, Appli
23	445	11.4	488	3 US-09-069-781B-5	Sequence 5, Appli
24	445	11.4	488	4 US-07-797-556-2	Sequence 5, Appli
25	445	11.4	488	4 US-08-864-564A-5	Sequence 5, Appli
26	445	11.4	488	4 US-09-094-410-5	Sequence 5, Appli
27	445	11.4	488	4 US-08-708-123D-5	Sequence 5, Appli

28	445	11.4	488	4 US-08-583-153A-5	Sequence 5, Appli
29	445	11.4	488	4 US-08-638-524B-5	Sequence 5, Appli
30	443.5	11.3	771	1 US-07-923-976-6	Sequence 6, Appli
31	408.5	10.5	1097	1 US-07-943-843-6	Sequence 6, Appli
32	408.5	10.5	1097	1 US-08-347-003-6	Sequence 6, Appli
33	404.5	10.4	1001	1 US-07-797-556-6	Sequence 6, Appli
34	404.5	10.4	1001	1 US-07-943-843-2	Sequence 2, Appli
35	404.5	10.4	1001	1 US-08-347-003-2	Sequence 2, Appli
36	401.5	10.3	620	2 US-08-419-652-7	Sequence 7, Appli
37	383	9.8	862	2 US-08-685-118-2	Sequence 2, Appli
38	383	9.8	862	2 US-08-915-495-2	Sequence 2, Appli
39	383	9.8	862	2 US-08-914-520-2	Sequence 2, Appli
40	375	9.6	979	1 US-08-308-881-6	Sequence 6, Appli
41	375	9.6	979	2 US-09-058-263-6	Sequence 6, Appli
42	375	9.6	979	2 US-09-059-099-6	Sequence 6, Appli
43	375	9.6	979	3 US-09-058-264-6	Sequence 6, Appli
44	375	9.6	979	4 US-09-455-962-6	Sequence 6, Appli
45	375	9.6	979	5 PCT-US95-06530-6	Sequence 6, Appli

## ALIGNMENTS

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RESULT 1
US-07-797-556-2
: Sequence 2, Application US/07797556
: Patent No. 5262522
: GENERAL INFORMATION:
: APPLICANT: Gearling, David P.
: TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
: NUMBER OF INVENTIONS: Inhibitory Factor
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/797,556
: FILING DATE: 19911122
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Seese, Kathryn A.
: REGISTRATION NUMBER: 32,172
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: TELEFAX: 206-587-0606
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 708 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-797-556-2

Query Match 17.4% Score 678.5; DB 1; Length 708;
Best Local Similarity 29.3%; Pred. No. 1.2e+54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKPNTSCVYVYRNLCITWSPGKESY-TQYTVK--RTYAGE--KHD--NCTN 71
DB 126 PEKPNLSCTIVNEGKKMKCEWDGGEHLETFNFKLSWATHTKADCAKADPTPTSCVD 185
QY 72 SSTSENKASCSFFLPRTIPNYTIEVANGDVIKS-HMTYVRLNIAETEPKIFRV 130
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Db 186 YST-----VFV-----NIEWVEAENALGKVTSDHINFPVYKV-KPNPHNLV 230  
QY 131 KPVIGIKRMIOIEWIKPELAPVSSDLKYTLRFRVNSTSWMEVNFARKRKNQTYNLTG 190  
Db 231 INSELSILKLTMTNPSIKSVII-LKYNIOYRTKDASTWSQIP-PEDTASTRSSFTYOD 288  
QY 191 LQPTTEVIALRCAYKESK-FWSDMSQKMGTEEARC-GLELMRYLKPADGRRPRV 248  
Db 289 LKPFTEYFRIKMKEDCKGYMSDSEASGITYEDRSKAPSFYWKIDPSHTQGYRTVQ 348  
QY 249 LLMKRGAPVLEKTLGYNIVYPSNTNLTETMNTNQOLEHLGSEFVMSISYNSL 308  
Db 349 LVMKTLPPFEANGKILDEYVLTFRKSHLQNTYVNAI-KLVNLTDYRATLTVRNLV 406  
QY 309 GKSPATLRIPAIQESFQCIENVQACVAEDOLVVKQSSALDVNTWMIEMFPVDSEPT 368  
Db 407 GKSDAAVLTIPACQFQATHPMDLKAFFPKDMLNVEWTPPRESKAKYILEMCLVSDKAPC 466  
QY 369 TLSWESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGEPSIOAVAKESVSEGEPTK 428  
Db 467 ITDQOEDGTVHRTYLRGNLAESKCYLITVPYVADGPGSPESIKAYLKQAPPSKGPYVR 526  
QY 429 VENIGVTVITTKMEIPKSEKGIICNTTIFYOAGGKGFSTYNSILOGLSLKRT 488  
Db 527 TKKYGKNEAVLEMDQLPVQNGFIRNTTIFYRTIIGNETAVNVDSSHTEYTLSSLTSDT 586  
QY 489 SYIVQVASTAGTNGTSINFKTLSEFVEILITSLIGGLILITLTVAYGLKRPNK 548  
Db 587 LYVMRMAVYDEGKDGPEFTTTPKPAQGEIEALVYVCLAFLLTLLGLVFCFNKRD 646  
QY 549 LTHLCPTVPNPAESSIATW-----HGDDFKKL 577  
Db 647 IKKHIMVNPDPKSHIAQMSPHTPRRHFNNSKDOM 682

## RESULT 2

US-08-308-881-2  
Sequence 2, Application US/08308881

Patent No. 5783672

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Macintosh

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881

FILING DATE: 12-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/249,553

FILING DATE: 26-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2614-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

2

LENGTH: 708 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-308-881-2

Query Match 17.4%, Score 678.5; DB 1; Length 708;  
Best Local Similarity 29.3%; Pred. No. 1.2e-54;  
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKENISCVYYKNNLTCTWSPGKETS-Y-QTYVKK---RTYAFGE---KHD---NCTTN 71  
Db 126 PEKPKNLSICVINECKKMKCEWDGGRHTLETNFTLKSEMAHMKFADCKAKRDTPTSCVTD 185  
QY 72 SSTSEGNRASCSEFIPRTIIPDNYITIEVEAEGDGVIS-HMTYRLENLAKTEPKIFRV 130  
Db 186 YST-----VFV-----NIEWVEAENALGKVTSDHINFPVYKV-KPNPHNLV 230  
QY 131 KPVIGIKRMIOIEWIKPELAPVSSDLKYTLRFRVNSTSWMEVNFARKRKNQTYNLTG 190  
Db 231 INSELSILKLTMTNPSIKSVII-LKYNIOYRTKDASTWSQIP-PEDTASTRSSFTYOD 288  
QY 191 LQPTTEVIALRCAYKESK-FWSDMSQKMGTEEARC-GLELMRYLKPADGRRPRV 248  
Db 289 LKPFTEYFRIKMKEDCKGYMSDSEASGITYEDRSKAPSFYWKIDPSHTQGYRTVQ 348  
QY 249 LLMKRGAPVLEKTLGYNIVYPSNTNLTETMNTNQOLEHLGSEFVMSISYNSL 308  
Db 349 LVMKTLPPFEANGKILDEYVLTFRKSHLQNTYVNAI-KLVNLTDYRATLTVRNLV 406  
QY 309 GKSPATLRIPAIQESFQCIENVQACVAEDOLVVKQSSALDVNTWMIEMFPVDSEPT 368  
Db 407 GKSDAAVLTIPACQFQATHPMDLKAFFPKDMLNVEWTPPRESKAKYILEMCLVSDKAPC 466  
QY 369 TLSWESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGEPSIOAVAKESVSEGEPTK 428  
Db 467 ITDQOEDGTVHRTYLRGNLAESKCYLITVPYVADGPGSPESIKAYLKQAPPSKGPYVR 526  
QY 429 VENIGVTVITTKMEIPKSEKGIICNTTIFYOAGGKGFSTYNSILOGLSLKRT 488  
Db 527 TKKYGKNEAVLEMDQLPVQNGFIRNTTIFYRTIIGNETAVNVDSSHTEYTLSSLTSDT 586  
QY 489 SYIVQVASTAGTNGTSINFKTLSEFVEILITSLIGGLILITLTVAYGLKRPNK 548  
Db 587 LYVMRMAVYDEGKDGPEFTTTPKPAQGEIEALVYVCLAFLLTLLGLVFCFNKRD 646  
QY 549 LTHLCPTVPNPAESSIATW-----HGDDFKKL 577  
Db 647 IKKHIMVNPDPKSHIAQMSPHTPRRHFNNSKDOM 682

## RESULT 3

US-09-058-263-2

Sequence 2, Application US/09058263

Patent No. 5891997

GENERAL INFORMATION:

APPLICANT: Mosley, Bruce

TITLE OF INVENTION: Receptor for Oncostatin M

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Macintosh

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/09/058,263  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,881  
FILING DATE: 12-SEP-1994  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 708 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-058-263-2

Query Match 17.4%; Score 678.5; DB 2; Length 708;  
Best Local Similarity 29.3%; Pred. No. 1.2e-54;  
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKPENISCVYYRKNTCTSPGKETS-TOYIVK---RYAGE---KHD---NCTTN 71  
DB 126 PEKPNLSICIVNEGKMKRCMDGGRHLETFILKSEMAWHKFDCKAKKRDTPSTCYD 185  
QY 72 SSTSNNRASCSEFLPRITIPDNYTIEVAENGDIYKIS-HMTYMLEIAKTEPPKIRY 130  
DB 186 YST-----YFV-----NIEVWEAEALGKVTSDHINFDVYRV-KPNPHNL 230  
QY 131 KPVIGIKRMIOEWIKPELAPVSSDLKYLFRFVNSTSMWEVNFARKNRKDKNTYNTLG 190  
DB 231 INSELSILKLTWNPISIKSVII-LKYNIOYRTDASTWGI-P-PEDTASRSSFYVD 288  
QY 191 LOPFTEYIALRCAYKESK-FWSDMSOEKMGTEEAPC-GLEIMRYLKPADAGRPRY 248  
DB 289 LKPFLEYFRIRCKMEDKGWSDMSEASGITYEDRSKAPSEFYKIDPSHTOGYRTYQ 348  
QY 249 LLMKARCAPYLEKTLGYNINWYPPESNNTLETMTNTNOQLHLHGSEFWMSMYSNL 308  
DB 349 LVMKTLPPFEANGKILDIYEVLLTRKSHLONTYVAT--KLTVNLTNDRIYATLTIVRLV 406  
QY 309 GKSPVATLRIPALIOESFQCIENVQACVAEDOLVVKMOSSALDVNTMMIEWFPDVSPT 368  
DB 407 GKSDAVALTIPACDQATHPVMDLKAPEKDNMLWEMTTPRESVAKYILLEMCVLSDKAPC 466  
QY 369 TLSMESVSQATNWTIOQDKLKEPFCYNISVYPMLDKXGEPYSIOAYKEGVPSEGPETK 428  
DB 467 ITDMOQEDGTVHRTYLRGNLAESEKCYLITVTPVYADGSGSPESIKAYLQKAPPSKGPYR 526  
QY 429 VENISGTVTLTWKREIPKSEKGIICNTTIFYOAGSGKFSKTVSSILQGLSELRKKT 488  
DB 527 TKRVKNAVALIEMDOLPVDVONGFIRNTTIFRTITIGETAIVNVDSSHTEITLSLSDT 586  
QY 489 SYIVQMASTAGNGTSTINEKTLFSVFELLITSLIGGLLILILVAYAGLKPKNK 548  
DB 587 LYVMAAYLTDEGKDGPEFTFTTPKFAOGEIEALVYVCLALLTTLGLVLCFNKNDL 646  
QY 549 LTHLCMPYVNPASSTIATW-----HGDDFKDL 577  
DB 647 IKKHIMPNVPDSKSHIAQWSPHPTPPRHNSKDM 682

RESULT 4  
US-09-059-099-2  
Sequence 2, Application US/09059099  
Patent No. 5925740

GENERAL INFORMATION:  
APPLICANT: Mosley, Bruce  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: Receptor for Oncostatin M  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/059,099  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,881  
FILING DATE: 12-SEP-1994  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 708 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-059-099-2

Query Match 17.4%; Score 678.5; DB 2; Length 708;  
Best Local Similarity 29.3%; Pred. No. 1.2e-54;  
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKPENISCVYYRKNTCTSPGKETS-TOYIVK---RYAGE---KHD---NCTTN 71  
DB 126 PEKPNLSICIVNEGKMKRCMDGGRHLETFILKSEMAWHKFDCKAKKRDTPSTCYD 185  
QY 72 SSTSNNRASCSEFLPRITIPDNYTIEVAENGDIYKIS-HMTYMLEIAKTEPPKIRY 130  
DB 186 YST-----YFV-----NIEVWEAEALGKVTSDHINFDVYRV-KPNPHNL 230  
QY 131 KPVIGIKRMIOEWIKPELAPVSSDLKYLFRFVNSTSMWEVNFARKNRKDKNTYNTLG 190  
DB 231 INSELSILKLTWNPISIKSVII-LKYNIOYRTDASTWGI-P-PEDTASRSSFYVD 288  
QY 191 LOPFTEYIALRCAYKESK-FWSDMSOEKMGTEEAPC-GLEIMRYLKPADAGRPRY 248  
DB 289 LKPFLEYFRIRCKMEDKGWSDMSEASGITYEDRSKAPSEFYKIDPSHTOGYRTYQ 348  
QY 249 LLMKARCAPYLEKTLGYNINWYPPESNNTLETMTNTNOQLHLHGSEFWMSMYSNL 308  
DB 349 LVMKTLPPFEANGKILDIYEVLLTRKSHLONTYVAT--KLTVNLTNDRIYATLTIVRLV 406  
QY 309 GKSPVATLRIPALIOESFQCIENVQACVAEDOLVVKMOSSALDVNTMMIEWFPDVSPT 368  
DB 407 GKSDAVALTIPACDQATHPVMDLKAPEKDNMLWEMTTPRESVAKYILLEMCVLSDKAPC 466  
QY 369 TLSMESVSQATNWTIOQDKLKEPFCYNISVYPMLDKXGEPYSIOAYKEGVPSEGPETK 428  
DB 467 ITDMOQEDGTVHRTYLRGNLAESEKCYLITVTPVYADGSGSPESIKAYLQKAPPSKGPYR 526

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Oy 429 VENICVKTVTITWKEIPSESEKGIICNTYITFYQAGGKGSEFSTVNSILIOGLESLKRT 488
Db 527 TKKGNKNAVLEMDPLPVDVONGFIRNTITFTRIIIGNETAANVDSHTEYLLSLTSOT 586
Oy 489 SYIVOVMASTAGAGTNGTSINFKTLFSVFEEIILITSLIGGULLIILTVAYGLKKPK 548
Db 587 LYVMAVAYDEGGKGDEGEFFFTTPKPAFAGEIAIVPCALFLTLLGLVLCFNKRL 646
Oy 549 LTHLCMPVTPNPAAESIATW-----HGDDPKDL 577
Db 647 IKRHVNPVDPFSKSHIAQWSPHTPRPHNFNSDKDM 682

RESULT 5
US-09-058-264-2
Sequence 2, Application US/09058264
Patent No. 601086
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058, 264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308, 881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249, 553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 264-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0450
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-264-2

Query Match 17.4%; Score 678.5; DB 3; Length 708;
Best Local Similarity 29.3%; Pred. No. 1,2e-54;
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14

Oy 22 PAKPENISCVYYRRNLNCTGTSPPGKETSQY-TOYTWK---RTYAFGE---KHD---NCTGN 71
Db 126 PERKNLNLSCTIYNEGKKMKCEMDGGETHLEINFTILKSEMAHFKFADCAKAKRTPTPSCTVD 185
Oy 72 STSENRAASCSEFLPRITIPDNYTITVEAENGDVYKS-HMTYWRLENIAKTEPKIRFV 130
Db 186 YST-----YFV-----NIEVWVAENALGKVTSDHINFDYVWK-KENPHNLISV 230
Oy 131 KPVGLIKRMIDIEWIKPELAVYSDLKTLTFRFRTVNSISWMEVNPAAKNKKDKNQYTNLTG 190

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Db	231	INSEELSSILKLTWNPBKSIVII-LKTNIOYRTDASTWQIP-PEDTASTRSSFTYOD	288
QY	191	LDPEFEYVALRCAYKESK-FWSDMSQEKMGNTBEEAPC-GLEIMRYLKPRAEDGRPRV	248
Db	289	LKPEFEYVFRICOMKEDGKGYSMDSEASGITYEDRPSKAPSFMYKIDPSHTQYRTQY	348
QY	249	LHKRKARGAPVLEKTLGYNIWYPPESNTNLEETNMNTTMOQELHGGESFMWSISVNSL	308
Db	349	LVMKTLPRPEANGKILIDEVTLTRKMSHLQNTYVNAI-KITVNLTDRIYLTATLYRNLV	406
QY	309	GKSPVATLRIPAIQKESFQCIIEVMQACVAEQLVVKMOSSALDVNTMMIEMFPDVSDEPT	368
Db	407	GKSDAVALITPACDPQATPHVMDLKAAPKDNMLMWEWTPRESVKKYLEMCVLSDKAPC	466
QY	369	TLSEWESVQATNWTITQDKLAFPCWYINISVYRMLHDKYGEFYISQIAYAKESVSECEPEK	428
Db	467	ITDMOEDDGTVHNTYLRGNLASKCYLLITVTPVYVADGSGPESIKAYLKAOPSPKGPYV	526
QY	429	VENIGVKTATITMKEIKPSEKSGIICNTTIFYOAGGGKGFKTYVNSSLDOYGLESJKRT	488
Db	527	TKVYGNEAVLEMDQLPVDYQNGFTRNTTIFRTITIGNEIYAVNVDSHTEYTLSSLSDT	586
QY	489	SYIVQYMASTSAAGTNGTSINFKLSFVSFEIILITSLGGGLLILILTVAYGKKRPP	548
Db	587	LYVMRAAATDDEGKGKRGPEFTPTPKFQAGEIATVAPVCIAFLITLLGLVLCFNKRL	646
QY	549	LTHLCWPTVPNPAESSIATW-----HGDEPKKL	577
Db	647	IKHIMPVNDPSKSHIAQWSPHTPRHNENSKDOM	682
RESULT 6			
US-09-455-962-2			
Sequence 2, Application US/09455962			
Patent No. 6524817			
GENERAL INFORMATION:			
APPLICANT: Mosley, Bruce			
APPLICANT: Cosman, David J.			
TITLE OF INVENTION: Receptor for Oncostatin M			
NUMBER OF SEQUENCES: 11			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Immunex Corporation			
STREET: 51 University Street			
CITY: Seattle			
STATE: WA			
COUNTRY: USA			
ZIP: 98101			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: Apple Macintosh			
OPERATING SYSTEM: Apple 7.1			
SOFTWARE: Microsoft Word, Version 5.1a			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/455, 962			
FILING DATE:			
CLASSIFICATION:			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 09/058, 264			
FILING DATE:			
APPLICATION NUMBER: US 08/249, 553			
FILING DATE: 26-MAY-1994			
ATTORNEY/AGENT INFORMATION:			
NAME: Seese, Kathryn A.			
REGISTRATION NUMBER: 32, 172			
REFERENCE/DOCKET NUMBER: 2614-A			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (206) 587-0430			
TELEFAX: (206) 233-0644			
TELEX: 756822			
INFORMATION FOR SEQ. ID NO. 2:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 708 amino acids			

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-455-962-2

Query Match 17.4%; Score 678.5; DB 4; Length 708;  
Best Local Similarity 29.3%; Pred. No. 1.2e-54;  
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKENISCVYYKKNLTCTSPGKETS-YQYTVK---RYAGE---KHD---NCTTN 71  
DB 126 PEKRNLSICVINEGKMKCEWDGGRHLETFNLKSEMAHFKPADKAKRDPTSCVD 185  
QY 72 SSTSENKASCFPLPRITIPDNTIYEAEAGDGVKS-HMTYRLENIAKTEPPKIFRY 130  
DB 186 YST-----YFV-----NIEWWEAENALGVSDHINFDPVYK-KPNPHNLV 230  
QY 131 KPVLGIRKMIQIEIKPELAPVSSDLKYLTFRTVNSTWMEVNFANRDKNOTYMLTG 190  
DB 231 INSEELSSILKLTWTNPSIKSVII-LKYNIOYRTKDASTWSQIP-PEDTASTRSSFTYOD 288  
QY 191 LQPTTEVYIARCAVKEK-FWSDMSOEKMGTEEEAPC-GLELMRYLKPRAAGRRPVYR 248  
DB 289 LKPTTEVYRIRCKEKEDGKGYSWSEASGITIEDRSKAPSFWKIDPSHTOGYRTVQ 348  
QY 249 LLMKARGAPVLEKTLGYNIMYPESTNLTETMNTTNOQLEHLHGSEFVMSISYSL 308  
DB 349 LVMKTLRPFEEANGKILDEYVLTTRMKSHLONYTNAT--KLTVALTNDRIYATLTIVRLV 406  
QY 309 GKSPVATLRIPAIQESFQCIENVQACVAEDQLVYKQSSALDVNTWMIEMFPDVSEPT 368  
DB 407 GKSDAAVLTIPACDFQATHPVMDLKAPKDNMLWVETTPRESVKKYILLEWCVLSDKAPC 466  
QY 369 TLSMESVQATNMTIQQOKLKPFMCYNISVYPMLDKVGEPYSIOAYAKESVPSGPEPTK 428  
DB 467 ITDMQOEDGVHRTYLRGNLAESKCYLITVPVADGSPESIKAYLKQAPSPKGPVYR 526  
QY 429 VENIGVKVTLTWKEIPKSEKGIICNTIIFYOAEKGFGFKTJNSILOGLESLKRT 488  
DB 527 TKYCKNNAVLEMOQLPVDVONGFIRNTITIRITIGMETAVNDSSTETETLSLSDT 586  
QY 489 SYIVQVMASTAGTNGTSINFKTLSEVFEIILITSLIGGLLILLLVAYGLKPNK 548  
DB 587 LYVWMAAYTDEGGDGEFTFTPKFAOGEIEAIVPVCLAFLLTLLGLVLCFNKRD 646  
QY 549 LTHLCMPTVPNPAESSTATW-----HGDDPKKL 577  
DB 647 IKKHIMPVDPDSKSHIAQWSPHTPPRHNFNSKDOM 682

RESULT 7  
PCT-US95-06530-2  
Sequence 2, Application PC/TUS9506530

GENERAL INFORMATION:  
APPLICANT: Mosley, Bruce  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: Receptor for Oncostatin M  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06530  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,881  
FILING DATE: 09-SEP-1994  
APPLICATION NUMBER: US 08/249,553  
FILING DATE: 26-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2614-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 708 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-06530-2

Query Match 17.4%; Score 678.5; DB 5; Length 708;  
Best Local Similarity 29.3%; Pred. No. 1.2e-54;  
Matches 169; Conservative 110; Mismatches 258; Indels 39; Gaps 14;

QY 22 PAKENISCVYYKKNLTCTSPGKETS-YQYTVK---RYAGE---KHD---NCTTN 71  
DB 126 PEKRNLSICVINEGKMKCEWDGGRHLETFNLKSEMAHFKPADKAKRDPTSCVD 185  
QY 72 SSTSENKASCFPLPRITIPDNTIYEAEAGDGVKS-HMTYRLENIAKTEPPKIFRY 130  
DB 186 YST-----YFV-----NIEWWEAENALGVSDHINFDPVYK-KPNPHNLV 230  
QY 131 KPVLGIRKMIQIEIKPELAPVSSDLKYLTFRTVNSTWMEVNFANRDKNOTYMLTG 190  
DB 231 INSEELSSILKLTWTNPSIKSVII-LKYNIOYRTKDASTWSQIP-PEDTASTRSSFTYOD 288  
QY 191 LQPTTEVYIARCAVKEK-FWSDMSOEKMGTEEEAPC-GLELMRYLKPRAAGRRPVYR 248  
DB 289 LKPTTEVYRIRCKEKEDGKGYSWSEASGITIEDRSKAPSFWKIDPSHTOGYRTVQ 348  
QY 249 LLMKARGAPVLEKTLGYNIMYPESTNLTETMNTTNOQLEHLHGSEFVMSISYSL 308  
DB 349 LVMKTLRPFEEANGKILDEYVLTTRMKSHLONYTNAT--KLTVALTNDRIYATLTIVRLV 406  
QY 309 GKSPVATLRIPAIQESFQCIENVQACVAEDQLVYKQSSALDVNTWMIEMFPDVSEPT 368  
DB 407 GKSDAAVLTIPACDFQATHPVMDLKAPKDNMLWVETTPRESVKKYILLEWCVLSDKAPC 466  
QY 369 TLSMESVQATNMTIQQOKLKPFMCYNISVYPMLDKVGEPYSIOAYAKESVPSGPEPTK 428  
DB 467 ITDMQOEDGVHRTYLRGNLAESKCYLITVPVADGSPESIKAYLKQAPSPKGPVYR 526  
QY 429 VENIGVKVTLTWKEIPKSEKGIICNTIIFYOAEKGFGFKTJNSILOGLESLKRT 488  
DB 527 TKYCKNNAVLEMOQLPVDVONGFIRNTITIRITIGMETAVNDSSTETETLSLSDT 586  
QY 489 SYIVQVMASTAGTNGTSINFKTLSEVFEIILITSLIGGLLILLLVAYGLKPNK 548  
DB 587 LYVWMAAYTDEGGDGEFTFTPKFAOGEIEAIVPVCLAFLLTLLGLVLCFNKRD 646  
QY 549 LTHLCMPTVPNPAESSTATW-----HGDDPKKL 577  
DB 647 IKKHIMPVDPDSKSHIAQWSPHTPPRHNFNSKDOM 682

RESULT 8  
US-08-825-558-6  
Sequence 6, Application US/08825558  
Patent No. 5965724  
GENERAL INFORMATION:  
APPLICANT: SHARKEY, ANDREW



```

Db 349 LMKRLPPEFANGKILDEYVTLTRMKSHLQNYTVNAT--KLTVNLINDRYLATLTVRLV 406
Oy 309 GKSPVATLRIPIAIDKESQCLIEVWQACAEOLVYKQSSALDVNTNMIEFPPVDSDPT 368
Db 407 GKSDAAVLTIPACDFQATHPMDLKAFPKDMLWEMWTPPRESVKKYLLEWCYLSDAKPC 466
Oy 369 TLMSEVSQATNMWITOODKLRPFMCYNISVYPMLDKGEPEYSIOAVAKEGVSPGPEPK 428
Db 467 ITDMQOEDGYHRTYLRKGNLAESKCYLITVPYVADGSPESIKAYIKQAPPSKGPYVR 526
Oy 429 VENIGKVTVTITWKEIPKSEKRGIIICNYTIFYQAEKGKFSKYVNSSILOGLSLKRT 488
Db 527 TKYGNKNAVLEMDQLPVDQNGEIRNYTIFYRTIGNETAVNDSHTEYLSLSDT 586
Oy 489 SYIOVMASTAGTNGTSINFKLSFVFELIITSLIGGLLILITVAYGLKRNK 548
Db 587 LYVWMAVYDEGKGDEFTFTTPKQGEIEALVVPCLAFLLITLLGLVFCFNKDL 646
Oy 549 LTHLCMPTVPNPAESSIATW-----HGDDFKDL----- 577
Db 647 IKHIMVWPDPSPKSHIAQWSPHPPRNHNSKQMSDGNFTDVSVEIANDKKRPE 706
Oy 578 NLKESD---DSVNT 589
Db 707 DLKSLDLFKKKEKINTE 722

```

# RESULT 10

```

US-09-313-942-9
: Sequence 9, Application US/09313942
: Patent No. 6472179
: GENERAL INFORMATION:
: APPLICANT: REGENERON PHARMACEUTICALS, INC.
: TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
: FILE REFERENCE: REG 203-A
: CURRENT APPLICATION NUMBER: US/09/313,942
: PRIOR FILING DATE: 1999-05-19
: PRIOR APPLICATION NUMBER: 09/313,942
: PRIOR FILING DATE: 1999-05-19
: PRIOR APPLICATION NUMBER: 60/101,858
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 951
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-313-942-9

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Query Match 16.1%; Score 629; DB 4; Length 951;

Best Local Similarity 26.7%; Pred. No. 8.7e-50;

Matches 193; Conservative 113; Mismatches 286; Indels 132; Gaps 26;

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Oy 22 PAKPENISCVYYRRKLNCTWSPKETSYSY--TOYTVK---RTYARGE---KHD---NCTTN 71
Db 126 PEKRNLSCLIVNEGKKMKCEMDGGRHLETFNLTKSEMAHFKEDCAKADTPTSCYVD 185
Oy 72 STSENRASSCFLLPRITIPDNYTIEVENGDGVKIS--HMTYMLENIARTPEPKIPRY 130
Db 186 YST-----YFV-----NIEVWEAENALGVTSDHINFDVYAV--KPNPHNLSV 230
Oy 131 KPVIGIKMIQIEMWKPELAVYSSDLKTLKFRYVNSTSMKEVNFARNRKDKNOTYNLTG 190
Db 231 INSELSILKLTWNPISKSVII--LKYNIOYRTDASTWSQIP--PEDTASTRSSFTYOD 288
Oy 191 LOPFEYVIALRCAYKESK--FMSDMSOKMGWTEERAPC--GLELMRVLKPAEADGRPRVR 248
Db 289 LKPFLEYFRIRCKMEDKGYWSDNSEASGITTYEDRSKAPSEFYKIDPSTOQYRYVQ 348
Oy 249 LLMKARGAPVLEKTLGINIWIYPPESNTNLETNMTNQQOLELHGSEFWVSMISYSL 308

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Db 349 LMKRLPPEFANGKILDEYVTLTRMKSHLQNYTVNAT--KLTVNLINDRYLATLTVRLV 406
Oy 309 GKSPVATLRIPIAIDKESQCLIEVWQACAEOLVYKQSSALDVNTNMIEFPPVDSDPT 368
Db 407 GKSDAAVLTIPACDFQATHPMDLKAFPKDMLWEMWTPPRESVKKYLLEWCYLSDAKPC 466
Oy 369 TLMSEVSQATNMWITOODKLRPFMCYNISVYPMLDKGEPEYSIOAVAKEGVSPGPEPK 428
Db 467 ITDMQOEDGYHRTYLRKGNLAESKCYLITVPYVADGSPESIKAYIKQAPPSKGPYVR 526
Oy 429 VENIGKVTVTITWKEIPKSEKRGIIICNYTIFYQAEKGKFSKYVNSSILOGLSLKRT 488
Db 527 TKYGNKNAVLEMDQLPVDQNGEIRNYTIFYRTIGNETAVNDSHTEYLSLSDT 586
Oy 489 SYIOVMASTAGTNGTSINFKLSFVFELIITSLIGGLLILITVAYGLKRNK 548
Db 587 LYVWMAVYDEGKGDEFTFTTPKQGEIEGASTKGPSVPLADSSKSGGYAAL 646
Oy 535 IILVAYGLKRNKLTHLCMPTVPNPAESSIATWHDGDFKDLN-----LKES----- 582
Db 647 GCLVKDY-----PEPYTVS---WNSGALJTGCVHFTFPAVLQSSGLYSLS 688
Oy 583 -----DSVNTEDRIL---KCSGPSDKLVYDKLVNFGVNLQEIFTEARTGOENNLG 633
Db 689 VVTVPSSSLGTQYICANNHKKPSMTKVDKVV-----EPKSCDKTH-- 728
Oy 634 GEKNQYVTCPPRPDCLPKSFEELPVSPET---PPR--KSQYLRSMPGCT-----R 680
Db 729 -----TC-----PCPA-----PELLGGSVLEFPKPKDITLMISRTPEVTCCVVVDVSHED 774
Oy 681 PEAK 684
Db 775 PEVK 778

```

# RESULT 11

```

US-08-419-652-5
: Sequence 5, Application US/08419652
: Patent No. 5831007
: GENERAL INFORMATION:
: APPLICANT: Chua, Anne O
: APPLICANT: Gubler, Ulrich A
: TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESS: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: United States of America
: ZIP: 07110-1199
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: PC compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/419,652
: FILING DATE: 11-APR-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/248,532
: FILING DATE: 31-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/094,713
: FILING DATE: 19-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Kass, Alan P
: REGISTRATION NUMBER: 32142
: REFERENCE/DOCKET NUMBER: CD 9174
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201) 235-4205
: TELEFAX: (201) 235-3500

```

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 572 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..572  
OTHER INFORMATION: /note="Represents residues 124 to  
OTHER INFORMATION: 742 of human gp130."  
US-08-419-652-5

Query Match 16.0%; Score 625; DB 2; Length 572;  
Best Local Similarity 26.8%; Pred. No. 8,9e-50;

Matches 165; Conservative 104; Mismatches 235; Indels 112; Gaps 15;

QY 22 PAKPENISCVYRRKRLTCTWSPGKETST-TOYIVK---RYYAGE---KHD---NCSTN 71  
DB 3 PEKPNLSCIVNEGKKMKCEMDGREGTHLETNFTLSEMAVTHKFDCKAKRDTPTSCYVD 62  
QY 72 STSENRRASCSEFLPRITIPDNYTIEVAENGDVYKS-HMTYMRLENIATKTEPKIFRV 130  
DB 63 YST-----YFV-----NIEVVEAENALGKVTSDHNF----- 91  
QY 131 KPVLGIRKMIQIEWIKPELAPVSSDLKYLTRFRVTNSTSMMEVNEAKNRKDKNOTYNLTG 190  
DB 92 -----QYRTKDASTWQIP-PEDTASTRSSEFTYQD 120  
QY 191 LQPTFEYVIALRCVAVKESK-FWSDMSQKMGKTEAEAC-GLELMRVLKPAEADGRVYR 248  
DB 121 LKPFEEYVFRIRCKMDEKGYMSDSEASGITYEDRSKAPSEFYKKIDPSHTGGYRVQ 180  
QY 249 LLMKARCAPVLEKTLGYNINWYPPESNTNLTETMNTTNOQLEHLHGSEFWMSYSL 308  
DB 181 LVMKTLRPFEEANGKILDEYVTLTRKSHLQNTYVAT--KLVNLTNDRIYATLTVRLV 238  
QY 309 GKSPVATLRIPAIQKESFOCIEVMQACVAEDQLVYKMOSSALDVNTWMIEMFPDVSEPT 368  
DB 239 GKSDAAVLTIPACDQOATHPYMDLKAFFPKDNLWEMTTPRESYVKKYILEMCVLSDKAPC 298  
QY 369 TLMSEVSQATNWTIQOQKLRPFMCYNISVYPMLDKXGEPSYIOAVAKGEPSPGPTK 428  
DB 299 ITDMQOEDGYHRYTLRGNLAESKCYLITVTPVADGSPESIKAYLKQAPSPSGPTVR 358  
QY 429 VENIGKVTITWKEIPKSERKGIICNTYIFVOAGGKGFSTVSSILQGLSELRKRT 488  
DB 359 TKYVKNNAVLEMOQLPVDQNGFIRNTYIFRTIIGMETAVNDSSTHTETLSLSJSDT 418  
QY 489 SYIVOVMASTAGTNGTSINFKTLSFVFEIILITSLIGGLLILITVAVYGLKRPK 548  
DB 419 LYVMAAYVTDEGGKDGCEFTFTTPKFAQGEIEAIVPVCLAFLLTLGLVCFNRKDL 478  
QY 549 LTHLCMPVPPNPASTATW-----HGDEKDL----- 577  
DB 479 IKKHTMPVPPSPSKSHIQWSPHPPRRHNSKDDMYSDGNFTDVSVEIEANDKKPPE 538  
QY 578 NLKESD---DSVNT 589  
DB 539 DLKSLDLRKKKEKINE 554

## RESULT 12

US-09-313-942-7

Sequence 7, Application US/09313942

Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: 60/101,858  
PRIOR FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO: 7  
LENGTH: 859  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-313-942-7

Query Match 15.8%; Score 619; DB 4; Length 859;  
Best Local Similarity 29.0%; Pred. No. 6.4e-49;

Matches 160; Conservative 98; Mismatches 242; Indels 52; Gaps 15;

QY 22 PAKPENISCVYRRKRLTCTWSPGKETST-TOYIVK---RYYAGE---KHD---NCSTN 71  
DB 126 PEKPNLSCIVNEGKKMKCEMDGREGTHLETNFTLSEMAVTHKFDCKAKRDTPTSCYVD 185  
QY 72 STSENRRASCSEFLPRITIPDNYTIEVAENGDVYKS-HMTYMRLENIATKTEPKIFRV 130  
DB 186 YST-----YFV-----NIEVVEAENALGKVTSDHNF----- 230  
QY 131 KPVLGIRKMIQIEWIKPELAPVSSDLKYLTRFRVTNSTSMMEVNEAKNRKDKNOTYNLTG 190  
DB 231 INSELSISILKLTWNPISIKSVII-LKYNIGYRTKDASTWQIP-PEDTASTRSSEFTYQD 288  
QY 191 LQPTFEYVIALRCVAVKESK-FWSDMSQKMGKTEAEAC-GLELMRVLKPAEADGRVYR 248  
DB 289 LKPFEEYVFRIRCKMDEKGYMSDSEASGITYEDRSKAPSEFYKKIDPSHTGGYRVQ 348  
QY 249 LLMKARCAPVLEKTLGYNINWYPPESNTNLTETMNTTNOQLEHLHGSEFWMSYSL 308  
DB 349 LVMKTLRPFEEANGKILDEYVTLTRKSHLQNTYVAT--KLVNLTNDRIYATLTVRLV 406  
QY 309 GKSPVATLRIPAIQKESFOCIEVMQACVAEDQLVYKMOSSALDVNTWMIEMFPDVSEPT 368  
DB 407 GKSDAAVLTIPACDQOATHPYMDLKAFFPKDNLWEMTTPRESYVKKYILEMCVLSDKAPC 466  
QY 369 TLMSEVSQATNWTIQOQKLRPFMCYNISVYPMLDKXGEPSYIOAVAKGEPSPGPTK 428  
DB 467 ITDMQOEDGYHRYTLRGNLAESKCYLITVTPVADGSPESIKAYLKQAPSPSGPTVR 526  
QY 429 VENIGKVTITWKEIPKSERKGIICNTYIFVOAGGKGFSTVSSILQGLSELRKRT 488  
DB 527 TKYVKNNAVLEMOQLPVDQNGFIRNTYIFRTIIGMETAVNDSSTHTETLSLSJSDT 586  
QY 489 SYIVOVMASTAGTNGTSINFKTLSFVFEIILITSLIGGLLILITVAVYGLKRPK 548  
DB 587 LYVMAAYVTDEGGKDGCEFTFTTPKFAQGEI-----ESGEPKSCD 627  
QY 549 LTHLCMPVPPNP 560  
DB 628 KTHTC-PPCPAP 638

## RESULT 13

US-08-825-558-4

Sequence 4, Application US/08825558

Patent No. 5963724

GENERAL INFORMATION:

APPLICANT: SHARKEY, ANDREW

APPLICANT: SMITH, STEPHEN K.

APPLICANT: DELLOW, KIMBERLEY A.

TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX

STREET: 1100 NEW YORK AVENUE

CITY: WASHINGTON

STATE: DC

COUNTRY: USA







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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:15:41 ; Search time 28 Seconds  
(without alignments)  
3104.720 Million cell updates/sec

Title: US-09-892-949-2

Perfect score: 3908  
Sequence: 1 MMTWALMLPISLCKFSLAA.....VTAREFLVSEKLPHTKGEV 732

Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications\_AA:\*  
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3: /cgn2-6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
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8: /cgn2-6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3908	100.0	732	11	US-09-892-949-2 Sequence 2, Appl1
2	3896	99.7	745	11	US-09-972-708-4 Sequence 4, Appl1
3	3405.5	87.1	649	11	US-09-892-949-46 Sequence 46, Appl1
4	3405.5	87.1	662	11	US-09-972-708-15 Sequence 15, Appl1
5	3405.5	87.1	662	11	US-09-892-949-54 Sequence 54, Appl1
6	3405.5	87.1	662	11	US-10-006-265-17 Sequence 17, Appl1
7	3350	85.7	652	11	US-09-972-708-14 Sequence 14, Appl1
8	3350	85.7	652	15	US-10-006-265-2 Sequence 2, Appl1
9	2783	71.2	764	11	US-09-892-949-69 Sequence 92, Appl1
10	2546	65.1	582	15	US-10-230-163-92 Sequence 92, Appl1
11	2546	65.1	582	15	US-10-230-338-92 Sequence 92, Appl1
12	2546	65.1	582	15	US-10-218-631-92 Sequence 92, Appl1
13	2546	65.1	582	15	US-10-230-414-92 Sequence 92, Appl1
14	2546	65.1	582	15	US-10-216-159A-92 Sequence 92, Appl1
15	2546	65.1	582	15	US-10-216-159A-92 Sequence 92, Appl1

16	2546	65.1	582	15	US-10-218-849-92	Sequence 92, Appl1
17	2546	65.1	582	15	US-10-227-873-92	Sequence 92, Appl1
18	2546	65.1	582	15	US-10-227-883-92	Sequence 92, Appl1
19	2546	65.1	582	15	US-10-219-076-92	Sequence 92, Appl1
20	2546	65.1	582	15	US-10-230-434-92	Sequence 92, Appl1
21	2546	65.1	582	15	US-10-219-003-92	Sequence 92, Appl1
22	2546	65.1	582	15	US-10-219-075-92	Sequence 92, Appl1
23	2546	65.1	582	15	US-10-219-464-92	Sequence 92, Appl1
24	2546	65.1	582	15	US-10-219-466-92	Sequence 92, Appl1
25	2546	65.1	582	15	US-10-219-479-92	Sequence 92, Appl1
26	2546	65.1	582	15	US-10-219-481-92	Sequence 92, Appl1
27	2546	65.1	582	15	US-10-230-260-92	Sequence 92, Appl1
28	2546	65.1	582	15	US-10-232-231-92	Sequence 92, Appl1
29	2546	65.1	582	15	US-10-232-233-92	Sequence 92, Appl1
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31	2546	65.1	582	15	US-10-218-956-92	Sequence 92, Appl1
32	2546	65.1	582	15	US-10-219-468-92	Sequence 92, Appl1
33	2546	65.1	582	15	US-10-219-478-92	Sequence 92, Appl1
34	2546	65.1	582	15	US-10-219-536-92	Sequence 92, Appl1
35	2546	65.1	582	15	US-10-233-205-92	Sequence 92, Appl1
36	2546	65.1	582	15	US-10-219-072-92	Sequence 92, Appl1
37	2546	65.1	582	15	US-10-219-470-92	Sequence 92, Appl1
38	2546	65.1	582	15	US-10-219-474-92	Sequence 92, Appl1
39	2546	65.1	582	15	US-10-219-524-92	Sequence 92, Appl1
40	2546	65.1	582	15	US-10-219-528-92	Sequence 92, Appl1
41	2546	65.1	582	15	US-10-227-880-92	Sequence 92, Appl1
42	2546	65.1	582	15	US-10-227-881-92	Sequence 92, Appl1
43	2546	65.1	582	15	US-10-227-882-92	Sequence 92, Appl1
44	2546	65.1	582	15	US-10-230-436-92	Sequence 92, Appl1
45	2546	65.1	582	15	US-10-232-223-92	Sequence 92, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-892-949-2 Application US/09892949.  
: Sequence 2, Appl1  
: Publication No. US20030096339A1  
GENERAL INFORMATION:  
: APPLICANT: Sprechel, Cindy A.  
: APPLICANT: Presnell, Scott R.  
: APPLICANT: Gao, Zeren  
: APPLICANT: Whitmore, Theodore E.  
: APPLICANT: Kuijper, Joseph L.  
: APPLICANT: Maurer, Mark F.  
: TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
: FILE REFERENCE: 00-42  
: CURRENT APPLICATION NUMBER: US/09/892,949  
: PRIOR APPLICATION NUMBER: 2001-06-26  
: PRIOR FILING DATE: 2000-06-26  
: PRIOR FILING DATE: 2000-06-26  
: PRIOR APPLICATION NUMBER: US 60/214,955  
: PRIOR FILING DATE: 2000-06-29  
: PRIOR APPLICATION NUMBER: US 60/267,963  
: PRIOR FILING DATE: 2001-08-02  
: NUMBER OF SEQ ID NOS: 93  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 2  
: LENGTH: 732  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-892-949-2

Query Match 100.0%; Score 3908; DB 11; Length 732;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTWALMLPISLCKFSLAAIPAKRENISCVYYRKNTCTWSPCKETSYQYVKKRYA 60  
DB 1 MMTWALMLPISLCKFSLAAIPAKRENISCVYYRKNTCTWSPCKETSYQYVKKRYA 60  
QY 61 FGEKHNDCTNNTSENKSCSFLPRTIPDNTVEAENGCGVIAKSHMTWRLLENIA 120

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Db 61 FGEKHDNCTNNTSSSENBRASCFFLPRTITPDNTYEVEAENGDCVISHMTYMRLENIA 120
Qy 121 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKRRK 180
Db 121 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKRRK 180
Qy 181 DKNQTYNLTGLQPFTEYIALRCAYEKESKFMDSMQEKMGT EEPAPCGLEIMRLKPAE 240
Db 181 DKNQTYNLTGLQPFTEYIALRCAYEKESKFMDSMQEKMGT EEPAPCGLEIMRLKPAE 240
Qy 241 ADGRPRVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTNNOOLEHLGSESPV 300
Db 241 ADGRPRVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTNNOOLEHLGSESPV 300
Qy 301 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDOLVYKQSSALDYNMTMIMF 360
Db 301 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDOLVYKQSSALDYNMTMIMF 360
Qy 361 PDVDEPTLTSWESVSQATNMTIOODKLPFCYNI SYVPMHLHDKVGPYSIOAYAKBGV 420
Db 361 PDVDEPTLTSWESVSQATNMTIOODKLPFCYNI SYVPMHLHDKVGPYSIOAYAKBGV 420
Qy 421 PSEGETVENIGVATVITWKEIPKSERKGIICNYTIFYOAEKGKFSKTYNSSILOYG 480
Db 421 PSEGETVENIGVATVITWKEIPKSERKGIICNYTIFYOAEKGKFSKTYNSSILOYG 480
Qy 481 LESLKRKTSYIVQWASTSAGTNGTSINFKTLSTSVFEIILITSLIGGLILITLVA 540
Db 481 LESLKRKTSYIVQWASTSAGTNGTSINFKTLSTSVFEIILITSLIGGLILITLVA 540
Qy 541 YGLKPKNKLTHLCWPTVNPAPASSIATWHGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
Db 541 YGLKPKNKLTHLCWPTVNPAPASSIATWHGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
Qy 601 DKLVIDKLVNFGNVLQEIFTDEARTGOENNLGCKNGYVTCPPRPDCPLKSEELPVS 660
Db 601 DKLVIDKLVNFGNVLQEIFTDEARTGOENNLGCKNGYVTCPPRPDCPLKSEELPVS 660
Qy 661 PEIPPRKSOYLRSRMPBECTRPEAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 720
Db 661 PEIPPRKSOYLRSRMPBECTRPEAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 720
Qy 721 SEKLPEHTKGEV 732
Db 721 SEKLPEHTKGEV 732

RESULT 2
US-09-972-708-4
; Sequence 4, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-4
Query Match 99.7%; Score 3896; DB 11: Length 745;
Best Local Similarity 99.7%; Pred. No. 0;
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Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MMTWALMLPSLCKFSUALPAKPNESCYYYYRKNLTCTWSPCKENSTQYTKRYA 60
Db 14 MMTWALMLPSLCKFSUALPAKPNESCYYYYRKNLTCTWSPCKENSTQYTKRYA 73
Qy 61 FGEKHDNCTNNTSSSENBRASCFFLPRTITPDNTYEVEAENGDCVISHMTYMRLENIA 120
Db 74 FGEKHDNCTNNTSSSENBRASCFFLPRTITPDNTYEVEAENGDCVISHMTYMRLENIA 133
Qy 121 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKRRK 180
Db 124 KTEPKIRRVKPVIGIKRMIOEWIKPELAPVSSDLKTLRRTYNSMMEVNAKRRK 193
Qy 181 DKNQTYNLTGLQPFTEYIALRCAYEKESKFMDSMQEKMGT EEPAPCGLEIMRLKPAE 240
Db 194 DKNQTYNLTGLQPFTEYIALRCAYEKESKFMDSMQEKMGT EEPAPCGLEIMRLKPAE 253
Qy 241 ADGRPRVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTNNOOLEHLGSESPV 300
Db 254 ADGRPRVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTNNOOLEHLGSESPV 313
Qy 301 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDOLVYKQSSALDYNMTMIMF 360
Db 314 SMISYNSLGKSPVATLRIPALOEKSFQCI EVMQACVAEDOLVYKQSSALDYNMTMIMF 373
Qy 361 PDVDEPTLTSWESVSQATNMTIOODKLPFCYNI SYVPMHLHDKVGPYSIOAYAKBGV 420
Db 374 PDVDEPTLTSWESVSQATNMTIOODKLPFCYNI SYVPMHLHDKVGPYSIOAYAKBGV 433
Qy 421 PSEGETVENIGVATVITWKEIPKSERKGIICNYTIFYOAEKGKFSKTYNSSILOYG 480
Db 434 PSEGETVENIGVATVITWKEIPKSERKGIICNYTIFYOAEKGKFSKTYNSSILOYG 493
Qy 481 LESLKRKTSYIVQWASTSAGTNGTSINFKTLSTSVFEIILITSLIGGLILITLVA 540
Db 494 LESLKRKTSYIVQWASTSAGTNGTSINFKTLSTSVFEIILITSLIGGLILITLVA 553
Qy 541 YGLKPKNKLTHLCWPTVNPAPASSIATWHGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
Db 554 YGLKPKNKLTHLCWPTVNPAPASSIATWHGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 613
Qy 601 DKLVIDKLVNFGNVLQEIFTDEARTGOENNLGCKNGYVTCPPRPDCPLKSEELPVS 660
Db 614 DKLVIDKLVNFGNVLQEIFTDEARTGOENNLGCKNGYVTCPPRPDCPLKSEELPVS 673
Qy 661 PEIPPRKSOYLRSRMPBECTRPEAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 720
Db 674 PEIPPRKSOYLRSRMPBECTRPEAKQQLFSGOSLVPHLCEGAPNPLKNSVTAREPLV 733
Qy 721 SEKLPEHTKGEV 732
Db 734 SEKLPEHTKGEV 745

RESULT 3
US-09-892-949-46
; Sequence 46, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprechet, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Geo, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
```

```

: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: US 60/267,963
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO: 46
: LENGTH: 649
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-892-949-46

```

Query Match	87.1%	Score 3405.5;	DB 11;	Length 649;
Best local Similarity	99.1%;	Pred. NO. 5.2e-291;		
Matches 640; Conservative	1;	Mismatches 2;	Indels 3;	Gaps 1.

OY	MMWTWALMMPLPSLCRKSIALPAKPKPMISCVYVYRKNLCTMSPGKETSOTQYAKRYA	60
Db	1 MMWTWALMMPLPSLCRKSIALPAKPKPMISCVYVYRKNLCTMSPGKETSOTQYAKRYA	60
OY	61 FGEKHDCNTSSSTSENBRASCSPFLPRITPDWVTEVEAENGDVYKSHMYWRLENIA	12
Db	61 FGEKHDCNTSSSTSENBRASCSPFLPRITPDWVTEVEAENGDVYKSHMYWRLENIA	12
OY	121 KTEPRKTEFRKPVGLIKRMIOIWIPELAPVSSDLKYTLRERTVNSTSMMEVNFKNRK	18
Db	121 KTEPRKTEFRKPVGLIKRMIOIWIPELAPVSSDLKYTLRERTVNSTSMMEVNFKNRK	18
OY	181 DKNOTYUJLQJPFTEYVILRCVAVESKFWMSQSEKKGMTPEELAPGLTEMLRYLPAE	24
Db	181 DKNOTYUJLQJPFTEYVILRCVAVESKFWMSQSEKKGMTPEELAPGLTEMLRYLPAE	24
OY	241 ADGRRPVRLMKKARGAPVLEKTLGYNIMYPESANTLLETJNTNTNOOLEHLHGSEFVY	30
Db	241 ADGRRPVRLMKKARGAPVLEKTLGYNIMYPESANTLLETJNTNTNOOLEHLHGSEFVY	30
OY	301 SMTSYNSLGSPVATLIRPAIOEKSPQCEVMAQCAEOLVYKMOSSALDVNTWMIEMF	36
Db	301 SMTSYNSLGSPVATLIRPAIOEKSPQCEVMAQCAEOLVYKMOSSALDVNTWMIEMF	36
OY	361 PDVDSSEPTLMSWSVSQATWMTIOODKLRPFMCYNISYVPLMDHXGEPYSIOAYAKCEV	42
Db	361 PDVDSSEPTLMSWSVSQATWMTIOODKLRPFMCYNISYVPLMDHXGEPYSIOAYAKCEV	42
OY	421 PSEBPEFKVENIGKYTYITWKELPSEKGIICNTITYQABGCGSEKTVNNSILOYG	48
Db	421 PSEBPEFKVENIGKYTYITWKELPSEKGIICNTITYQABGCGSEKTVNNSILOYG	48
OY	481 LESLKRRTSYIOVMASTAGTNGNSINFKTLSPFVPELITLSLGGILLILITLYA	54
Db	481 LESLKRRTSYIOVMASTAGTNGNSINFKTLSPFVPELITLSLGGILLILITLYA	54
OY	541 YGLKRPKKLTHLCMPYVNPFAESSIATWHDDEKDKLNTKESDVSNTEDRLKPCSTPS	60
Db	541 YGLKRPKKLTHLCMPYVNPFAESSIATWHDDEKDKLNTKESDVSNTEDRLKPCSTPS	60
OY	601 DKLVLDKLVNFGVNLDEITFDARQGEQNNLGGKNGRILSSCP	66
Db	601 DKLVLDKLVNFGVNLDEITFDARQGEQNNLGGKNGRILSSCP	66

RESULT 4  
US-09-972-708-15  
Sequence 15, Application US/09972708  
Publication No. US2003005987A1  
GENERAL INFORMATION:  
APPLICANT: Immunex Corporation  
APPLICANT: Cosman, David J.  
APPLICANT: Mosley, Bruce A.  
APPLICANT: Bird, Timothy A.  
APPLICANT: Dubose, Robert F.  
APPLICANT: Wiley, Steven R.  
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS  
FILE REFERENCE: 3160-B  
HPR1 AND HPR2

: CURRENT APPLICATION NUMBER: US/09/972,708  
 : CURRENT FILING DATE: 2001-10-05  
 : NUMBER OF SEQ ID NOS: 29  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 15  
 : LENGTH: 662  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : US-09-972-708-15

Query Match	87.1%;	Score 3405.5;	DB 11;	Length 662;
Best Local Similarity	99.1%;	Pred. No. 5.3e-291;		
Matches 640; Conservative	1;	Mismatches 2;	Indels 3;	Gaps 1;

QY	MMTALMMPLSCKRSLAALPAKRNISCVYYKRLITCMWSGKESYQYVAKRTYA	60
Db	MMTALMMPLSCKRSLAALPAKRNISCVYYKRLITCMWSGKESYQYVAKRTYA	73
QY	FGKHNDCTTNSSTSENBRASCFFLPRTIPDNYTIEVEANGDGVIKSHMTYRLNIA	120
Db	FGKHNDCTTNSSTSENBRASCFFLPRTIPDNYTIEVEANGDGVIKSHMTYRLNIA	133
QY	KTERPKIFRKPVPVLGIKRMIOIEMIKPELAPVSSDLKTLAPRYVNSTSMVEVFAKNRK	180
Db	KTERPKIFRKPVPVLGIKRMIOIEMIKPELAPVSSDLKTLAPRYVNSTSMVEVFAKNRK	193
QY	DKNOTYVLGLOPFTEYVIALRCAYKESKFSWSDMSQEMKMGTEEBAPCGELMVLKPAE	240
Db	DKNOTYVLGLOPFTEYVIALRCAYKESKFSWSDMSQEMKMGTEEBAPCGELMVLKPAE	253
QY	ADGRAPRYRLMKKARGAPVLEKTLGYNIMYBESNTNLETMTNTNOOLEHLGSGSFVW	300
Db	ADGRAPRYRLMKKARGAPVLEKTLGYNIMYBESNTNLETMTNTNOOLEHLGSGSFVW	313
QY	SMTSYNLSGSPALTRIPALIOEKSPNOCELVNOACVAEDOLVYWKOSSALDVNMTMEWF	360
Db	SMTSYNLSGSPALTRIPALIOEKSPNOCELVNOACVAEDOLVYWKOSSALDVNMTMEWF	373
QY	PVDVSEPTTLSMESVSQATNMWTIOODKILPFMCNMISVYPMILHDKVGEPSYIOAYAKEGV	420
Db	PVDVSEPTTLSMESVSQATNMWTIOODKILPFMCNMISVYPMILHDKVGEPSYIOAYAKEGV	433
QY	PSBEPREFKVNIGCVKVTYTTWKELERKSEKGIICMTTFYOAEGSKGFSKTVNSSIIQYG	480
Db	PSBEPREFKVNIGCVKVTYTTWKELERKSEKGIICMTTFYOAEGSKGFSKTVNSSIIQYG	493
QY	LESJAKRTSYIYOVMASTSGAGTNGSINFKTLPSVFEIILITSJIGGGLIILITLVA	540
Db	LESJAKRTSYIYOVMASTSGAGTNGSINFKTLPSVFEIILITSJIGGGLIILITLVA	553
QY	YGLKPKPKLTLHLCPVTPVPAPAESIATWNGDQFKRLMLKESDVSUNTEDRLKPCSTPS	600
Db	YGLKPKPKLTLHLCPVTPVPAPAESIATWNGDQFKRLMLKESDVSUNTEDRLKPCSTPS	613
QY	DKLVYDKLVVNGVNLQOEIETDEARPGOENNLGGCKNSTRILISSCP	650
Db	DKLVYDKLVVNGVNLQOEIETDEARPGOENNLGGCKNSTRILISSCP	663

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RESULT 5
US-09-892-949-54
; Sequence 54, Application US/09892949
; Publication No. US2003096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949

```

```
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 54
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-54
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Query Match      87.1%; Score 3405.5; DB 11; Length 662:
Best Local Similarity 99.1%; Pred. No. 5.3e-291;
Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
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OY 1 MMTWALMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKETSQYTVKRTYA 60
DB 14 MMTWALMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKETSQYTVKRTYA 73
OY 61 FGEKHDNCTNSTSENKASCSFLLPRITIPDNTTIEVEAENGGVKSHMTYRLENIA 120
DB 74 FGEKHDNCTNSTSENKASCSFLLPRITIPDNTTIEVEAENGGVKSHMTYRLENIA 133
OY 121 KTEPPKIFRVKPVLGIRKMIQIEMIKPELAVSSDLKYTLFRVNSTSMVEVFAKRRK 180
DB 134 KTEPPKIFRVKPVLGIRKMIQIEMIKPELAVSSDLKYTLFRVNSTSMVEVFAKRRK 193
OY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPACGLEMLVRLPAE 240
DB 194 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPACGLEMLVRLPAE 253
OY 241 ADGRRPVRLMKKARGAVLEKTLGYNIMYPESNTNLTETMNTTNOQLHLGGESEFW 300
DB 254 ADGRRPVRLMKKARGAVLEKTLGYNIMYPESNTNLTETMNTTNOQLHLGGESEFW 313
OY 301 SMISYNSLGKSPVATLRIPAIQKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEF 360
DB 314 SMISYNSLGKSPVATLRIPAIQKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEF 373
OY 361 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 420
DB 374 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 433
OY 421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVOAEGGKFSKTVNSSILOYG 480
DB 434 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVOAEGGKFSKTVNSSILOYG 493
OY 481 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPSVFEIILITSLIGGGLLILITLVA 540
DB 494 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPSVFEIILITSLIGGGLLILITLVA 553
OY 541 YGLKPKMLTHLCPTVPNPAESSIATWHDGDFDKLNLKESDVSNTEDRIILPCSTPS 600
DB 554 YGLKPKMLTHLCPTVPNPAESSIATWHDGDFDKLNLKESDVSNTEDRIILPCSTPS 613
OY 601 DKLVIDKLVVFGNVLOEIFTDEARTQENNLGGEKNG---YVTCP 643
DB 614 DKLVIDKLVVFGNVLOEIFTDEARTQENNLGGEKNGTRLISCP 659
```

```
RESULT 6
US-10-006-265-17
; Sequence 17, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
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; CURRENT APPLICATION NUMBER: US/10/006,265
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 17
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-17
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Query Match      87.1%; Score 3405.5; DB 15; Length 662:
Best Local Similarity 99.1%; Pred. No. 5.3e-291;
Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
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```
OY 1 MMTWALMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKETSQYTVKRTYA 60
DB 14 MMTWALMLPSLCKFSLAALPAKPENISCVYYRKNLTCTWSPGKETSQYTVKRTYA 73
OY 61 FGEKHDNCTNSTSENKASCSFLLPRITIPDNTTIEVEAENGGVKSHMTYRLENIA 120
DB 74 FGEKHDNCTNSTSENKASCSFLLPRITIPDNTTIEVEAENGGVKSHMTYRLENIA 133
OY 121 KTEPPKIFRVKPVLGIRKMIQIEMIKPELAVSSDLKYTLFRVNSTSMVEVFAKRRK 180
DB 134 KTEPPKIFRVKPVLGIRKMIQIEMIKPELAVSSDLKYTLFRVNSTSMVEVFAKRRK 193
OY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPACGLEMLVRLPAE 240
DB 194 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPACGLEMLVRLPAE 253
OY 241 ADGRRPVRLMKKARGAVLEKTLGYNIMYPESNTNLTETMNTTNOQLHLGGESEFW 300
DB 254 ADGRRPVRLMKKARGAVLEKTLGYNIMYPESNTNLTETMNTTNOQLHLGGESEFW 313
OY 301 SMISYNSLGKSPVATLRIPAIQKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEF 360
DB 314 SMISYNSLGKSPVATLRIPAIQKSFQIEYMAQVADOLVVKWSSALDVTNMTLMEF 373
OY 361 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 420
DB 374 PDVDSPTTSLMESVSQATNMTIOODKLRPWCYNISYVPMHDKVGEPSIOAYAKEGV 433
OY 421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVOAEGGKFSKTVNSSILOYG 480
DB 434 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVOAEGGKFSKTVNSSILOYG 493
OY 481 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPSVFEIILITSLIGGGLLILITLVA 540
DB 494 LESLKRTSYIVQYMASTAGTNGTSTINFKTLSPSVFEIILITSLIGGGLLILITLVA 553
OY 541 YGLKPKMLTHLCPTVPNPAESSIATWHDGDFDKLNLKESDVSNTEDRIILPCSTPS 600
DB 554 YGLKPKMLTHLCPTVPNPAESSIATWHDGDFDKLNLKESDVSNTEDRIILPCSTPS 613
OY 601 DKLVIDKLVVFGNVLOEIFTDEARTQENNLGGEKNG---YVTCP 643
DB 614 DKLVIDKLVVFGNVLOEIFTDEARTQENNLGGEKNGTRLISCP 659
```

```
RESULT 7
US-09-972-708-14
; Sequence 14, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
```

APPLICANT: Bird, Timothy A.  
APPLICANT: Dubose, Robert F.  
APPLICANT: Wiley, Steven R.  
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
FILE REFERENCE: 3160-B  
CURRENT APPLICATION NUMBER: US/09/972.708  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 14  
LENGTH: 652  
TYPE: PR1  
ORGANISM: Homo sapiens  
US-09-972-708-14

Query Match 85.7%; Score 3350; DB 11; Length 652;  
Best Local Similarity 99.8%; Pred. No. 4e-286;  
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MMTWALMMLPSLCKFSLALPAKPNISCVYYRKNLCTWSPGKETSYQYVKKRYA 60  
14 MMTWALMMLPSLCKFSLALPAKPNISCVYYRKNLCTWSPGKETSYQYVKKRYA 73  
61 FGEKHDNCTNNSSTSENASCSEFLPRITTPDNTTIEAENGSGVSKSHMTYRLNIA 120  
74 FGEKHDNCTNNSSTSENASCSEFLPRITTPDNTTIEAENGSGVSKSHMTYRLNIA 133  
121 KTEPKIFRYKPVIGIKRMIOIEMIKPELAVSSDLKYTLFRVNSTSWMEVFAKRNK 180  
134 KTEPKIFRYKPVIGIKRMIOIEMIKPELAVSSDLKYTLFRVNSTSWMEVFAKRNK 193  
181 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLPKPAE 240  
194 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLPKPAE 253  
241 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSESPV 300  
254 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSESPV 313  
301 SMISYNSLGSPVATLRIPAIQKSFQCIEMQACVADOLVVKQSSALDVNTWMIEMF 360  
314 SMISYNSLGSPVATLRIPAIQKSFQCIEMQACVADOLVVKQSSALDVNTWMIEMF 373  
361 PDVNSEPTLSMESVSQATNMTIOODKLRPWCYNISYVPMHLKRGVGPYSIOAYAKEGV 420  
374 PDVNSEPTLSMESVSQATNMTIOODKLRPWCYNISYVPMHLKRGVGPYSIOAYAKEGV 433  
421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEGGKFSKTVNSIIQYG 480  
434 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEGGKFSKTVNSIIQYG 493  
481 LESLKRTSYIVQYMASTAGTNGTSINFTLSFSVEIILLITSLIGGGLIIIIITLVA 540  
494 LESLKRTSYIVQYMASTAGTNGTSINFTLSFSVEIILLITSLIGGGLIIIIITLVA 553  
541 YGLKPKPKLTHLCPTVPNPRESSIATWHDGDFDKLNLKESDSDSVNTEDEILKPCSTPS 600  
554 YGLKPKPKLTHLCPTVPNPRESSIATWHDGDFDKLNLKESDSDSVNTEDEILKPCSTPS 613  
601 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 629  
614 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 642

RESULT 8  
US-10-006-265-2  
Sequence 2, Application US/10006265  
Publication No. US20030125520A1  
GENERAL INFORMATION:  
APPLICANT: Maeda, Masatsugu  
APPLICANT: Yaguchi, No. US20030125520A1ko  
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10  
FILE REFERENCE: 06501-096001

CURRENT APPLICATION NUMBER: US/10/006.265  
CURRENT FILING DATE: 2003-01-06  
PRIOR APPLICATION NUMBER: PCT/JP00/03556  
PRIOR FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: JP 11/155797  
PRIOR FILING DATE: 1999-06-02  
PRIOR APPLICATION NUMBER: JP 11/217797  
PRIOR FILING DATE: 1999-07-30  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 652  
TYPE: PR1  
ORGANISM: Homo sapiens  
US-10-006-265-2

Query Match 85.7%; Score 3350; DB 15; Length 652;  
Best Local Similarity 99.8%; Pred. No. 4e-286;  
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MMTWALMMLPSLCKFSLALPAKPNISCVYYRKNLCTWSPGKETSYQYVKKRYA 60  
14 MMTWALMMLPSLCKFSLALPAKPNISCVYYRKNLCTWSPGKETSYQYVKKRYA 73  
61 FGEKHDNCTNNSSTSENASCSEFLPRITTPDNTTIEAENGSGVSKSHMTYRLNIA 120  
74 FGEKHDNCTNNSSTSENASCSEFLPRITTPDNTTIEAENGSGVSKSHMTYRLNIA 133  
121 KTEPKIFRYKPVIGIKRMIOIEMIKPELAVSSDLKYTLFRVNSTSWMEVFAKRNK 180  
134 KTEPKIFRYKPVIGIKRMIOIEMIKPELAVSSDLKYTLFRVNSTSWMEVFAKRNK 193  
181 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLPKPAE 240  
194 DKNOTYMLTGLOPTEEVIALRCVAKESKFSMDWSOEKMGTEBEAPCGLEMLVLPKPAE 253  
241 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSESPV 300  
254 ADGRPRVRLMKKRGAPVLEKTLGYNIWYYPESNTNLTETMNTNOOLEHLGSESPV 313  
301 SMISYNSLGSPVATLRIPAIQKSFQCIEMQACVADOLVVKQSSALDVNTWMIEMF 360  
314 SMISYNSLGSPVATLRIPAIQKSFQCIEMQACVADOLVVKQSSALDVNTWMIEMF 373  
361 PDVNSEPTLSMESVSQATNMTIOODKLRPWCYNISYVPMHLKRGVGPYSIOAYAKEGV 420  
374 PDVNSEPTLSMESVSQATNMTIOODKLRPWCYNISYVPMHLKRGVGPYSIOAYAKEGV 433  
421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEGGKFSKTVNSIIQYG 480  
434 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFVQAEGGKFSKTVNSIIQYG 493  
481 LESLKRTSYIVQYMASTAGTNGTSINFTLSFSVEIILLITSLIGGGLIIIIITLVA 540  
494 LESLKRTSYIVQYMASTAGTNGTSINFTLSFSVEIILLITSLIGGGLIIIIITLVA 553  
541 YGLKPKPKLTHLCPTVPNPRESSIATWHDGDFDKLNLKESDSDSVNTEDEILKPCSTPS 600  
554 YGLKPKPKLTHLCPTVPNPRESSIATWHDGDFDKLNLKESDSDSVNTEDEILKPCSTPS 613  
601 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 629  
614 DKLVIDKLIVNFGNVLOEIFTDEARTGOE 642

RESULT 9  
US-09-892-949-69  
Sequence 69, Application US/09892949  
Publication No. US20030096339A1  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Presnell, Scott R.  
APPLICANT: Gao, Zeren

APPLICANT: Whitmore, Theodore E.  
APPLICANT: Kullper, Joseph L.  
APPLICANT: Maurer, Mark F.  
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTORL7  
FILE REFERENCE: 00-42  
CURRENT APPLICATION NUMBER: US/09/892,949  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: US 60/214,282  
PRIOR FILING DATE: 2000-06-26  
PRIOR APPLICATION NUMBER: US 60/214,955  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 60/267,963  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 69  
LENGTH: 764  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Human zcytorl7-Fc4 fusion polypeptide  
US-09-892-949-69

Query Match 71.2%; Score 2783; DB 11; Length 764;  
Best Local Similarity 93.8%; Pred. No. 4.6e-236;  
Matches 525; Conservative 2; Mismatches 9; Indels 24; Gaps 2;

QY 1 MMTWALMLPLSLCKFSALAPAKPENISCVYYRKNNLTCTMSPGKENSYYQYVKKRYA 60  
DB 14 MMTWALMLPLSLCKFSALAPAKPENISCVYYRKNNLTCTMSPGKENSYYQYVKKRYA 73  
QY 61 FGEKHDNCTNSTSENASCSPFLPRITIPDNTYIEVEANGDVINKSHNTYRLNENIA 120  
DB 74 FGEKHDNCTNSTSENASCSPFLPRITIPDNTYIEVEANGDVINKSHNTYRLNENIA 133  
QY 121 KTEPPKIFRVKPVVIGIKMIQIEMTKPELAYSSDLKTLFRVYNSTSMMEVNFAPKRRK 180  
DB 134 KTEPPKIFRVKPVVIGIKMIQIEMTKPELAYSSDLKTLFRVYNSTSMMEVNFAPKRRK 193  
QY 181 DKNQTYNLGTGQPTFEYVIALRCVAKESKFSWDSOEKMGTEEPAPCGLELMRYLKPAE 240  
DB 194 DKNQTYNLGTGQPTFEYVIALRCVAKESKFSWDSOEKMGTEEPAPCGLELMRYLKPAE 253  
QY 241 ADGRRPVRLMKKARGAVLEKTLGYNIMYYPESNTNLTETMNTNNOLEHLGSESFW 300  
DB 254 ADGRRPVRLMKKARGAVLEKTLGYNIMYYPESNTNLTETMNTNNOLEHLGSESFW 313  
QY 301 SMIVYNSLGSKSPVATLRIPATQESFQCIEMQACVADOLVVKWQSALDVNTWMEWF 360  
DB 314 SMIVYNSLGSKSPVATLRIPATQESFQCIEMQACVADOLVVKWQSALDVNTWMEWF 373  
QY 361 PDVDEPTTSLMESVSQATNMTIQODKLPFCYNISVYPMALHPCVGPYSIQAVAKEGV 420  
DB 374 PDVDEPTTSLMESVSQATNMTIQODKLPFCYNISVYPMALHPCVGPYSIQAVAKEGV 433  
QY 421 PSEBPEIKVENIGVYVITTWKEIKPKSERKGIICNYTIFYOAEKGKGSFTVNSSIIQYG 480  
DB 434 PSEBPEIKVENIGVYVITTWKEIKPKSERKGIICNYTIFYOAEKGKGSFTVNSSIIQYG 493  
QY 481 LESLKRTSYIVQYMASSAGTNGTSINFKTSLFSVFEIILITSLIGGLILILITVA 540  
DB 494 LESLKRTSYIVQYMASSAGTNGTSINFKTSLFSVFEIILITSLIGGLILILITVA 532  
QY 541 YGLKPNKTLHLCWPTVNP 560  
DB 533 --EPRSSDKHTHC--PPCAP 549

RESULT 10  
US-10-227-884-92  
Sequence 92, Application US/10227884  
Publication No. US20030027988A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Collin L.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C79  
CURRENT APPLICATION NUMBER: US/10/227,884  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089905  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090691  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/095302  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095318  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095916  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096146

PRIOR FILING DATE: 1998-08-11  
PRIOR APPLICATION NUMBER: 60/096791  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/097986  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098544  
PRIOR FILING DATE: 1998-08-31  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099811  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100038  
PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/106877  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/106801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/106849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10

PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 60/126773  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: 60/127887  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/131270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/131445  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/140650  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/140723  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: 60/141037  
PRIOR FILING DATE: 1999-06-23  
PRIOR APPLICATION NUMBER: 60/144758  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/146222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: 60/146963  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/149320  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149638  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/151733  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/164418  
PRIOR FILING DATE: 1999-11-09  
PRIOR APPLICATION NUMBER: 60/166361  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/169445  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.1%; Score 2546; DB 15; Length 582;  
Best Local Similarity 98.7%; Pred. No. 2.2e-215;  
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MMTWALMMLPSLCLFSLAALPAKRENISCVYYIRKNTLCTWSPCKEISTYQYTKRYA 60  
DB 33 MMTWALMMLPSLCLFSLAALPAKRENISCVYYIRKNTLCTWSPCKEISTYQYTKRYA 92  
QY 61 FGEKHNDCTNSTSENASCSEFLPRITIPDNTYIEVEAENGDCVISHMTYWRLEMA 120  
DB 93 FGEKHNDCTNSTSENASCSEFLPRITIPDNTYIEVEAENGDCVISHMTYWRLEMA 152  
QY 121 KTEPKIFRVKPVGLGIRKMIQIEWIKPELAPVSSDLKTYLRFRTVNSTSMWEVNAKRR 180  
DB 153 KTEPKIFRVKPVGLGIRKMIQIEWIKPELAPVSSDLKTYLRFRTVNSTSMWEVNAKRR 212  
QY 181 DKNQYNTLTGLOPFVEYIALRCVAKESKFSMDSQEMKGMTBEERAPGGLMLRVLKPAE 240  
DB 213 DKNQYNTLTGLOPFVEYIALRCVAKESKFSMDSQEMKGMTBEERAPGGLMLRVLKPAE 272  
QY 241 ADGRPRVRLMKKARGADVLEKTLGYNIMWYPESNTNLTETMNTTNOGLELHLGGESEWV 300

|||||  
Db 273 ADGRPRVLLMKAGCAVLEKTLGYNITWYDESNTNLEFNTNNOQLHLGSEFW 332  
QY 301 SMISVNSIGKSPVATLRIPAIORSEFOCIENVQACVADOLVYKQSSALDVTNMTMEF 360  
Db 333 SMISVNSIGKSPVATLRIPAIORSEFOCIENVQACVADOLVYKQSSALDVTNMTMEF 392  
QY 361 PDVDSPTLLSMESVSQATNMTIQODKLKPEWCYNISVYPMHLDRKGEPSIOAYAKGV 420  
Db 393 PDVDSPTLLSMESVSQATNMTIQODKLKPEWCYNISVYPMHLDRKGEPSIOAYAKGV 452  
QY 421 PSEGETVENIGVTVITITWKEIPKSERKGIICNTTIFYOAGSGKFSKTVNSSI 476  
Db 453 PSEGETVENIGVTVITITWKEIPKSERKGIICNTTIFYOAGSGKFSKTVNSSI 508  
  
RESULT 11  
US-10-230-163-92  
Sequence 92, Application US/10230163  
Publication No. US20030036635A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin I.  
TITLE OF INVENTION: SECRETED- AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C96  
CURRENT APPLICATION NUMBER: US/10/230,163  
CURRENT FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
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PRIOR FILING DATE: 1998-05-13  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086392  
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PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090691  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/095302  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095318  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095916  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096146  
PRIOR FILING DATE: 1998-08-11  
PRIOR APPLICATION NUMBER: 60/096791  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/097986  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098544  
PRIOR FILING DATE: 1998-08-31  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099811  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100038  
PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787



;; PRIOR FILING DATE: 1998-11-17  
;; PRIOR APPLICATION NUMBER: 60/108801  
;; PRIOR FILING DATE: 1998-11-17  
;; PRIOR APPLICATION NUMBER: 60/108849  
;; PRIOR FILING DATE: 1998-11-18  
;; PRIOR APPLICATION NUMBER: 60/112422  
;; PRIOR FILING DATE: 1998-12-15  
;; PRIOR APPLICATION NUMBER: 60/113296  
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;; PRIOR APPLICATION NUMBER: 60/113605  
;; PRIOR FILING DATE: 1998-12-23  
;; PRIOR APPLICATION NUMBER: 60/113621  
;; PRIOR FILING DATE: 1998-12-23  
;; PRIOR APPLICATION NUMBER: 60/115558  
;; PRIOR FILING DATE: 1999-01-12  
;; PRIOR APPLICATION NUMBER: 60/115549  
;; PRIOR FILING DATE: 1999-02-10  
;; PRIOR APPLICATION NUMBER: 60/123618  
;; PRIOR FILING DATE: 1999-03-10  
;; PRIOR APPLICATION NUMBER: 60/125259  
;; PRIOR FILING DATE: 1999-03-19  
;; PRIOR APPLICATION NUMBER: 60/125775  
;; PRIOR FILING DATE: 1999-03-23  
;; PRIOR APPLICATION NUMBER: 60/126773  
;; PRIOR FILING DATE: 1999-03-29  
;; PRIOR APPLICATION NUMBER: 60/127887  
;; PRIOR FILING DATE: 1999-04-05  
;; PRIOR APPLICATION NUMBER: 60/130232  
;; PRIOR FILING DATE: 1999-04-21  
;; PRIOR APPLICATION NUMBER: 60/131022  
;; PRIOR FILING DATE: 1999-04-26  
;; PRIOR APPLICATION NUMBER: 60/131270  
;; PRIOR FILING DATE: 1999-04-27  
;; PRIOR APPLICATION NUMBER: 60/131291  
;; PRIOR FILING DATE: 1999-04-27  
;; PRIOR APPLICATION NUMBER: 60/131445  
;; PRIOR FILING DATE: 1999-04-28  
;; PRIOR APPLICATION NUMBER: 60/134287  
;; PRIOR FILING DATE: 1999-05-14  
;; PRIOR APPLICATION NUMBER: 60/140650  
;; PRIOR FILING DATE: 1999-06-22  
;; PRIOR APPLICATION NUMBER: 60/140723  
;; PRIOR FILING DATE: 1999-06-22  
;; PRIOR APPLICATION NUMBER: 60/141037  
;; PRIOR FILING DATE: 1999-06-23  
;; PRIOR APPLICATION NUMBER: 60/144758  
;; PRIOR FILING DATE: 1999-07-20  
;; PRIOR APPLICATION NUMBER: 60/145698  
;; PRIOR FILING DATE: 1999-07-26  
;; PRIOR APPLICATION NUMBER: 60/146222  
;; PRIOR FILING DATE: 1999-07-28  
;; PRIOR APPLICATION NUMBER: 60/146963  
;; PRIOR FILING DATE: 1999-08-03  
;; PRIOR APPLICATION NUMBER: 60/149320  
;; PRIOR FILING DATE: 1999-08-17  
;; PRIOR APPLICATION NUMBER: 60/149638  
;; PRIOR FILING DATE: 1999-08-17  
;; PRIOR APPLICATION NUMBER: 60/151733  
;; PRIOR FILING DATE: 1999-08-31  
;; PRIOR APPLICATION NUMBER: 60/164418  
;; PRIOR FILING DATE: 1999-11-09  
;; PRIOR APPLICATION NUMBER: 60/166361  
;; PRIOR FILING DATE: 1999-11-16  
;; PRIOR APPLICATION NUMBER: 60/169445  
;; PRIOR FILING DATE: 1999-12-07  
;; PRIOR APPLICATION NUMBER: 60/169495  
;; PRIOR FILING DATE: 1999-12-07  
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.1%; Score 2546; DB 15; Length 582;  
Best Local Similarity 98.7%; Pred. No. 2,2e-215;  
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MMWTWALMMLPSLCKFSLALPAKPENISCVYYRRKULCTWSPGKETSTQYTVKRTYA 60  
|||||  
Db 33 MMWTWALMMLPSLCKFSLALPAKPENISCVYYRRKULCTWSPGKETSTQYTVKRTYA 92  
61 FGEKHNCTNNTSSSENKASCSFPLRITTPDNTTVEVANGGVKSHMTVRLLENIA 120  
OY 93 FGEKHNCTNNTSSSENKASCSFPLRITTPDNTTVEVANGGVKSHMTVRLLENIA 152  
Db 121 KTEPPKIFRVKPVGLIRMIQIEIKPELAPVSSDLKYTLRFRTVNSTSMVEVFAKNRK 180  
|||||  
Db 153 KTEPPKIFRVKPVGLIRMIQIEIKPELAPVSSDLKYTLRFRTVNSTSMVEVFAKNRK 212  
OY 181 DKNOTVNLGTLOPTEVIALRCAVKSKEFWSQKMGMTTEEADPCGLEMLRVLPKPAE 240  
|||||  
Db 213 DKNOTVNLGTLOPTEVIALRCAVKSKEFWSQKMGMTTEEADPCGLEMLRVLPKPAE 272  
OY 241 ADGRRPVRLLMKKRGAAPVLEKTGYNIWYYPESNTNLTETMNTNOOLEHLGGESEFW 300  
|||||  
Db 273 ADGRRPVRLLMKKRGAAPVLEKTGYNIWYYPESNTNLTETMNTNOOLEHLGGESEFW 332  
OY 301 SMISYNSLGKSPVTLRIPATQESFOCIEYMOACVAEDOLVYKMOSSALDVNTMTIEMF 360  
|||||  
Db 333 SMISYNSLGKSPVTLRIPATQESFOCIEYMOACVAEDOLVYKMOSSALDVNTMTIEMF 392  
OY 361 PDVDEPTLTSWESVSQATMTTIOODKLKPEWCYNISVYPMALHDVGEPSYQAYAREGV 420  
|||||  
Db 393 PDVDEPTLTSWESVSQATMTTIOODKLKPEWCYNISVYPMALHDVGEPSYQAYAREGV 452  
OY 421 PSEGPETKVENIGKVTYITIMKELPKSEKGCICNTYITIFQAEKGKFSKTVNSI 476  
|||||  
Db 453 PSEGPETKVENIGKVTYITIMKELPKSEKGCICNTYITIFQAEKGKFSKTVNSI 508

RESULT 12  
US-10-230-338-92  
;; Sequence 92, Application US/10230338  
;; Publication No. US2003004934A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Gerritsen, Mary  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Stephan, Jean-Philippe F.  
;; APPLICANT: Watanabe, Colin L.  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P3530P1C92  
;; CURRENT APPLICATION NUMBER: US/10/230,338  
;; PRIOR FILING DATE: 2002-08-28  
;; PRIOR APPLICATION NUMBER: 10/119,480  
;; PRIOR FILING DATE: 2002-04-09  
;; PRIOR APPLICATION NUMBER: 60/059113  
;; PRIOR FILING DATE: 1997-09-17  
;; PRIOR APPLICATION NUMBER: 60/062287  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/063549  
;; PRIOR FILING DATE: 1997-10-28  
;; PRIOR APPLICATION NUMBER: 60/064103  
;; PRIOR FILING DATE: 1997-10-31  
;; PRIOR APPLICATION NUMBER: 60/069873  
;; PRIOR FILING DATE: 1997-12-17  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/079294

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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-92

Query Match
Best Local Similarity 98.7%; Score 2546; DB 15; Length 582;
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 60
DB 33 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 92
OY 61 FGEKHDNCTTSSSENASCSEFLPRITPDNTTIEVEAENGCVIKSHMTYRLNIA 120
DB 93 FGEKHDNCTTSSSENASCSEFLPRITPDNTTIEVEAENGCVIKSHMTYRLNIA 152
OY 121 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMHEVNFARKRK 180
DB 153 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMHEVNFARKRK 212
OY 181 DKNOTYNTLGLQPTFEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 240
DB 213 DKNOTYNTLGLQPTFEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 272
OY 241 ADGRRPVLLMKKARGAVLEKTLGYNIMYYPESNTNLTETMNTTNOOLELHLCGESFW 300
DB 273 ADGRRPVLLMKKARGAVLEKTLGYNIMYYPESNTNLTETMNTTNOOLELHLCGESFW 332
OY 301 SMISYNSLGKSPVATLRIPALQEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 360
DB 333 SMISYNSLGKSPVATLRIPALQEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 392
OY 361 PDVNSEPTTSLMESVSQATNMTIOODKLPKWCNINISYPMHLHDKVGPYSIOAYAKGV 420
DB 393 PDVNSEPTTSLMESVSQATNMTIOODKLPKWCNINISYPMHLHDKVGPYSIOAYAKGV 452
OY 421 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGGKGFCKHAHSEV 476
DB 453 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGGKGFCKHAHSEV 508

RESULT 13
US-10-218-631-92
; Sequence 92, Application US/10218631
; Publication NO. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Victoria
; APPLICANT: Smith, Austin L.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218,631
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-92

Query Match
Best Local Similarity 98.7%; Score 2546; DB 15; Length 582;
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 60
DB 33 MMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSQYTVKRTYA 92
OY 61 FGEKHDNCTTSSSENASCSEFLPRITPDNTTIEVEAENGCVIKSHMTYRLNIA 120
DB 93 FGEKHDNCTTSSSENASCSEFLPRITPDNTTIEVEAENGCVIKSHMTYRLNIA 152
OY 121 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMHEVNFARKRK 180
DB 153 KTEPKIFRVPVLGIRKMIQIEMIKPELAPVSSDLKTLFRFVNSTSMHEVNFARKRK 212
OY 181 DKNOTYNTLGLQPTFEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 240
DB 213 DKNOTYNTLGLQPTFEYVIALRCAYKESKFSWDSQEMKMGTEEBAPCGLELMLVLPKPAE 272
OY 241 ADGRRPVLLMKKARGAVLEKTLGYNIMYYPESNTNLTETMNTTNOOLELHLCGESFW 300
DB 273 ADGRRPVLLMKKARGAVLEKTLGYNIMYYPESNTNLTETMNTTNOOLELHLCGESFW 332
OY 301 SMISYNSLGKSPVATLRIPALQEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 360
DB 333 SMISYNSLGKSPVATLRIPALQEKSFQCI EYMOACVAEDQLVVKMOSSALDVNTMIMEF 392
OY 361 PDVNSEPTTSLMESVSQATNMTIOODKLPKWCNINISYPMHLHDKVGPYSIOAYAKGV 420
DB 393 PDVNSEPTTSLMESVSQATNMTIOODKLPKWCNINISYPMHLHDKVGPYSIOAYAKGV 452
OY 421 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGGKGFCKHAHSEV 476
DB 453 PSEGPETKVENIGKVTYITTKETPKSERKGIICNTYITFYAEGGKGFCKHAHSEV 508

RESULT 14
US-10-230-414-92
; Sequence 92, Application US/10230414
; Publication NO. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC98  
CURRENT APPLICATION NUMBER: US/10/230,414  
CURRENT FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 92  
LENGTH: 582  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-230-414-92

Query Match 65.1%; Score 2546; DB 15; Length 582;  
Best Local Similarity 98.7%; Pred. No. 2.2e-215;  
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MAMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 60  
DB 33 MAMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 92  
QY 61 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEAENGGVIKSHMTYRLENIA 120  
DB 93 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEAENGGVIKSHMTYRLENIA 152  
QY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKTLFRFVNSTSMMEVNFANKRK 180  
DB 153 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKTLFRFVNSTSMMEVNFANKRK 212  
QY 181 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAGCLELMRYLKPAAE 240  
DB 213 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAGCLELMRYLKPAAE 272  
QY 241 ADGRRPVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGGESEFW 300  
DB 273 ADGRRPVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGGESEFW 332  
QY 301 SMISYNSLGKSPVATLRIPATOEKSFQIEVMOACVADOLVVKWQSSALDVNTMTWMEF 360  
DB 333 SMISYNSLGKSPVATLRIPATOEKSFQIEVMOACVADOLVVKWQSSALDVNTMTWMEF 392  
QY 361 PDVSEPTTSLMESVSQATNWTIOODKLPFCWCYNISVYPMUHDKVGEPYSIOAYAKGCV 420  
DB 393 PDVSEPTTSLMESVSQATNWTIOODKLPFCWCYNISVYPMUHDKVGEPYSIOAYAKGCV 452  
QY 421 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFYAEGGKGFCKTAVNSSI 476  
PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFYAEGGKGFCKTAVNSSI 476

DB 453 PSEGPETKVENIGVKTVTITWKEIPKSERKGIICNTTIFYAEGGKGFCKTAVNSSEV 508  
RESULT 15  
US-10-216-159A-92  
Sequence 92, Application US/10216159A  
Publication No. US20030069397A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC6  
CURRENT APPLICATION NUMBER: US/10/216,159A  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 92  
LENGTH: 582  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-216-159A-92  
Query Match 65.1%; Score 2546; DB 15; Length 582;  
Best Local Similarity 98.7%; Pred. No. 2.2e-215;  
Matches 470; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MAMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 60  
DB 33 MAMTWALMLPSLCKFSLAALPAKPNISCVYYRRKNTCTWSPGKETSYYQYVKKRYA 92  
QY 61 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEAENGGVIKSHMTYRLENIA 120  
DB 93 FGEKHDNCTNSTSENASCSPFLPRITIPDNTTIEVEAENGGVIKSHMTYRLENIA 152  
QY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKTLFRFVNSTSMMEVNFANKRK 180  
DB 153 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAVSSDLKTLFRFVNSTSMMEVNFANKRK 212  
QY 181 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAGCLELMRYLKPAAE 240  
DB 213 DKNOTYNTLTGLOPTEYVIALRCVAKESKFSWDSQEMGMTTEEPAGCLELMRYLKPAAE 272  
QY 241 ADGRRPVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGGESEFW 300  
ADGRRPVRLMKKARGAVLEKTLGYNIMWYPESNTNLTETMNTTNOOLELHLGGESEFW 300

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Db 273 ADGRRPVRLLMKKARGAVLEKTLGYNIMYPESNTNLETMTNTNOOLELHIGSEFW 332
QY 301 SMISYNSLGKSPVATLRIPAIQKSFQCI EYMOACVAEDOLVYKWOSSALDVNTWMIWF 360
Db 333 SMISYNSLGKSPVATLRIPAIQKSFQCI EYMOACVAEDOLVYKWOSSALDVNTWMIWF 392
QY 361 PDVDEPTTLSMESYSQATNMTIOODKLPFCYNI SVYPM LHDKVGEPSIOAYAKEGV 420
Db 393 PDVDEPTTLSMESYSQATNMTIOODKLPFCYNI SVYPM LHDKVGEPSIOAYAKEGV 452
QY 421 PSEGPEKVENIGVKTVTITWKELPKSERKGI CNVTI FYOAGGKGF SKTVNSSI 476
Db 453 PSEGPEKVENIGVKTVTITWKELPKSERKGI CNVTI FYOAGGKGF CKHAHSEV 508
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Search completed: August 4, 2003, 11:21:07  
Job time : 30 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2003, 11:16:41 ; Search time 85 Seconds  
(without alignments)  
1366.916 Million cell updates/sec

Title: US-09-892-949-2

Perfect score: 3908

Sequence: 1 MMTWALMLPISLCKFSLAA.....VTAREFLVSEKLPENTKGEV 732

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3908	100.0	732	23	ABBO5730
2	3908	100.0	764	24	ABP54364
3	3908	100.0	764	23	ABP54365
4	3896	99.7	745	23	AAE24024
5	3405.5	87.1	649	23	ABBO5738
6	3405.5	87.1	662	22	ABP54364
7	3405.5	87.1	662	22	AAE24029
8	3405.5	87.1	662	23	ABBO5741
9	3405.5	87.1	681	24	ABP54363

10	3350	85.7	652	22	ABP51242
11	3350	85.7	652	23	AAE24028
12	3074	78.7	627	24	ABP54366
13	2908	74.4	581	24	ABP54367
14	2783	71.2	764	23	ABBO5743
15	2764	70.7	549	24	ABP54368
16	2763	70.7	549	24	ABP54369
17	2546	65.1	582	23	ABBO5742
18	2546	65.1	582	23	ABBO5742
19	2546	65.1	582	23	ABBO5742
20	2132.5	54.6	716	24	ABP54370
21	2132.5	54.6	726	23	AAE24037
22	2128.5	54.5	716	24	ABP54371
23	1954	50.0	662	23	ABBO5742
24	1750	44.8	324	23	ABBO5732
25	1567	40.1	620	22	ABBO5707
26	1553	39.7	547	23	ABBO5745
27	1222	31.3	239	23	ABBO5733
28	1222	31.3	252	22	ABBO5743
29	1222	31.3	252	23	ABBO5743
30	690.5	17.7	917	13	AAE24027
31	688.5	17.6	917	13	AAE24027
32	681.5	17.4	918	12	AAE24027
33	679.5	17.4	918	15	AAE24027
34	679.5	17.4	918	21	AAE24027
35	679.5	17.4	918	21	AAE24027
36	679.5	17.4	918	24	ABP54367
37	678.5	17.4	708	17	AAE24027
38	677.5	17.3	918	17	AAE24027
39	665.5	17.0	708	14	AAE24027
40	630	16.1	961	21	AAE24027
41	629	16.1	951	20	AAE24027
42	629	16.1	951	21	AAE24027
43	619	15.8	859	20	AAE24027
44	619	15.8	859	21	AAE24027
45	618	15.8	658	17	AAE24027

#### ALIGNMENTS

RESULT 1	ABBO5730	standard; Protein: 732 AA.
ID	ABBO5730;	
AC	ABBO5730;	
XX		
DT	01-MAY-2002 (first entry)	
XX		
DE	Human zcytor17 protein sequence seq ID NO:2.	
XX		
KW	zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;	
KW	antihematopoietic; antileukemic; antirheumatic; antithrombotic; cytostatic;	
KW	muscular; lymphoid; immune; inflammatory; splenic; bone;	
KW	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;	
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;	
KW	inflammatory disease; pancreatitis; inflammatory bowel disease.	
OS	Homo sapiens.	
XX		
PN	WO200200721-A2.	
XX		
PD	03-JAN-2002.	
XX		
PF	26-JUN-2001; 2001WO-US20484.	
XX		
PR	26-JUN-2000; 2000US-214282P.	
XX		
PR	29-JUN-2000; 2000US-214955P.	
XX		
PR	08-FEB-2001; 2001US-267963P.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;	



Db 93 GGEKNDCTNTSSSENASCSPFLPRITPDNTTIEVEANGGVKISHMTYRLENIA 152  
 QY 121 KTEPPKIFRVKPVIGIKRMIOIEWIKPELAVSSDLKYTLTFRVNSTSMNEVFAKRR 180  
 Db 153 KTEPPKIFRVKPVIGIKRMIOIEWIKPELAVSSDLKYTLTFRVNSTSMNEVFAKRR 212  
 QY 181 DKNOTYNTLGQPTFEYVIALRCVAKESKFSWDSQEMGMTTEEPACGLELMRYLRAE 240  
 Db 213 DKNOTYNTLGQPTFEYVIALRCVAKESKFSWDSQEMGMTTEEPACGLELMRYLRAE 272  
 QY 241 ADGRPRVRLMKKARGAVLEKTLGYNIMYIPESNTNLTETMNTNOOLEHLGSEFW 300  
 Db 273 ADGRPRVRLMKKARGAVLEKTLGYNIMYIPESNTNLTETMNTNOOLEHLGSEFW 332  
 QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVAEDQLVVKQSSALDVNTMTEMF 360  
 Db 333 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVAEDQLVVKQSSALDVNTMTEMF 392  
 QY 361 PDVDEPTTLTSMESVSQATNMTTIOODKLKPFMCYNISYVPMHDKVGPYSIOAYAKGV 420  
 Db 393 PDVDEPTTLTSMESVSQATNMTTIOODKLKPFMCYNISYVPMHDKVGPYSIOAYAKGV 452  
 QY 421 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTLFYQAEKGKFSKTVNSSILOYG 480  
 Db 453 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTLFYQAEKGKFSKTVNSSILOYG 512  
 QY 481 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVFEILLITSLIGGGLILLITLVA 540  
 Db 513 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVFEILLITSLIGGGLILLITLVA 572  
 QY 541 YGLKPKPKLTHLCWPTVNPRESSIATWHGDDFKDKLNLKESDVSNTEDRILKPCSTPS 600  
 Db 573 YGLKPKPKLTHLCWPTVNPRESSIATWHGDDFKDKLNLKESDVSNTEDRILKPCSTPS 632  
 QY 601 DKLVYDKLVNFGVNLQELFTDEARTGOENNLGGEKNKYVTCPPRPDCPLKSFPEELPVS 660  
 Db 633 DKLVYDKLVNFGVNLQELFTDEARTGOENNLGGEKNKYVTCPPRPDCPLKSFPEELPVS 692  
 QY 661 PEIPPRKSOYLRSRMPECTREPEAKEQLLFSQSGLVPHLCEGAPNPLKNSVAREFLV 720  
 Db 693 PEIPPRKSOYLRSRMPECTREPEAKEQLLFSQSGLVPHLCEGAPNPLKNSVAREFLV 752  
 QY 721 SEKLPEHTKGEV 732  
 Db 753 SEKLPEHTKGEV 764

RESULT 3  
 ABP54365  
 ID ABP54365 standard; Protein: 764 AA.

XX AC ABP54365;  
 XX 20-JAN-2003 (first entry)  
 DE Human NR10.4 splicing variant protein seq ID NO:6.  
 XX NR10; splicing variant; haematopoietin receptor; immunomodulator;  
 KW haemostatic; haematopoietic factor; immunological disease;  
 KW haematopoietic disease; haematopoietic cell regulation.  
 XX Homo sapiens.  
 OS  
 XX WO200277230-A1.  
 PN 03-OCT-2002.  
 PD 22-MAR-2002; 2002WO-JP02769.  
 PF 26-MAR-2001; 2001JP-0087298.  
 PR (CHUS) CHUGAI SEIYAKU KK.  
 PA

PI Maeda M, Yaguchi N, Hasegawa M;  
 XX WPI: 2003-018925/01.  
 DR N-PSDB; AB083365.  
 XX NR10 splicing variants of haematopoietin receptor proteins and encoded  
 PT genes, applicable in searching haematopoietic factors and developing  
 PT remedies for immunological and haematopoietic diseases  
 XX Claim 1; Fig 7-9; 250pp; Japanese.  
 PS  
 CC The present invention describes haematopoietic receptor NR10 splicing  
 CC variants (I). (I) have immunomodulator and haemostatic activities. The  
 CC proteins and encoded genes are applicable in searching for novel  
 CC haematopoietic factors, and developing remedies for immunological and  
 CC haematopoietic diseases. The haematopoietin receptor genes participate  
 CC in vivo immunomodulation and haematopoietic cell regulation, and in  
 CC the search for haematopoietic factors capable of functionally binding  
 CC to the receptors. The present sequence represents the human NR10.4  
 CC protein from the present invention.

Sequence 764 AA:

Query Match 100.0%; Score 3908; DB 24; Length 764;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTWALMLPDLCKFSLAALPAKRENISCVYYRRKNTCTWSPCKETSYYQYVYKRYA 60  
 Db 33 MMTWALMLPDLCKFSLAALPAKRENISCVYYRRKNTCTWSPCKETSYYQYVYKRYA 92  
 QY 61 GGEKNDCTNTSSSENASCSPFLPRITPDNTTIEVEANGGVKISHMTYRLENIA 120  
 Db 93 GGEKNDCTNTSSSENASCSPFLPRITPDNTTIEVEANGGVKISHMTYRLENIA 152  
 QY 121 KTEPPKIFRVKPVIGIKRMIOIEWIKPELAVSSDLKYTLTFRVNSTSMNEVFAKRR 180  
 Db 153 KTEPPKIFRVKPVIGIKRMIOIEWIKPELAVSSDLKYTLTFRVNSTSMNEVFAKRR 212  
 QY 181 DKNOTYNTLGQPTFEYVIALRCVAKESKFSWDSQEMGMTTEEPACGLELMRYLRAE 240  
 Db 213 DKNOTYNTLGQPTFEYVIALRCVAKESKFSWDSQEMGMTTEEPACGLELMRYLRAE 272  
 QY 241 ADGRPRVRLMKKARGAVLEKTLGYNIMYIPESNTNLTETMNTNOOLEHLGSEFW 300  
 Db 273 ADGRPRVRLMKKARGAVLEKTLGYNIMYIPESNTNLTETMNTNOOLEHLGSEFW 332  
 QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVAEDQLVVKQSSALDVNTMTEMF 360  
 Db 333 SMISYNSLGKSPVATLRIPAIQEKSFQCIEMQACVAEDQLVVKQSSALDVNTMTEMF 392  
 QY 361 PDVDEPTTLTSMESVSQATNMTTIOODKLKPFMCYNISYVPMHDKVGPYSIOAYAKGV 420  
 Db 393 PDVDEPTTLTSMESVSQATNMTTIOODKLKPFMCYNISYVPMHDKVGPYSIOAYAKGV 452  
 QY 421 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTLFYQAEKGKFSKTVNSSILOYG 480  
 Db 453 PSEGETKVENIGVKTIVITWKEIPKSERKGIICNTYTLFYQAEKGKFSKTVNSSILOYG 512  
 QY 481 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVFEILLITSLIGGGLILLITLVA 540  
 Db 513 LESLKRKTSYIVQVMASTAGTNGTSTINFKTLSPSVFEILLITSLIGGGLILLITLVA 572  
 QY 541 YGLKPKPKLTHLCWPTVNPRESSIATWHGDDFKDKLNLKESDVSNTEDRILKPCSTPS 600  
 Db 573 YGLKPKPKLTHLCWPTVNPRESSIATWHGDDFKDKLNLKESDVSNTEDRILKPCSTPS 632  
 QY 601 DKLVYDKLVNFGVNLQELFTDEARTGOENNLGGEKNKYVTCPPRPDCPLKSFPEELPVS 660  
 Db 633 DKLVYDKLVNFGVNLQELFTDEARTGOENNLGGEKNKYVTCPPRPDCPLKSFPEELPVS 692  
 QY 661 PEIPPRKSOYLRSRMPECTREPEAKEQLLFSQSGLVPHLCEGAPNPLKNSVAREFLV 720

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DB      693 PEIPRKSQYLNRSMPEGRPEAKEQLLFSGSLVPHDLCEGAPNPKNSVTAREFLV 752
OY      721 SEKLPEHTRKEV 732
        |||||
DB      753 SEKLPEHTRKEV 764

RESULT 4
AAE24024
ID      AAE24024 standard: Protein: 745 AA.
XX
AC      AAE24024;
XX
DT      23-SEP-2002 (first entry)
XX
DE      Human haematopoietin receptor 1 (HPR1) protein.
XX
KW      Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
KW      pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
KW      neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
KW      cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
KW      ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
KW      osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
KW      anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease;
KW      demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
KW      vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
KW      stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
KW      ischaemic disease.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Location/Qualifiers
FT      20..32
FT      /Label= Signal_peptide
FT      33..745
FT      /note= "Human mature HPR1 protein"
FT      33..241
FT      /note= "Cytokine receptor domain"
FT      83
FT      /note= "This residue changes to Ala during
FT      allelic variation"
FT      135..138
FT      /note= "Proline-rich linker"
FT      139..241
FT      /note= "C-terminal cytokine receptor subdomain"
FT      168
FT      /note= "This residue changes to Asn during
FT      allelic variation"
FT      187
FT      /note= "This residue changes to Thr during
FT      allelic variation"
FT      224..228
FT      /note= "MSXMS motif"
FT      242..515
FT      /note= "Fibronectin repeat"
FT      361
FT      /note= "This residue changes to Pro during
FT      allelic variation"
FT      362
FT      /note= "This residue changes to Gly during
FT      allelic variation"
FT      510
FT      /note= "This residue changes to Asn during
FT      allelic variation"
FT      517
FT      /note= "Encoded by GAC; This residue changes to
FT      Asp during allelic variation"
FT      526..556
FT      /note= "Extended transmembrane domain"
FT      533..552
FT      /note= "Core transmembrane domain"
FT      553..745
FT      /note= "Cytoplasmic domain"

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FT      Domain
FT      563..573
FT      /note= "Box1 conserved motif"
FT      588..592
FT      /note= "Repeat peptide"
FT      597..601
FT      /note= "Repeat peptide"
FT      603..607
FT      /note= "Repeat peptide"
FT      614..618
FT      /note= "Repeat peptide"
FT      619..623
FT      /note= "Repeat peptide"
FT      631..641
FT      /note= "Repeat peptide"
FT      635..639
FT      /note= "Box2 conserved motif"
FT      679
FT      /note= "Repeat peptide"
FT      679
FT      /note= "This residue changes to Gly during
FT      allelic variation"

WO200229060-A2.
11-APR-2002.
05-OCT-2001; 2001WO-US31634.
06-OCT-2000; 2000US-238706P.
13-OCT-2000; 2000US-240476P.
20-FEB-2001; 2001US-270282P.
(IMMUNEX CORP.
Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
WPT: 2002-330172/36.
N-PSDB; AAD38772.

Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,
useful for treating cell proliferation, metabolic, and reproductive
hormone related conditions -

Claim 1; Page 84-87; 156pp; English.

The present invention relates to human and murine haematopoietin receptor
polypeptides HPR1 and HPR2. Sequences of the invention are useful for
treating cell proliferation conditions e.g., pancytopenia, leukopenia,
anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
resulting from a lack of bone-forming cells. They are also useful for
treating cell proliferation conditions such as leukaemia and tumour
metastasis, osteoporosis resulting from an excess of bone-resorbing
cells. HPR sequences are also useful for treating medical conditions and
diseases such as cell proliferation, metabolic and reproductive hormone
related conditions. They are useful for treating various haematologic and
oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
squamous cell carcinoma), haematologic disorders, anemias (e.g., anaemia
of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
dysplastic syndromes (including refractory anaemia, refractory anaemia
CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
paenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
myeloid metaplasia, osteoclast disorders that lead to bone loss such
as osteoporosis including post-menopausal osteoporosis, periodontitis
resulting in tooth loosening or loss, prosthesis loosening after joint
replacement, neurodegenerative conditions (e.g., acute polynuropathy,
Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
Guillain-Barre syndrome, Creutzfeld-Jacob disease, demyelinating neuropathy,
myasthenia gravis, chronic neuronal degeneration, stroke including
cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
for treating various other disorders such as osteoporosis, obesity,

```



CC deficient mammary development and infertility. The present sequence  
is human HPRI protein.

XX Sequence 745 AA;

Query Match 99.7%; Score 3896; DB 23; Length 745;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLTCTWSGKETSTYQYVKKRYA 60
DB 14 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLTCTWSGKETSTYQYVKKRYA 73
QY 61 FGEKHDNCTNSTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 120
DB 74 FGEKHDNCTNSTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 133
QY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMMEVFAKRRK 180
DB 134 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMMEVFAKRRK 193
QY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPAPCGLELMRYLKPAAE 240
DB 194 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPAPCGLELMRYLKPAAE 253
QY 241 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTNTOLEHLGSEFWV 300
DB 254 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTNTOLEHLGSEFWV 313
QY 301 SMISYNSLGKSPVATLIRPAIQEKSFQCIEMVACVADOLVYKMOSSALDVTMTMEWF 360
DB 314 SMISYNSLGKSPVATLIRPAIQEKSFQCIEMVACVADOLVYKMOSSALDVTMTMEWF 373
QY 361 PDVSEPTTSMESVSQATMTTIOODKLKPCWCYNISVYPLHDKVGEPSIQAYAREGV 420
DB 374 PDVSEPTTSMESVSQATMTTIOODKLKPCWCYNISVYPLHDKVGEPSIQAYAREGV 433
QY 421 PSEGPETKVENIGKVTYITWKEIPKSEKGIICNTTIFYOAEKGKFSKTVNSIIQYG 480
DB 434 PSEGPETKVENIGKVTYITWKEIPKSEKGIICNTTIFYOAEKGKFSKTVNSIIQYG 493
QY 481 LESLKRTSYIVQVMASTAGTNGTSINFKTLISFVEIILLTSLIGGGLILLITLVA 540
DB 494 LESLKRTSYIVQVMASTAGTNGTSINFKTLISFVEIILLTSLIGGGLILLITLVA 553
QY 541 YGLKKPKKTLHLCPYTPNPRESSIATWHGDDFKDLNLSKSDSVNTEEDILKPCSTPS 600
DB 554 YGLKKPKKTLHLCPYTPNPRESSIATWHGDDFKDLNLSKSDSVNTEEDILKPCSTPS 613
QY 601 DKLVLDLVNFGVNLQEIFTEARTGOENNLGGEKNGYVCPRPDCCPLGKSPHEELPV 660
DB 614 DKLVLDLVNFGVNLQEIFTEARTGOENNLGGEKNGYVCPRPDCCPLGKSPHEELPV 673
QY 661 PEIPPKRSQYLRSRMEPGSTRPEAKEQLLFSGOSLVPHLCBEGANPYLKNSTVAREFLV 720
DB 674 PEIPPKRSQYLRSRMEPGSTRPEAKEQLLFSGOSLVPHLCBEGANPYLKNSTVAREFLV 733
QY 721 SEKLPEHTKGEV 732
DB 734 SEKLPEHTKGEV 745

```

RESULT 5

ABBO5738 standard; Protein: 649 AA.

XX ABO5738;

XX 01-MAY-2002 (first entry)

DE Human zcytor17 protein sequence SEQ ID NO:46.

KW zcytor17: chromosome 5; 5q11: cytokine receptor; immunomodulatory;

KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;  
muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
inflammatory disease; pancreatitis; inflammatory bowel disease.

OS Homo sapiens.

XX WO200200721-A2.

XX 03-JAN-2002.

XX 26-JUN-2001; 2001WO-US20484.

XX 26-JUN-2000; 2000US-214282P.

XX 29-JUN-2000; 2000US-214955P.

XX 08-FEB-2001; 2001US-267963P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Sprechner CA, Presnell SR, Gao Z, Whitmore TE, Kuiper JJ;

XX Maurer ME;

XX WPI; 2002-090519/12.

XX N-PSDB; ABA93803.

XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
XX useful for treating and diagnosing lymphoid, immune, inflammatory,  
XX splenic, blood or bone disorders.

XX Claim 18: Page 195-197; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17.  
zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
antirheumatic, antiarthritic and muscular activities. The zcytor17  
proteins are useful for treating and diagnosing lymphoid, immune,  
inflammatory, splenic, blood or bone disorders. Agonists or  
anti-zcytor17 antibodies are useful in stimulating cell-mediated  
immunity and for stimulating lymphocyte proliferation, such as in the  
treatment of infections involving immunosuppression, including certain  
viral infections. They are also useful for inducing cytotoxicity and  
for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to  
chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
ABA93843 and ABO5730 to ABO5745 represent sequences used in the  
exemplification of the present invention.

XX Sequence 649 AA;

Query Match 87.1%; Score 3405.5; DB 23; Length 649;

Best Local Similarity 99.1%; Pred. No. 81e-280;

Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

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QY 1 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLTCTWSGKETSTYQYVKKRYA 60
DB 1 MMNTWALMLPDLCKFSLAALPAKPNISCYYYIRKRLTCTWSGKETSTYQYVKKRYA 60
QY 61 FGEKHDNCTNSTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 120
DB 61 FGEKHDNCTNSTSENKASCSFLLPRITPDNTTIEVEANGGVKSHMTYRLNIA 120
QY 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMMEVFAKRRK 180
DB 121 KTEPPKIFRVKPVGLIKRMIOIEMIKPELAPVSSDLKTYTLRFRTVNSTSMMEVFAKRRK 180
QY 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPAPCGLELMRYLKPAAE 240
DB 181 DKNOTYNTGLQPTFEYVIALRCVAKESKFSWDSQEKMGTEEPAPCGLELMRYLKPAAE 240
QY 241 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTNTOLEHLGSEFWV 300
DB 241 ADGRRPVLLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTNTOLEHLGSEFWV 300

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```

Db 241 ADGRPRVRLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLGESFMV 300
QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCI EVMQACVAEDQLVVKQSSALDVNTMIMWF 360
Db 301 SMISYNSLGKSPVATLRIPAIQEKSFQCI EVMQACVAEDQLVVKQSSALDVNTMIMWF 360
QY 361 PDVDSPTTSLMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
Db 361 PDVDSPTTSLMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
QY 421 PSEGETVENIGVATVITTKKEIPKSERKGIICNTTFYQAEKGKSKTYNSSILOYG 480
Db 421 PSEGETVENIGVATVITTKKEIPKSERKGIICNTTFYQAEKGKSKTYNSSILOYG 480
QY 481 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFSVEIILITSLIGGLIILITLVA 540
Db 481 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFSVEIILITSLIGGLIILITLVA 540
QY 541 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
Db 541 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
QY 601 DKLYIDKLVNFGNVLOEIFTDEARTGQENNLGGEKNG---YVTCF 643
Db 601 DKLYIDKLVNFGNVLOEIFTDEARTGQENNLGGEKNGTRLSSCP 646

RESULT 6
AAB51244
ID AAB51244 standard; Protein: 662 AA.
AC AAB51244;
XX 26-MAR-2001 (first entry)
DT
DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.
XX
KM Human: haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KM Immunoregulation; haematopoietic cell regulation; transmembrane;
KM Immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KM metal allergy; pollen allergy.
XX
OS Homo sapiens.
XX
PN WO200075314-A1.
PD 14-DEC-2000.
XX
PE 01-JUN-2000; 2000WO-JP03556.
XX
PR 02-JUN-1999; 99JP-0155797.
PR 30-JUL-1999; 99JP-0217797.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Yaguchi N;
XX WPI: 2001-061720/07.
XX N-PSDB: AAC92350.
DR
XX Hematopoietin receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies.
XX
PS Claim 1: Fig 13-14; 127pp; Japanese.
XX
CC The present sequence represents a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell
CC regulation in vivo, and is useful in searching for haematopoietic
CC factors capable of binding to the receptor. NR10 can be used for the
CC identification of substances for the treatment and prevention of immune

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CC and haematopoietic disorders including autoimmune diseases and allergies
CC such as metal and pollen allergy.
XX
SQ Sequence 662 AA.
Query Match 87.1%; Score 3405.5; DB 22; Length 662;
Best local similarity 99.1%; Pred. No. 8.3e-280;
Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 MMNTWALMLPSLCKFSLAALPARKENISCYYYRKNLTCTWSPEKETSYYQYVKKRYA 60
Db 14 MMNTWALMLPSLCKFSLAALPARKENISCYYYRKNLTCTWSPEKETSYYQYVKKRYA 73
QY 61 FGEKHNDCTTSSSENASCSEFLPRITPDNTYIEEANGDGVISHMTYMRLENIA 120
Db 74 FGEKHNDCTTSSSENASCSEFLPRITPDNTYIEEANGDGVISHMTYMRLENIA 133
QY 121 KTEPPKIFRVRPVLGIRKRIQIEWIKPELAVSSDLKYTLRFRVNSTSMMEVFAKNRK 180
Db 134 KTEPPKIFRVRPVLGIRKRIQIEWIKPELAVSSDLKYTLRFRVNSTSMMEVFAKNRK 193
QY 181 DKNQTYNTLGIQPTFEYVIALRCAYKESKFSNDSQEMMGNTDEEAPCGLEMLRVLAKAE 240
Db 194 DKNQTYNTLGIQPTFEYVIALRCAYKESKFSNDSQEMMGNTDEEAPCGLEMLRVLAKAE 253
QY 241 ADGRPRVRLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLGESFMV 300
Db 254 ADGRPRVRLMKKARGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLELHLGESFMV 313
QY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCI EVMQACVAEDQLVVKQSSALDVNTMIMWF 360
Db 314 SMISYNSLGKSPVATLRIPAIQEKSFQCI EVMQACVAEDQLVVKQSSALDVNTMIMWF 373
QY 361 PDVDSPTTSLMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 420
Db 374 PDVDSPTTSLMESVSQATNMTIQODKLKPFWCYNISYVPMHDKVGPYSIOAYAKGV 433
QY 421 PSEGETVENIGVATVITTKKEIPKSERKGIICNTTFYQAEKGKSKTYNSSILOYG 480
Db 434 PSEGETVENIGVATVITTKKEIPKSERKGIICNTTFYQAEKGKSKTYNSSILOYG 493
QY 481 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFSVEIILITSLIGGLIILITLVA 540
Db 494 LESLKRKTSYIVQVASTSAGTNGTSINFKTLSPFSVEIILITSLIGGLIILITLVA 553
QY 541 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 600
Db 554 YGLKKPNKLTHLCPMTVPNPASSIATWHDGDFKDKLNLKESDSDSVNTEDRILKPCSTPS 613
QY 601 DKLYIDKLVNFGNVLOEIFTDEARTGQENNLGGEKNG---YVTCF 643
Db 614 DKLYIDKLVNFGNVLOEIFTDEARTGQENNLGGEKNGTRLSSCP 659

RESULT 7
AAE24029
ID AAE24029 standard; Protein: 662 AA.
AC AAE24029;
XX 23-SEP-2002 (first entry)
DT
DE Human HPR1 variant protein #3.
XX
KM Human: haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
KM pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
KM neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
KM cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
KM ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
KM osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
KM anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
KM demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;

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KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
 KM ischaemic disease; variant.  
 XX Homo sapiens.  
 OS  
 PN WO200229060-A2.  
 PD 11-APR-2002.  
 XX  
 PF 05-OCT-2001; 2001WO-US31634.  
 XX  
 PR 06-OCT-2000; 2000US-2238706P.  
 PR 13-OCT-2000; 2000US-240476P.  
 PR 20-FEB-2001; 2001US-270282P.  
 XX  
 PA (IMMUNEX CORP.  
 XX  
 PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;  
 DR WPI; 2002-330172/36.  
 XX  
 PT Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,  
 PT useful for treating cell proliferation, metabolic, and reproductive  
 PT hormone related conditions -  
 XX  
 PS Disclosure; Page 112-115; 136pp; English.  
 XX  
 CC The present invention relates to human and murine hematopoietin receptor  
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 CC resulting from a lack of bone-forming cells. They are also useful for  
 CC treating cell proliferation conditions such as leukaemia and tumour  
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
 CC cells. HPR sequences are also useful for treating medical conditions and  
 CC diseases such as cell proliferation, metabolic and reproductive hormone  
 CC related conditions. They are useful for treating various hematologic and  
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,  
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such  
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis  
 CC resulting in tooth loosening or loss, prosthesis loosening after joint  
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,  
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 CC amyotrophic lateral sclerosis, chronic neuronal degeneration, stroke including  
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful  
 CC for treating various other disorders such as osteoporosis, obesity,  
 CC deficient mammary development and infertility. The present sequence  
 CC is human HPR1 variant protein.  
 CC  
 XX  
 SQ Sequence 662 AA;  
 Query Match 87.1%; Score 3405.5; DB 23; Length 662;  
 Best Local Similarity 99.1%; Pred. No. 8.3e-280;  
 Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
 QY 1 MMTWTALMLPSLCFSLALPAKPNISCVYYRKNLTCTWSPGKETSQYVKKRYA 60  
 DB 14 MMTWTALMLPSLCFSLALPAKPNISCVYYRKNLTCTWSPGKETSQYVKKRYA 73  
 QY 61 FGEKHNDCTNNSSTENRASCFFLPRIITPDNTTIEVEANGDGVKSHMTYRLENTIA 120  
 DB 74 FGEKHNDCTNNSSTENRASCFFLPRIITPDNTTIEVEANGDGVKSHMTYRLENTIA 133

QY 121 KTEPKIEFRVYPVIGIKRMIOEMIKPELAPVSSDLKYTLRFRVNSTSMWEVFAKNR 180  
 DB 134 KTEPKIEFRVYPVIGIKRMIOEMIKPELAPVSSDLKYTLRFRVNSTSMWEVFAKNR 193  
 QY 181 DKNOTYNLGLQPFTEVEVALRCVAKESKFWSDMSQEMKMTDEAPCGLELVRVLPAP 240  
 DB 194 DKNOTYNLGLQPFTEVEVALRCVAKESKFWSDMSQEMKMTDEAPCGLELVRVLPAP 253  
 QY 241 ADGRPRVRLMKARCAPVEKTLGNINWYPPSSNTNLETMTNTNOQLEHLGGSFVW 300  
 DB 254 ADGRPRVRLMKARCAPVEKTLGNINWYPPSSNTNLETMTNTNOQLEHLGGSFVW 313  
 QY 301 SMISYNSLGKSPATLIRIPAIQKSPCIEVMQACVADQDLYVKMOSALDVTMTMEF 360  
 DB 314 SMISYNSLGKSPATLIRIPAIQKSPCIEVMQACVADQDLYVKMOSALDVTMTMEF 373  
 QY 361 PDVDSPTLWSVESQATNMTIOODKLKPPWCYNISVYPMLDHDKVGEPSIOAYAKEG 420  
 DB 374 PDVDSPTLWSVESQATNMTIOODKLKPPWCYNISVYPMLDHDKVGEPSIOAYAKEG 433  
 QY 421 PSEGPETKVENIGKYTTITWKEIPKSEKGIICNTYIFQABGKGFSTVWSSIIQYG 480  
 DB 434 PSEGPETKVENIGKYTTITWKEIPKSEKGIICNTYIFQABGKGFSTVWSSIIQYG 493  
 QY 481 LESLKRKTSYIVOMASTSAGTNGTSINFKTISFVFEIILITSLIGGGLITLITVA 540  
 DB 494 LESLKRKTSYIVOMASTSAGTNGTSINFKTISFVFEIILITSLIGGGLITLITVA 553  
 QY 541 YGLKRPKRLHLCPVNPNAESSIATWHDGDKLNLKESDVSNTEDRIILKPCSTPS 600  
 DB 554 YGLKRPKRLHLCPVNPNAESSIATWHDGDKLNLKESDVSNTEDRIILKPCSTPS 613  
 QY 601 DKLYIDLVNFGVNLQEIFTDEARTQENNLGCKNG---YVTCP 643  
 DB 614 DKLYIDLVNFGVNLQEIFTDEARTQENNLGCKNGTRILSCP 659  
 RESULT 8  
 ID ABB05741 standard; Protein: 662 AA.  
 XX  
 AC ABB05741;  
 XX  
 DT 01-MAY-2002 (first entry)  
 XX  
 DE Human zcytor17 protein sequence SEQ ID NO:54.  
 XX  
 KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;  
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200721-A2.  
 PD 03-JAN-2002.  
 XX  
 PD 26-JUN-2001; 2001WO-US20484.  
 XX  
 PF 26-JUN-2000; 2000US-214282P.  
 PR 26-JUN-2000; 2000US-214955P.  
 PR 29-JUN-2000; 2000US-214955P.  
 PR 08-FEB-2001; 2001US-267963P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;  
 PI Maurer MF;  
 XX  
 DR WPI; 2002-090519/12.

DR N-PSDB: ABA93808.

XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is  
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,  
 PI splenic, blood or bone disorders -

XX Example 1: Page 204-206; 235pp; English.

XX The present invention describes a cytokine receptor designated zcytor17.  
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,  
 CC antirheumatic, antirhectic and muscular activities. The zcytor17  
 CC proteins are useful for treating and diagnosing lymphoid, immune,  
 CC inflammatory, splenic, blood or bone disorders. Agonists or  
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated  
 CC immunity and for stimulating lymphocyte proliferation, such as in the  
 CC treatment of infections involving immunosuppression, including certain  
 CC viral infections. They are also useful for inducing cytotoxicity and  
 CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful  
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple  
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,  
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to  
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to  
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the  
 CC exemplification of the present invention.

XX Sequence 662 AA:

Query Match 87.1%; Score 3405.5; DB 23; Length 662;

Best Local Similarity 99.1%; Pred. No. 8.3e-280;

Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

```

QY 1 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKETSQTQYTKRYA 60
DB 14 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKETSQTQYTKRYA 73
QY 61 FGEHNDCTNTSSSENKASCFFLPRTTIPDNTTIEVEANGGVKISHMTYRLNIA 120
DB 74 FGEHNDCTNTSSSENKASCFFLPRTTIPDNTTIEVEANGGVKISHMTYRLNIA 133
QY 121 KTEPPKIFRVPVIGIKRMIOIEMIKPELAPVSSDLKTLFRVNSTSMWEVFAKNRK 180
DB 134 KTEPPKIFRVPVIGIKRMIOIEMIKPELAPVSSDLKTLFRVNSTSMWEVFAKNRK 193
QY 181 DKNOTYNTLGLQPTTEYVIALRCVAKESKFSWDSOEMKMGTEEPACGLELMLVLPKPAE 240
DB 194 DKNOTYNTLGLQPTTEYVIALRCVAKESKFSWDSOEMKMGTEEPACGLELMLVLPKPAE 253
QY 241 ADGRPRVRLMKKARGAPVLEKTLGYNINWYPSNTNLTETMTNTNOOLELHLCGESFW 300
DB 254 ADGRPRVRLMKKARGAPVLEKTLGYNINWYPSNTNLTETMTNTNOOLELHLCGESFW 313
QY 301 SMISYNSIGKSPVATLRIPAIOEKSFQIEYMOACVADOLVVKMOSSALDVNTMIMLMEF 360
DB 314 SMISYNSIGKSPVATLRIPAIOEKSFQIEYMOACVADOLVVKMOSSALDVNTMIMLMEF 373
QY 361 PDVDSPTTISWESVSQATMNTIQODKLPKWCYNISVYPMALHDKVGEPSYQIAYAREGV 420
DB 374 PDVDSPTTISWESVSQATMNTIQODKLPKWCYNISVYPMALHDKVGEPSYQIAYAREGV 433
QY 421 PSEPEPEKVENIGKYTYITWKELPKSEKGTICNTYITFOAEGKGESKTVNSSIIQYG 480
DB 434 PSEPEPEKVENIGKYTYITWKELPKSEKGTICNTYITFOAEGKGESKTVNSSIIQYG 493
QY 481 LESAKRTSYIVQMASTAGCTNGTSINFRTLSFSVEEILLTSLIGGGILLITITLVA 540
DB 494 LESAKRTSYIVQMASTAGCTNGTSINFRTLSFSVEEILLTSLIGGGILLITLVA 553
QY 541 YGLKKPKLTLHLCPYVNPAPASSIATWGDGDKDLNLKESDSDVNTEDRIKPCSTPS 600
DB 554 YGLKKPKLTLHLCPYVNPAPASSIATWGDGDKDLNLKESDSDVNTEDRIKPCSTPS 613
QY 601 DKLYIDLVNFGVNLQEIFTEDEARTGOENNLGGEKNG---YVTCF 643
      |||||||

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DB 614 DKLYIDLVNFGVNLQEIFTEDEARTGOENNLGGEKNGTRILSSCP 659

RESULT 9

ABP54363

ID ABP54363 standard; Protein: 681 AA.

AC ABP54363;

DT 20-JAN-2003 (first entry)

DE Human NR10.3 splicing variant protein SEQ ID NO:2.

KW NR10: splicing variant; haematopoietin receptor; immunomodulator;

KW haematopoietic factor; immunological disease;

KW haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

PN WO200277230-A1.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

PA (CHUS ) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

DR WPI: 2003-018925/01.

XX N-PSDB: ABO83363.

PT NR10 splicing variants of hematopoietin receptor proteins and encoded  
 PT genes, applicable in searching hematopoietic factors and developing  
 PT remedies for immunological and hematopoietic diseases -

PS Example 2: Fig 3; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing  
 CC variants (I). (i) have immunomodulator and haemostatic activities. The  
 CC proteins and encoded genes are applicable in searching for novel  
 CC haematopoietic factors, and developing remedies for immunological and  
 CC haematopoietic diseases. The haematopoietin receptor genes participate  
 CC in in vivo immunomodulation and haematopoietic cell regulation, and in  
 CC the search for haematopoietic factors capable of functionally binding  
 CC to the receptors. The present sequence represents the human NR10.3  
 CC protein from the present invention.

XX Sequence 681 AA:

Query Match 87.1%; Score 3405.5; DB 24; Length 681;

Best Local Similarity 99.1%; Pred. No. 8.7e-280;

Matches 640; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

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QY 1 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKETSQTQYTKRYA 60
DB 33 MMTWALMLPDLCKFSLAALPAKPNISCVYYRKNLTCTWSPGKETSQTQYTKRYA 92
QY 61 FGEHNDCTNTSSSENKASCFFLPRTTIPDNTTIEVEANGGVKISHMTYRLNIA 120
DB 93 FGEHNDCTNTSSSENKASCFFLPRTTIPDNTTIEVEANGGVKISHMTYRLNIA 152
QY 121 KTEPPKIFRVPVIGIKRMIOIEMIKPELAPVSSDLKTLFRVNSTSMWEVFAKNRK 180
DB 153 KTEPPKIFRVPVIGIKRMIOIEMIKPELAPVSSDLKTLFRVNSTSMWEVFAKNRK 212
QY 181 DKNOTYNTLGLQPTTEYVIALRCVAKESKFSWDSOEMKMGTEEPACGLELMLVLPKPAE 240
DB 213 DKNOTYNTLGLQPTTEYVIALRCVAKESKFSWDSOEMKMGTEEPACGLELMLVLPKPAE 272
QY 241 ADGRPRVRLMKKARGAPVLEKTLGYNINWYPSNTNLTETMTNTNOOLELHLCGESFW 300
      |||||||

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|||||
Db 273 ADGRPRVRLMKKARGAPVLEKTLGYNIWYYPESNTNLTETMTNTNOOLEHLGGESEFW 332
OY 301 SMISYNSLGKSPVATLRIPIAIOEKSPFCIEYMOACVADOLVVKMOSSALDVNTWMIEMF 360
Db 333 SMISYNSLGKSPVATLRIPIAIOEKSPFCIEYMOACVADOLVVKMOSSALDVNTWMIEMF 392
OY 361 PDVDSPTLTSWESVSQATNMTIOQDKLKPRWCYNISVYPMHDKVGEPSYIAVAKGV 420
Db 393 PDVDSPTLTSWESVSQATNMTIOQDKLKPRWCYNISVYPMHDKVGEPSYIAVAKGV 452
OY 421 PSEGEPTKVENIGKVTYITWKELPKSERKICITNYITFYAEGGKSKTVNSIIQYG 480
Db 453 PSEGEPTKVENIGKVTYITWKELPKSERKICITNYITFYAEGGKSKTVNSIIQYG 512
OY 481 LESLKRTSYIVQWMASTAGTNGTSINFKTLSPFVEIILITSLIGGLILITLVA 540
Db 513 LESLKRTSYIVQWMASTAGTNGTSINFKTLSPFVEIILITSLIGGLILITLVA 572
OY 541 YGLKPKPKLTHLCWPTVNPAPASSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 600
Db 573 YGLKPKPKLTHLCWPTVNPAPASSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 632
OY 601 DKLVYDKLVNFGVNLQEIFTDEARTGOENNLGGEKNG--YVACP 643
Db 633 DKLVYDKLVNFGVNLQEIFTDEARTGOENNLGGEKNGTRILSSCP 678

RESULT 10
AAB51242
ID AAB51242 standard; Protein: 652 AA.
AC AAB51242;
XX
DT 26-MAR-2001 (first entry)
DE Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.
XX
KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW immunoregulation; haematopoietic cell regulation; transmembrane;
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW metal allergy; pollen allergy.
OS Homo sapiens.
XX
PN WO200075314-A1.
XX
PD 14-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-JP03556.
XX
PR 02-JUN-1999; 99JP-0155797.
PR 30-JUL-1999; 99JP-0217797.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Yaguchi N;
XX
DR WPI: 2001-061720/07.
DR N-PSDB; AAC92337.
XX
PT Hematopoietin receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies -
XX
PS Claim 1; Fig 3-5; 127pp; Japanese.
XX
CC The present sequence represents a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell
CC regulation in vivo, and is useful in searching for haematopoietic
CC factors capable of binding to the receptor. NR10 can be used for the

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CC identification of substances for the treatment and prevention of immune
CC and haematopoietic disorders including autoimmune diseases and allergies
CC such as metal and pollen allergy.
XX
SQ Sequence 652 AA:
Query Match 85.7%; Score 3350; DB 22; Length 652;
Best Local Similarity 99.8%; Pred. No. 4.2e-275;
Matches 628; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 MMTWALMLMPLSLCKFSLALPAPENISCYYYRKNLTCTWSGKESTYQYVKKRYA 60
Db 14 MMTWALMLMPLSLCKFSLALPAPENISCYYYRKNLTCTWSGKESTYQYVKKRYA 73
OY 61 FGEKNDCTTSSSENASCSPFLPRTTIDNTIEVEANGGVKISHMTYRLENTA 120
Db 74 FGEKNDCTTSSSENASCSPFLPRTTIDNTIEVEANGGVKISHMTYRLENTA 133
OY 121 KTEPPKIFRVPVGLIKRMIOIEMIKPELAVSSDLKTYLFRVTNSTWMEVFAKNRK 180
Db 134 KTEPPKIFRVPVGLIKRMIOIEMIKPELAVSSDLKTYLFRVTNSTWMEVFAKNRK 193
OY 181 DKNOTYNLGTQPTFEYIALRCVAKESKFSMDSQEMKGTBEBAPCGELMRYLPAE 240
Db 194 DKNOTYNLGTQPTFEYIALRCVAKESKFSMDSQEMKGTBEBAPCGELMRYLPAE 253
OY 241 ADGRPRVRLMKKARGAPVLEKTLGYNIWYYPESNTNLTETMTNTNOOLEHLGGESEFW 300
Db 254 ADGRPRVRLMKKARGAPVLEKTLGYNIWYYPESNTNLTETMTNTNOOLEHLGGESEFW 313
OY 301 SMISYNSLGKSPVATLRIPIAIOEKSPFCIEYMOACVADOLVVKMOSSALDVNTWMIEMF 360
Db 314 SMISYNSLGKSPVATLRIPIAIOEKSPFCIEYMOACVADOLVVKMOSSALDVNTWMIEMF 373
OY 361 PDVDSPTLTSWESVSQATNMTIOQDKLKPRWCYNISVYPMHDKVGEPSYIAVAKGV 420
Db 374 PDVDSPTLTSWESVSQATNMTIOQDKLKPRWCYNISVYPMHDKVGEPSYIAVAKGV 433
OY 421 PSEGEPTKVENIGKVTYITWKELPKSERKICITNYITFYAEGGKSKTVNSIIQYG 480
Db 434 PSEGEPTKVENIGKVTYITWKELPKSERKICITNYITFYAEGGKSKTVNSIIQYG 493
OY 481 LESLKRTSYIVQWMASTAGTNGTSINFKTLSPFVEIILITSLIGGLILITLVA 540
Db 494 LESLKRTSYIVQWMASTAGTNGTSINFKTLSPFVEIILITSLIGGLILITLVA 553
OY 541 YGLKPKPKLTHLCWPTVNPAPASSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 600
Db 554 YGLKPKPKLTHLCWPTVNPAPASSIATWHDGDFDKLNLKESDSDSVNTEDRILKPCSTPS 613
OY 601 DKLVYDKLVNFGVNLQEIFTDEARTGOE 629
Db 614 DKLVYDKLVNFGVNLQEIFTDEARTGOE 642

RESULT 11
AAE24028
ID AAE24028 standard; Protein: 652 AA.
AC AAE24028;
XX
DT 23-SEP-2002 (first entry)
DE Human HPR1 variant protein #2.
XX
KW Human; haematopoietin receptor; HPR1; HPR2; cell proliferation;
KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
KW ITP; sickle cell vasocclusive crisis; amyloid fibrosis; myeloid metaplasia;
KW osteoclast disorder; peridontitis; acute polyneuropathy; Bell's palsy;
KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;

```

KW	vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
KV	stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
KW	ischaemic disease; variant.
XX	
OS	Homo sapiens.
XX	
PN	WO200229060-A2.
XX	
PD	11-APR-2002.
XX	
PF	05-OCT-2001; 2001WO-US51634.
XX	
PR	06-OCT-2000; 2000US-238706P.
PR	13-OCT-2000; 2000US-240476P.
PR	20-FEB-2001; 2001US-270282P.
XX	
PA	(IMMV ) IMMUNEX CORP.
XX	
PI	Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
XX	
DR	WPI: 2002-330172/36.
XX	
PT	Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
PT	useful for treating cell proliferation, metabolic, and reproductive
XX	hormone related conditions -
XX	
PS	Disclosure; Page 110-112; 136pp; English.

CC The present invention relates to human and murine haematopoietic receptor  
CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
CC resulting from a lack of bone-forming cells. They are also useful for  
CC treating cell proliferation conditions such as leukaemia and tumour  
CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
CC cells. HPR sequences are also useful for treating medical conditions and  
CC diseases such as cell proliferation, metabolic and reproductive hormone  
CC related conditions. They are useful for treating various haematologic and  
CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,  
CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
CC myeloid metaplasia, osteoclast disorders that lead to bone loss such  
CC as osteoporosis including post-menopausal osteoporosis, periodontitis  
CC resulting in tooth loosening or loss, prostheses loosening after joint  
CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,  
CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
CC amyotrophic lateral sclerosis, chronic neuronal degeneration, stroke including  
CC cerebral ischaemic diseases, HPR1 and HPR2 polypeptides are also useful  
CC for treating various other disorders such as osteoporosis, obesity,  
CC deficient mammary development and infertility. The present sequence  
CC is human HPR1 variant protein.

Query Match	85.7%	Score 3350	DB 23	Length 652
Best Local Similarly	99.8%	Pred. No. 4.2e-275		
Matches 628	Conservative 1	Mismatches 0	Indels 0	Gaps 0

QY 1 MMTATLMTLPSCIKESLALPAKPEINISCVYYKKNLTQWSPGKESTYQTYVKTYYA 60  
Db 14 MMTATLMTLMTLPSCIKESLALPAKPEINISCVYYKKNLTQWSPGKETSYQTYVKTYYA 73  
QY 61 FGKHNCNTNSTSPNASCSEFLPRITIPDNTYIEVEANGGVYIKSHMTYRLENTIA 120  
|||||

Dd	74	FGEKHNDCTTNSSTSENRA	SCSEFLPRITIPDNITYIEVA	ENGDCVIXSHMTYRL	ENIA	1333	
Qy	121	KTEPPKIFRKPVPALGI	KRMIOIEMI KPELAPV	SDLKTTLRFRTVNST	SMWEVFAKNRK	180	
Dd	134	KTEBPKIFRKPVPALGI	KRMIOIEMI KPELAPV	SDLKTTLRFRTVNST	SMWEVFAKNRK	193	
Qy	181	DKNOTYNLGLDPFTEY	YIALCAVAKESKFWSD	MSQEKMGTEEDAPCG	LELMRYLPAE	240	
Dd	194	DKNOTYNLGLDPFTEY	YIALCAVAKESKFWSD	MSQEKMGTEEDAPCG	LELMRYLPAE	253	
Qy	241	ADGRPRRLIMKAKAR	APVLEKTYCINIMY	YESNTNLTEMNNT	NOLEHJOGESFW	300	
Dd	254	ADGRPRRLIMKAKAR	APVLEKTYCINIMY	YESNTNLTEMNNT	NOLEHJOGESFW	313	
Qy	301	SMISYNSLGKSPATL	RIAPAIQESFOCIEV	QACVAEDOLVVMK	OSSALDVNTWML	EMF 360	
Dd	314	SMISYNSLGKSPATL	RIAPAIQESFOCIEV	QACVAEDOLVVMK	OSSALDVNTWML	EMF 373	
Qy	361	PVDVSEPTLMSWES	QOATNMTIOQDKL	PWCYNI SVYPM	LHDKVGEPSIQAYAK	EGV 420	
Dd	374	PVDVSEPTLMSWES	QOATNMTIOQDKL	PWCYNI SVYPM	LHDKVGEPSIQAYAK	EGV 433	
Qy	421	PSSGPEPKVENIGV	KVTYITTKKEIPK	SEKGICTYITFY	QAEGBGKFSKTW	SSLIQYG 480	
Dd	434	PSSGPEPKVENIGV	KVTYITTKKEIPK	SEKGICTYITFY	QAEGBGKFSKTW	SSLIQYG 493	
Qy	481	LESJLKRTSYIYO	VMASTAGGTNG	NSINFKLSV	VEIILISLJGGGLI	ILITLVA 540	
Dd	494	LESJLKRTSYIYO	VMASTAGGTNG	NSINFKLSV	VEIILISLJGGGLI	ILITLVA 553	
Qy	541	YGLKRPNKLTJL	HCMPVPNPAP	ESSIATYHGD	DFDKMLKESDS	SVMTEDRI	LKPCSTPS 600
Dd	554	YGLKRPNKLTJL	HCMPVPNPAP	ESSIATYHGD	DFDKMLKESDS	SVMTEDRI	LKPCSTPS 613
Qy	601	DKLVIDKLVYNG	VNLQELFT	DEARTGOE		629	
Dd	614	DKLVIDKLVYNG	VNLQELFT	DEARTGOE		642	

```

RESULT 12
ABP54366
ID ABP54366 standard; Protein: 627 AA.
XX
XX ABP54366;
XX
XX 20-JAN-2003 (first entry)
XX
XX
XX DE Human NR10.5 splicing variant protein SEQ ID NO:8.
XX
XX NR10: splicing variant; haematopoietin receptor; immunomodulator;
XX haemostatic; haematopoietic factor; immunological disease;
XX haematopoietic disease; haematopoietic cell regulation.
XX
XX Homo sapiens.
XX
XX WO200277230-A1.
XX
XX 03-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-JP02769.
XX
XX 26-MAR-2001; 2001JP-0087298.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Maeda M, Yaguchi N, Hasegawa M,
XX
XX WPI: 2003-018925/01.
XX
XX N-PSDB; ABQ83366.
XX
XX
XX NR10 splicing variants of hematopoietin receptor proteins and encoded
XX genes, applicable in searching hematopoietic factors and developing
XX remedies for immunological and hematopoietic diseases -
XX

```

XX Claim 1; Fig 10-12; 250pp; Japanese.

CC The present invention describes haematopoietic receptor NR10 splicing  
 CC variants (I). (I) have immunomodulator and haemostatic activities. The  
 CC proteins and encoded genes are applicable in searching for novel  
 CC haematopoietic factors, and developing remedies for immunological and  
 CC haematopoietic diseases. The haematopoietin receptor genes participate  
 CC in vivo immunomodulation and haematopoietic cell regulation, and in  
 CC the search for haematopoietic factors capable of functionally binding  
 CC to the receptors. The present sequence represents the human NR10.5  
 CC protein from the present invention.

XX Sequence 627 AA;

Query Match 78.7%; Score 3074; DB 24; Length 627;  
 Best Local Similarity 100.0%; Pred. No. 1e-251;  
 Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTWALMMLPSLCKFSLAALPAKPENISCVYYRRKMLCTWSPGKETSTQYTVKRTYA 60  
 |||||||  
 Db 33 MMTWALMMLPSLCKFSLAALPAKPENISCVYYRRKMLCTWSPGKETSTQYTVKRTYA 92  
 QY 61 FGEKHNDCTNNSSTSENKASCSEFLPRITIPDNTTIEVEANGDGVIKSHMTYWRLENIA 120  
 |||||||  
 Db 93 FGEKHNDCTNNSSTSENKASCSEFLPRITIPDNTTIEVEANGDGVIKSHMTYWRLENIA 152  
 QY 121 KTEPRKIFRYKPVVIGIRMIQIEWIKPELAPVSSDLKTYLRFRTVNSTSMWEVFAKNRK 180  
 |||||||  
 Db 153 KTEPRKIFRYKPVVIGIRMIQIEWIKPELAPVSSDLKTYLRFRTVNSTSMWEVFAKNRK 212  
 QY 181 DKNOTYMLTGLQPTTEVIALRCVAKESKFSWDSQKMGTEEEAPCGLELWVLPKPAE 240  
 |||||||  
 Db 213 DKNOTYMLTGLQPTTEVIALRCVAKESKFSWDSQKMGTEEEAPCGLELWVLPKPAE 272  
 QY 241 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTMLTETMNTNOOLEHLGGESEFW 300  
 |||||||  
 Db 273 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTMLTETMNTNOOLEHLGGESEFW 332  
 QY 301 SMISYNSLGKSPVATLRIPAIQESFOCIEMQACVAEDOLVVKWSSALDVTNMTIEMF 360  
 |||||||  
 Db 333 SMISYNSLGKSPVATLRIPAIQESFOCIEMQACVAEDOLVVKWSSALDVTNMTIEMF 392  
 QY 361 PDVDSPTTSLSWESVSQATNMTIQODKLKPFWCYNISVYPMALHDKVEPYSIQAYAREGV 420  
 |||||||  
 Db 393 PDVDSPTTSLSWESVSQATNMTIQODKLKPFWCYNISVYPMALHDKVEPYSIQAYAREGV 452  
 QY 421 PSBGPETKVENIGKVTYITWKEIPKSEKGIICNTYITFYQAEKGKFSKTVNSSIIQYG 480  
 |||||||  
 Db 453 PSBGPETKVENIGKVTYITWKEIPKSEKGIICNTYITFYQAEKGKFSKTVNSSIIQYG 512  
 QY 481 LESIKRRTSYIVQWMASTAGTNGTSINFKTISFSEFEILLTSLIGGLILLITLVA 540  
 |||||||  
 Db 513 LESIKRRTSYIVQWMASTAGTNGTSINFKTISFSEFEILLTSLIGGLILLITLVA 572  
 QY 541 YGLKKPKNLTHLCWTPVNPAAESSIATWHDGDF 574  
 |||||||  
 Db 573 YGLKKPKNLTHLCWTPVNPAAESSIATWHDGDF 606

RESULT 13

ABP54367 ID ABP54367 standard; Protein; 581 AA.

XX ABP54367;

XX 20-JAN-2003 (first entry)

DE Human NR10.6 splicing variant protein SEQ ID NO:10.

KW NR10; splicing variant; haematopoietin receptor; immunomodulator;

KW haemostatic; haematopoietic factor; immunological disease;

KW haematopoietic disease; haematopoietic cell regulation.

XX Homo sapiens.

OS W0200277230-A1.

XX 03-OCT-2002.

PE 22-MAR-2002; 2002WO-JP02769.

XX 26-MAR-2001; 2001JP-0087298.

XX (CHUS ) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

DR WPI; 2003-018925/01.

DR N-PSDB; AB083367.

PT NR10 splicing variants of haematopoietin receptor proteins and encoded  
 PT genes, applicable in searching haematopoietic factors and developing  
 PT remedies for immunological and haematopoietic diseases

PS Claim 1; Fig 13-15; 250pp; Japanese.

CC The present invention describes haematopoietic receptor NR10 splicing  
 CC variants (I). (I) have immunomodulator and haemostatic activities. The  
 CC proteins and encoded genes are applicable in searching for novel  
 CC haematopoietic factors, and developing remedies for immunological and  
 CC haematopoietic diseases. The haematopoietin receptor genes participate  
 CC in vivo immunomodulation and haematopoietic cell regulation, and in  
 CC the search for haematopoietic factors capable of functionally binding  
 CC to the receptors. The present sequence represents the human NR10.6  
 CC protein from the present invention.

XX Sequence 581 AA;

Query Match 74.4%; Score 2908; DB 24; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-237;  
 Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTWALMMLPSLCKFSLAALPAKPENISCVYYRRKMLCTWSPGKETSTQYTVKRTYA 60  
 |||||||  
 Db 33 MMTWALMMLPSLCKFSLAALPAKPENISCVYYRRKMLCTWSPGKETSTQYTVKRTYA 92  
 QY 61 FGEKHNDCTNNSSTSENKASCSEFLPRITIPDNTTIEVEANGDGVIKSHMTYWRLENIA 120  
 |||||||  
 Db 93 FGEKHNDCTNNSSTSENKASCSEFLPRITIPDNTTIEVEANGDGVIKSHMTYWRLENIA 152  
 QY 121 KTEPRKIFRYKPVVIGIRMIQIEWIKPELAPVSSDLKTYLRFRTVNSTSMWEVFAKNRK 180  
 |||||||  
 Db 153 KTEPRKIFRYKPVVIGIRMIQIEWIKPELAPVSSDLKTYLRFRTVNSTSMWEVFAKNRK 212  
 QY 181 DKNOTYMLTGLQPTTEVIALRCVAKESKFSWDSQKMGTEEEAPCGLELWVLPKPAE 240  
 |||||||  
 Db 213 DKNOTYMLTGLQPTTEVIALRCVAKESKFSWDSQKMGTEEEAPCGLELWVLPKPAE 272  
 QY 241 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTMLTETMNTNOOLEHLGGESEFW 300  
 |||||||  
 Db 273 ADGRRPRLMKKARGAPVLEKTLGYNIWYYPESNTMLTETMNTNOOLEHLGGESEFW 332  
 QY 301 SMISYNSLGKSPVATLRIPAIQESFOCIEMQACVAEDOLVVKWSSALDVTNMTIEMF 360  
 |||||||  
 Db 333 SMISYNSLGKSPVATLRIPAIQESFOCIEMQACVAEDOLVVKWSSALDVTNMTIEMF 392  
 QY 361 PDVDSPTTSLSWESVSQATNMTIQODKLKPFWCYNISVYPMALHDKVEPYSIQAYAREGV 420  
 |||||||  
 Db 393 PDVDSPTTSLSWESVSQATNMTIQODKLKPFWCYNISVYPMALHDKVEPYSIQAYAREGV 452  
 QY 421 PSBGPETKVENIGKVTYITWKEIPKSEKGIICNTYITFYQAEKGKFSKTVNSSIIQYG 480  
 |||||||  
 Db 453 PSBGPETKVENIGKVTYITWKEIPKSEKGIICNTYITFYQAEKGKFSKTVNSSIIQYG 512  
 QY 481 LESIKRRTSYIVQWMASTAGTNGTSINFKTISFSEFEILLTSLIGGLILLITLVA 540

Db 513 LESLKRTSYIVQWASTSAGTNGTSINFTLSFSVEEIIITLSLIGGLIIITLVA 572  
QY 541 YGLKRP 546  
Db 573.YGLKRP 578

RESULT 14

AB05743  
ID ABB05743 standard; Protein: 764 AA.

AC ABB05743;

DT 01-MAY-2002 (first entry)

DE Human zcytor17-Fc4 fusion protein SEQ ID NO:69.

XX zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;

KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;

KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;

KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;

KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;

XX inflammatory disease; pancreatitis; inflammatory bowel disease.

OS Homo sapiens.

OS Synthetic.

PN WO200200721-A2.

XX 03-JAN-2002.

PF 26-JUN-2001; 2001WO-US20484.

XX 26-JUN-2000; 2000US-214282P.

PR 29-JUN-2000; 2000US-214935P.

PR 08-FEB-2001; 2001US-267963P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuljper JL;

PI Maurer MF;

XX WPI; 2002-090519/12.

DR N-PSDB; ABA93821.

XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is

PT useful for treating and diagnosing lymphoid, immune, inflammatory,

PT splenic, blood or bone disorders -

XX Example 11; Page 221-223; 235pp; English.

XX The present invention describes a cytokine receptor designated zcytor17.

XX zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,

XX antirheumatic, antiarthritic and muscular activities. The zcytor17

XX proteins are useful for treating and diagnosing lymphoid, immune,

XX inflammatory, splenic, blood or bone disorders. Agonists or

XX anti-zcytor17 antibodies are useful in stimulating cell-mediated

XX immunity and for stimulating lymphocyte proliferation, such as in the

XX treatment of infections involving immunosuppression, including certain

XX viral infections. They are also useful for inducing cytotoxicity and

XX for treating leukopenias. Antagonist of zcytor17 polypeptides are useful

XX for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple

XX sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,

XX pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to

XX chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to

XX ABA93843 and ABB05730 to ABB05745 represent sequences used in the

XX exemplification of the present invention.

XX Sequence 764 AA;

XX Query Match 71.2%; Score 2783; DB 23; Length 764;

XX Best Local Similarity 93.8%; Pred. No. 7e-227;

Matches 525; Conservative 2; Mismatches 9; Indels 24; Gaps 2;

QY 1 MMWTFALMLPDLCKFSLAALPAKPNISCVYYRKNITCTWSPKESSTYQYTKRYA 60

Db 14 MMWTFALMLPDLCKFSLAALPAKPNISCVYYRKNITCTWSPKESSTYQYTKRYA 73

QY 61 FGEKHNDCTNSTSENASCSPFLPRITIPDNTIEVEANGDGVISHHTYMRLEMA 120

Db 74 FGEKHNDCTNSTSENASCSPFLPRITIPDNTIEVEANGDGVISHHTYMRLEMA 133

QY 121 KTEPKIFRVPVIGIKRMIOEWIKPELAVSSDLKTYLFRFVNSTSMMEVFNKRNK 180

Db 134 KTEPKIFRVPVIGIKRMIOEWIKPELAVSSDLKTYLFRFVNSTSMMEVFNKRNK 193

QY 181 DKNQTYNLTGLQPFVEYIALRCVAKESKESFMSQEMKMGTEEPAPCGLELMRYLKA 240

Db 194 DKNQTYNLTGLQPFVEYIALRCVAKESKESFMSQEMKMGTEEPAPCGLELMRYLKA 253

QY 241 ADGRPRVFLMKKARGAVLEKTLGYNTWYYPESNTNLTETMNTNNOOLEHLGSEFNV 300

Db 254 ADGRPRVFLMKKARGAVLEKTLGYNTWYYPESNTNLTETMNTNNOOLEHLGSEFNV 313

QY 301 SMISYNSLGKSPVATLRIPAIQENSFCIEYMQACVADQLVKMQSSALDVNTWMIEMF 360

Db 314 SMISYNSLGKSPVATLRIPAIQENSFCIEYMQACVADQLVKMQSSALDVNTWMIEMF 373

QY 361 PDVSEPTLSMESVQATNMTIOODKLPKPCVNIISVYPMHLKVGEPYSIQAVAKGV 420

Db 374 PDVSEPTLSMESVQATNMTIOODKLPKPCVNIISVYPMHLKVGEPYSIQAVAKGV 433

QY 421 PSEGETVENIGVKTIVITWKEIPKSERKGIICVYTFYQAEKGKFSKTVNSSILOYG 480

Db 434 PSEGETVENIGVKTIVITWKEIPKSERKGIICVYTFYQAEKGKFSKTVNSSILOYG 493

QY 481 LESLKRTSYIVQWASTSAGTNGTSINFTLSFSVEEIIITLSLIGGLIIITLVA 540

Db 494 LESLKRTSYIVQWASTSAGTNGTSINFTLSFSVEEIIITLSLIGGLIIITLVA 532

QY 541 YGLKPNKTLHLCMPTVNP 560

Db 533 --EPKSDKTHTC--PCCPAP 549

RESULT 15

ABP54368  
ID ABP54368 standard; Protein: 549 AA.

AC ABP54368;

DT 20-JAN-2003 (first entry)

DE Human NR10.7 splicing variant protein SEQ ID NO:12.

XX NR10; splicing variant; haematopoietin receptor; immunomodulator;

KW haemostatic; haematopoietic factor; immunological disease;

KW haematopoietic disease; haematopoietic cell regulation.

XX Homo sapiens.

XX WO200277230-A1.

XX 03-OCT-2002.

XX 22-MAR-2002; 2002WO-JP02769.

XX 26-MAR-2001; 2001JP-0087298.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Maeda M, Yaguchi N, Hasegawa M;

XX WPI; 2003-018925/01.

DR N-PSDB; ABQ83368.



xx NR10 splicing variants of hematopoietin receptor proteins and encoded  
pr genes, applicable in searching hematopoietic factors and developing  
pr remedies for immunological and hematopoietic diseases -

xx Claim 1; Fig 16-18; 250pp; Japanese.

xx The present invention describes haematopoietic receptor NR10 splicing  
cc variants (I). (I) have immunomodulator and haemostatic activities. The  
cc proteins and encoded genes are applicable in searching for novel  
cc haematopoietic factors, and developing remedies for immunological and  
cc haematopoietic diseases. The haematopoietin receptor genes participate  
cc in in vivo immunomodulation and haematopoietic cell regulation, and in  
cc the search for haematopoietic factors capable of functionally binding  
cc to the receptors. The present sequence represents the human NR10.7  
cc protein from the present invention.

xx Sequence 549 AA:

Query Match 70.7%; Score 2764; DB 24; Length 549;

Best Local Similarity 99.8%; Pred. No. 1.7e-225;

Matches 515; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MMTWALMPLSLCKFSLAALPAKPENISCVYYRKNLCTWSPCKETSYQYTKRYA 60
   |||
Db 33 MMTWALMPLSLCKFSLAALPAKPENISCVYYRKNLCTWSPCKETSYQYTKRYA 92
   |||

OY 61 FGEKHDNCTNSSTENRASCSEFLPRITIPDNTIEVAENGDCVYKSHMTYRLNIA 120
   |||
Db 93 FGEKHDNCTNSSTENRASCSEFLPRITIPDNTIEVAENGDCVYKSHMTYRLNIA 152
   |||

OY 121 KTEPKIFRVPVLGIRKRIQEWIKPELAPVSDLKXTLRPRTVNSTSMMEVNFKNRK 180
   |||
Db 153 KTEPKITFRVPVLGIRKRIQEWIKPELAPVSDLKXTLRPRTVNSTSMMEVNFKNRK 212
   |||

OY 181 DKNQYNTLGLQPTFEYVIALRCVAEKSEKFSWDSQEKMGTEEPGCLRLRVLPKPAE 240
   |||
Db 213 DKNQYNTLGLQPTFEYVIALRCVAEKSEKFSWDSQEKMGTEEPGCLRLRVLPKPAE 272
   |||

OY 241 ADGRPRVRLMKKAGAPVLEKTLGYNIMYPESNTNLEMTNNTNOOLEHLGSEFPV 300
   |||
Db 273 ADGRPRVRLMKKAGAPVLEKTLGYNIMYPESNTNLEMTNNTNOOLEHLGSEFPV 332
   |||

OY 301 SMISYNSLGKSPVATLRIPAIQEKSFQCIENVQACVAEDQVYKQSSALDVNTWMEWF 360
   |||
Db 333 SMISYNSLGKSPVATLRIPAIQEKSFQCIENVQACVAEDQVYKQSSALDVNTWMEWF 392
   |||

OY 361 PDVDSEPTLLSWESVSQATNMTIQODKLKPFWCYNISVYPMLDHKGVEPYSIQAYAKEGV 420
   |||
Db 393 PDVDSEPTLLSWESVSQATNMTIQODKLKPFWCYNISVYPMLDHKGVEPYSIQAYAKEGV 452
   |||

OY 421 PSEGPEYVENIGVTVITITWKEIPKSEKGLICNTTIFYQAGGKGFSTYVNSSILOYG 480
   |||
Db 453 PSEGPEYVENIGVTVITITWKEIPKSEKGLICNTTIFYQAGGKGFSTYVNSSILOYG 512
   |||

OY 481 LESLKRKTSYIVQVMASTAGTNGTSINFKTLSPS 516
   |||
Db 513 LESLKRKTSYIVQVMASTAGTNGTSINFKTLSPS 548
   |||
```

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Job time : 88 secs

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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:20:42 ; Search time 45 Seconds  
(without alignments)  
1564.344 Million cell updates/sec

Title: US-09-892-949-2  
Perfect score: 3508  
Sequence: 1 MMWTWALMLPISLCKFSLAA.....VFARFLVSEKLPHETKGEV 732

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688.5	17.6	917	2	I49699
2	682.5	17.5	918	2	A44257
3	679.5	17.4	918	2	A36337
4	513.5	13.1	783	2	JH0329
5	506	12.9	863	2	C38252
6	471.5	12.1	837	2	A34898
7	443.5	11.3	771	2	B38252
8	408.5	10.5	1097	2	S17308
9	405.5	10.4	1092	2	JX0332
10	242.5	6.2	1162	2	PC4184
11	231.5	5.9	662	2	I13782
12	231.5	5.9	895	2	S74225
13	227	5.8	1162	2	S68438
14	226	5.7	738	2	I49295
15	221	5.7	900	2	S68440
16	219.5	5.6	830	2	I50455
17	219.5	5.6	892	2	S68439
18	219.5	5.6	894	2	S68437
19	216	5.5	2222	2	T13924
20	207	5.3	636	2	JW0047
21	205	5.2	831	2	JU1655
22	200.5	5.1	610	2	A36116
23	199.5	5.1	610	2	A43631
24	192.5	4.9	1232	2	T43027
25	191	4.9	292	2	I77525
26	191	4.9	303	2	I77524
27	191	4.9	310	2	A29884
28	191	4.9	608	2	I53269
29	188.5	4.8	1898	2	S46216

30	188	4.8	26926	1	I38344	titin, cardiac mus
31	187.5	4.8	581	2	I45971	prolactin receptor
32	187	4.8	412	2	A41070	prolactin receptor
33	185.5	4.7	1894	2	C54689	protein-tyrosine-p
34	182.5	4.7	1897	1	TDHUK	leukocyte antigen
35	180.5	4.6	1691	1	D54689	protein-tyrosine-p
36	176.5	4.5	1912	2	A56178	leucocyte common a
37	175.5	4.5	1290	2	A56453	leucocyte common a
38	175	4.5	843	2	A40970	undulin 1 - human
39	175	4.5	6805	2	S20901	titin - rabbit (fr
40	174.5	4.5	1028	2	I58164	Big-1 protein (fr
41	174.5	4.5	1028	2	A53449	plasmacytoma-assoc
42	174.5	4.5	2481	2	A43908	fibronectin - Afri
43	174	4.5	1197	2	T30581	neural cell adhesi
44	171.5	4.4	805	2	S68441	leptin receptor, s
45	171	4.4	1447	2	A54100	tumor suppressor p

## ALIGNMENTS

## RESULT 1

I49699  
glycoprotein 130 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Jul-2000  
C:Accession: I49699; I48370  
R:Salto, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.  
J. Immunol. 148, 4066-4071, 1992  
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp  
A:Reference number: I48370; MUID:92291532; PMID:1602143  
A:Accession: I49699  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Status: translated from GB/EMBL/DBJ  
A:Residues: 1-917 <RES>  
A:Cross-references: GB:M63336; NID:9193591; PIDN:AAA37723.1; PID:9193592.  
A:Accession: I48370  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-917 <RES>  
A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA44515.1; PID:9840817  
A:Genetics:  
A:Gene: gp130  
A:Superfamily: cytokine receptor homology  
C:Keywords: glycoprotein  
P:134-314/Domain: cytokine receptor homology <CNS>

Query Match 17.6%; Score 688.5; DB 2; Length 917;  
Best Local Similarity 26.5%; Pred. No. 1.2e-41;  
Matches 204; Conservative 130; Mismatches 317; Indels 119; Gaps 24;

QY	22	PAKENICCVYYRKNLTCTSPGKETSY-QGYTKRYTAGEKHNDCTSSSENAS	80
DB	126	PDKPTNLICVINEGKMLCDMPGRETLENYTLKSEMA-TEKRPDCSKHG	179
QY	81	CSF-FLPRTIPDNTTIEVEAENGSGVKSHTWRLFNIAKTEPPKIFRPKPVLGIRK	139
DB	180	CWVSIMPTIYV-NIEVWEADENALGKVSSESINFDPAKKKPPPPYVLSLTNSSELSI	237
QY	140	IQIEWIKDELAPVSSDLKTYLRFRTVNSTSMVEVFAKRRDKDQNTNLGLQPTTEVYI	199
DB	238	LKLSWSSGLGGL-LDKASDIQYRTKASSTMIQVPL-EDTMSPRSPFVQDLKPTTEVYF	295
QY	200	ALRCVAKES--KFSMSDQSEKMGKTEEPAPC-GLEIMRYLKPAAEDGRPPVRLMKKRG	256
DB	296	RIR-SIKSGGKGYMSDEEASGTYIEDRPSRPPSFYKTKSHQEQERSVRLTWKAPL	354
QY	257	APVLEKTIQYINWYPPESNTNLTETMTNTNOOLEHLHGSEFWMSISYSLGSPVATL	316
DB	355	SEANCKIILDIYV--ILTOSKSVSQTYYTGTGLTYNLTNDRIYVSLAARNKVGSAAYL	412
QY	317	RIPALQKSFQCIIEYMQACVAEDOLVYKMOSSALDVNTMTIEMFPDVSPTTISWESVS	376

413 TIPSPHVAAYSVNLKAPKDNLLMVEWTPPPKVSXYILEMVCVLSNAPCEDWMOED 472  
414 QATNNTIOODKLKPPWCXINISVYVPMHDKVGEPSYIOAYAKGVSSEGETVENIGYKT 436  
415 ATVNTHTLGRLLSEKCYQITVTPFATGPGSESLKAYLKOAPARGVTRTKVGNNE 532  
416 VTIWKEIPKSEKRGIIICNYITFYQAEKGKFSKTVNSSILOYGESLKRTSYIVQYMA 496  
417 AVLAWDOI.PVDDQNGFINRYSISYRTSVGKEMVAVDSSHTEYTLSSLSPTLYMVHMAA 592  
418 STSAGCTGTSTINFTLSFSVFEIILLTSLGGGLLIILLTVAYGLKPKPKLHLCPPT 556  
419 YTEDEGKGPPEFTFTLPKFAOGEIAIVPCLAFLLTLLGLVLCFCFKRLDKIKHWP 652  
420 VNPFAESSIATW-----HGDDPKDKLNLKESDSDS-----VNTEDRLKPCSPSPK 603  
421 VPDPSKSHIAQMSPTPRPHNFNSKDM-----YSDGNFTDVSVLEANNKKPC--PDDLK 707  
422 VIDKLNVNFGVNLQEIFTDE--ARTGOENNLG----- 634  
423 SVD-----LFKKKYSTEGHSSGIGSSCMSSSRPSSISSENEASQSTASTV 755  
424 EKNGVYTPFRPDCPLGKSF-----EELPV-----SPEIPPKRSQYLRM 672  
425 EYSTVHSGYRHQVPSYOVFSRSESTOPLDSEERPEDLQLVDSVDSGDELLPRQPYKQ 815  
426 S-----RMPEGTRPEAKCOLLEFSG-----OSLVPHDLCEEGAPNRY 708  
427 NCSQPEACPEISHPERSNOVL--SGNEEDFVRLKQOQVSDHISO-----PY 859

## RESULT 2

Interleukin-6 signal transducing molecule gp130 - rat  
A:Accession: A44257  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Jul-2000  
C:Accession: A44257  
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.  
Genomics 14, 666-672, 1992  
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing  
A:Reference number: A44257; MUID:93052397; PMID:1427893  
A:Accession: A44257  
A:Status: Preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-918 <MAN>  
A:Experimental source: liver  
A:Note: sequence extracted from NCBI backbone (NCBI:118488)  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 17.5%; Score 682.5; DB 2; Length 918;  
Best Local Similarity 27.0%; Pred. No. 3.3e-41;  
Matches 214; Conservative 125; Mismatches 339; Indels 115; Gaps 25;

22 PAKPENISCVYYRKNLCTWSPKETSYSY-TOYTVKRYAFGEKHNDCTNSSTSENRS 80  
126 PDIFNLNLCIYNEGKNNMLCQDPGRFETLETNYTLKSEMA--TEKFPDORTKHGTS----S 180  
81 CSF-FLPRTITPDNTTIVEAENGDVYKSHMTYRLEINAKTEPKTFYKPVGLIKRM 139  
181 CMGCTPIYFV--NIEVWEAENALGNVSEPIINFDPADKKPSPPHMLSTYSEELSSI 238  
140 IOIEMIKELAPVSSDCLKYLRFRYVNSTSMVEVFNKRNKDKNOTYVLTGLOPTEVI 199  
239 LKLWVNSGLDSILR-LKSDIQYRKDASTWIVPL--EDIVSPRTSFVODLKPETEVF 296  
200 ALRCVAVES--KFSWDSQEKMGMTTEEPAC--GLMLVRLKPAEADGRPRLLMKARG 256  
297 RIR-SIKENGKGYMSDSEASGTTIEDRPSKAPSFYKVNANHPQERSRARLLWKTLPL 355  
257 APVLEKTLGVIWYIPESNTNLTETMTNTNOOLELHGGESEFWWSMISYNSLGKSPVATL 316

356 SEANGKILDEYVLTOSKSVQSYTVNCT--ELIYVLTNNRNVASLAARNVYKSPATVL 413  
317 RLPALQESFOCIEVMQACVADOLVYKMOSSALDVNTWMHMEFPDVDSSEPTLSMESVS 376  
414 TIPSGHFRASHPVVDLKAAPPKDNLLMVEWTPPPKVVNNYILEMVCVLSNSPCLIPWMOED 473  
317 QATNNTIOODKLKPPWCXINISVYVPMHDKVGEPSYIOAYAKGVSSEGETVENIGYKT 436  
414 GTVNTHTLGRLLSEKCYLITVTPFPGGPPSPESKAYLKOAPRSKPTVTRTKVGNNE 533  
415 VTIWKEIPKSEKRGIIICNYITFYQAEKGKFSKTVNSSILOYGESLKRTSYIVQYMA 496  
416 AVLEMDHLPVDDQNGFINRYSISYRTSVGKEMVAVDSSHTEYTLSSLSPTLYMVHMAA 593  
417 STSAGCTGTSTINFTLSFSVFEIILLTSLGGGLLIILLTVAYGLKPKPKLHLCPPT 556  
418 YTEDEGKGPPEFTFTLPKFAOGEIAIVPCLAFLLTLLGLVLCFCFKRLDKIKHWP 653  
419 VNPFAESSIATW-----HGDDPKDKL--NLKESDSDS--VNTEDRLKPCSPSPK 606  
420 VPDPSKSHIAQMSPTPRPHNFNSKDMYSDANFTDVSVLEANNKKPC--PDDLKSLD 711  
421 KLVNFGVNLQEIFTDE--ARTGOENNLG-----EKN----- 637  
422 KLVNFGVNLQEIFTDE--ARTGOENNLG-----EKN----- 637  
423 GYVNCFFRPDCPLGKSF-----EELPV-----VSPETPPKRSQYLRM 675  
424 TVVHSGYRHQVPSYOVFSRSESTOPLDSEERPEDLQLVDSVDSGDELLPRQOYFKQSCS 819  
425 PEGTRPE-----AKEOLLEFSQGLVPHDLCEEGAPNRYLNKSTAREF--L 719  
426 QPGASPDVSHRGSRSSQVPSGSEDEDFVRLKQOQVSDHISE-----PY--GSDORRLFOGCS 872  
427 VSEKLPENTKGEV 732  
428 VADALGTGTDCOI 885

## RESULT 3

membrane glycoprotein gp130 precursor - human  
A:Accession: A36337  
C:Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 28-Jul-2000  
C:Accession: A36337  
R:Hihi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.  
Cell 63, 1149-1157, 1990  
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.  
A:Reference number: A36337; MUID:91084844; PMID:2261637  
A:Accession: A36337  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-918 <HIB>  
A:Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354  
A:Gene: GDB:IL6ST; GP130  
A:Cross-references: GDB:126725; OMIM:600694  
A:Map position: 5q11-5q11  
C:Superfamily: cytokine receptor homology  
C:Keywords: glycoprotein; membrane protein  
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 17.4%; Score 679.5; DB 2; Length 918;  
Best Local Similarity 28.4%; Pred. No. 5.5e-41;  
Matches 173; Conservative 113; Mismatches 261; Indels 67; Gaps 16;

22 PAKPENISCVYYRKNLCTWSPKETSYSY-TOYTVK--RTYAFGE--KHD--NCTTN 71  
126 PEKPNLNLCIYNEGKNNKRCDEGRFETLETNYTLKSEMAHKKRADCKAKDPTSCVD 185  
72 STISENRSKCSFELPRTITPDNTTIVEAENGDVYKSHMTYRLEINAKTEPKTFYRV 130  
186 YST-----YFV-----NIEVWEAENALKVSDHINFDPYKVV--KPNPHNLV 230

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QY 131 KPVLGIRKMIQIEMIKELAPVSSDLKYTLRFTVNSTWMEVFAKRRDKNOTYNLTG 190
D 231 INSEELSLIKLWTNPSIKSVII-LKYNQYRTKQASTWSQIP-PEDTASTRSSFLYOD 288
QY 191 LOPPEYVALRCVAESK-FMSDWSOEKMGTEEEAPC-GLEMLRVLKAPEADRRPR 248
D 289 LKPEEYVFRICMKEDGKGYMSDSEASGITYEDRPSKAPSFMYKIDESHQGYRTYQ 348
QY 249 LMKKAGAPVLEKTLGYNWYPESENTNLEMTNTNOOLELHGESEWVSISNSL 308
D 349 LVMKTLRPFEPANGKIDYEVTLTRKSHLONVYNAT--KLTVNLMDRYLATITVRNLV 406
QY 309 GKSPVALTRIPALOESEFQIEVWQACVADOLVKKQSSALDVNTMMIEMFDPVDEPT 368
D 407 GKSDAVALTIPACDFQFTHVMDLKAFKDNMLMVEITTPRESKKKILMECVLSDKAPC 466
QY 369 TLMSESQATNMNTIQQDKLPWCYISYVPMHDKVGEPTYSIOAYAKGVPSEGETK 428
D 467 ITDMQOEDGTVHRFTYELGKNLAESKCYLITVTPYADDPGSPESIKAKLQAPSPKPTVR 526
QY 429 VENIGVTVITTKKEIPKSEKGIICVTLTFQAEKGKFSKTVNSLLOGLESLKRT 488
D 527 TKVYKKEAVLEMDQLPDVQNGFIRNVTTLFTYRTIGNEAVNVDSHTEYTLSTLSDT 586
QY 489 SYIVQVASTSAGTNGTSINFKTLSPFVEIILITSLIGGLILITLVAYGLKRPNK 548
D 587 LYVWMAAYTDEGKQDEFTFTTPKFAQGEIEIAIVPVCLAFLLTLGLVLPFNKRL 646
QY 549 LTHLCWTPVNPASSIATW-----HGDFKDKL----- 577
D 647 IKHIMVNPDPSPSHIAQWSPHPTPRHFNNSKQDMYSDGNFTDVSVEIEANDKRPPE 706
QY 578 NIKESD-----DSVNT 589
D 707 LKSLDLFKKEKINTE 722

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## RESULT 4

```

JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C:Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Sor
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757; PMID:2147944
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <LAR>
A:Cross-references: GB:X55720; NID:g31698; PIDN:CA39252.1; PID:g31699
A:Experimental source: Placenta
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <
F:25-783/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 13.1%; Score 513.5; DB 2; Length 783;
Best Local Similarity 26.8%; Pred. No. 4.9e-29;
Matches 195; Conservative 95; Mismatches 278; Indels 159; Gaps 34;

```

## RESULT 5

```

JH0329
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C:Accession: C38252; A38252; JH0330; A46486; S66332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348; PMID:1701053
A:Accession: C38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FKR>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A:Note: clones pHC11 and pHC5
A:Accession: A38252
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FU2>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A:Note: clone pHC3
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757; PMID:2147944
A:Accession: JH0330

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QY 130 VKPVLGIRKMIQIEMIKELAPVSS-----DKYTLRFTVN--NSTSWME 172
D 235 MDP-----SPEAPRQAGCLOQCEWEPQGLHINQKCELRHHPQGEASMAL 281
QY 173 VNFANRRDKNNQYNTLGTLPFTYVALRC-AVKESEFMSDWSOEKMGTEEEAP-CGL 230
D 282 VG---PLPLALQELCGLLPAPYATLIQICIRMPLEIGHMSDMSPSLELTTERAPVRL 338
QY 231 ELW---RVLPAAEDGRRPRLLMKKARGAPVLE---KTIGYNWYPESENTN-LTETPN 283
D 339 DTMWRQOLDP-----RTVQLEWKP--VPLEDSGRIGGYVSWRPSQACALPLCN 389
QY 284 TTNQOLELHGESEFWVSMTSYNSLGKSPV--ATLRIPALOESEFQIEVWQACVAE 338
D 390 TTLCSTCFHLPSAEQVALVAYNSAGTSRPTPVVFSRSRQALURLH-----AMAR 440
QY 339 D--QLVKKQSSALDVNTW-----MIEFP---PDVDEPTTLTLMSESQATNMNTIQQDKL 389
D 441 DPHSLWGWMEPP-----NPMWQGYVIEWGLGPPSASNSNKTWRMQRNGRATGFLKEN-IR 495
QY 390 PEMCYNISYVPMHDKVGEPTYSIOAYAKGVPSEGETKVENIGVTVITTKKEIPKSER 449
D 496 PQLTEITVTPYODTTPGSOHVAYISQEMAPSHAPLHLKHGKTWAQLEWPEPELG 555
QY 450 KGIICNTYTFQAEKGKFSKTVNSLLOGLESLKRTSYIVQVASTSAGTNGTSIN 509
D 556 KSPITHTYITWTNQNQSFALINASSRGVFLHLEPASLYHLHMAASQAGATNSVLT 615
QY 510 FKTLSPFVEIILITSLIGGLILITLVAYGLKRPNKLTLCWTPVNPASSIATW- 568
D 616 LMTLPREGSELHILGLFGLLLTLCGTAMLCCSPNRKPL-WPSVPPAHNSLGSWV 674
QY 569 -----HGDFK-----DKLNKESD-----DSVNTEDRLKCPSPDKLVYDKL 608
D 675 PTMEEDAFQLPGLGTPPTITLVLEDEKKVPWESHNSE---TGLPT-----L 723
QY 609 VVNFQVLOEITFDEARTGOENNLGCKNGVYTCPPDPCLGKSFEEPLVSPPIPPRS 668
D 724 VQTY--VLQ-----GDPRAVST---QPGQSGNS-----DQAGPPRRS 756
QY 669 QYLRSM 675
D 757 AYFKDQI 763

```



Db 716 SG--NGSLPALVQAVYLQGDPREISNOSQPPSRITGDVLYGVLESPTSGV---MQYI 769  
OY 672 RSRMEGRNP 681  
Db 770 RS---DSTDP 776

## RESULT 7

B38252  
granulocyte colony-stimulating factor receptor precursor (clone pHQ2) - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 05-Nov-1999  
C:Accession: B38252  
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990  
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor receptor.  
A:Reference number: A38252; MUID:91062348; PMID:1701053  
A:Accession: B38252  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-771 <PUNK>  
A:Cross-references: GB:M59819; GB:M38026; NID:9485363; PIDN:AAA63177.1; PID:9485364

Query Match 11.3%; Score 443.5; DB 2; Length 771;  
Best Local Similarity 25.4%; Pred. No. 5.7e-24;  
Matches 189; Conservative 90; Mismatches 297; Indels 169; Gaps 34;

OY 22 PAKENISCVYYRKNTLCTWSBCKETSY--TOYTKRYTAFGEKHNDCTNNSST- 74  
Db 123 PAIHNLSCLE---MNLTSLLICOMEGPETHLPTSTFLKSKFSK---NCOTGDSI 174  
OY 75 -----SENRAKSCFFLPRTIPDNVTIEVEANGDGVKSHMTYRLNIAKTEPKIFR 129  
Db 175 LDCVPKDGQSHCCIPRKHLLIYQMMGLWQAEHALGTSMSPOLCLDPMDVVKLEPPMILT 234  
OY 130 VKPVLGIRMIQIEWKPELAPVSS-----DLKTYLRFRTV--NSTSME 172  
Db 235 MDP-----SPEARPOAGCLOLCWEPWQPLHINOKCELHNRKQORGEASVAL 281  
OY 173 VNFANKRKDKQNTNLGLQPTFEYVIALRC-AVKESKFWSDMSQEKMGTEBEAP-CGL 230  
Db 282 VG---PLPLEALQYELGGLPATYTLQIRCIKMPDPGMSDWSLSLELRTTERAPYVRL 338  
OY 231 ELW---RYLKPAEDGRRPVRLMKKAGAPVLE---KTLGYNIMYIPESNTN-LLETMN 283  
Db 339 DTWKRQOLDP-----RTVQLFMPK---VPLEEDSGRIQGYVSWRSGQAGAILPLCN 389  
OY 284 TTNOOLELHIGGESFWWSMISNLSGNS--PV--ATLRIPAIOEKSFQCLIEVMQCYAE 338  
Db 390 TTETSCFHEHPSEAOEVALVAVNSAGTSRPTPVFSESGPALTRLH-----AMAR 440  
OY 339 D--QLVYKMOSSALDVNTM---MIEWF---PDVDSEPTTILSWESVSQATMTTQOQK 389  
Db 441 DPHSLWGWEP---NPMPOGYVIEWGLGPPSASNSKRTWRMEONGRATFLLEKEN-IR 495  
OY 390 PFCWYNISVYPMLDKDGEPYSIOAYAKEGVSESGEPENKVENIGKVTITIMKEIPKBER 449  
Db 496 PFOLEIITVPLYODTGPQSOHYAYISOEMAPSHAPLHLKHIGKTAQOLMWPEPPPLG 555  
OY 450 KGIICNTIIFYOAGGKGFSTVNSILQYGLSILKRTSYIVOMASTAGTNGTSIN 509  
Db 556 KSPILHTIIFWTNQNQSFALINASSRGFVLHGLEPASTLVHILMAASQAGATSTYLT 615  
OY 510 FKTSFSVFELIILITSLIGGLIILITVAAGLKP---NKLHLKCPYTPNPAESSIA 566  
Db 616 LMTLTPAP-----TGRIPGOVSOTQTLTAAAPCCPCQSWMRMPSSCPALRHSPSS-Q 668  
OY 567 TWHGDDFKDLINKESDSDSVNTEPRILKPCSTPSDKLIDLVVAFGVNLQEIFDEART 626  
Db 669 CW-----RRMKRSRCPGSPITIAQRPVAS----- 691  
OY 627 GOENNLGEGKNGYVTCPE--RPDCPLKSFELPLVSPETIPPKSQYLRSRME- GTRPEA 683

Db 692 -----PLMSRPMCSRGHQ--DQPPSPN--PSLAPAIRSFGSCWAAPQA 732  
OY 684 KEQLLFSGQS-LVPDHLCBEGAPNP 707  
Db 733 QGGGTISAVTPLSPSWRASPPAPSP 757

## RESULT 8

S17308  
leukemia inhibitory factor receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S17308  
R:Gearing, D.P.; Thut, C.J.; Vandembos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Pr  
EMBO J. 10, 2839-2848, 1991  
A:Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 sign  
A:Reference number: S17308; MUID:92007727; PMID:1915266  
A:Accession: S17308  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1097 <GPA>  
A:Cross-references: GB:X61615; NID:934365; PIDN:CAA43805.1; PID:934366

Query Match 10.5%; Score 408.5; DB 2; Length 1097;  
Best Local Similarity 21.3%; Pred. No. 3.4e-21;  
Matches 178; Conservative 139; Mismatches 292; Indels 225; Gaps 40;

OY 22 PAKENISCVYYRKNTLCTWSBCKETSY--TOYTKRYTAFGEKHNDCTNNSSTSE 76  
Db 333 PDTEQQLNCETHDLKEIKSWMNPGRYTALVGPRTSYTLVESFS-GKYVRLKRAEAPNE 391  
OY 77 NRASCFPLRPIITIPDNVTIEVEANGDGVKSHMTYRLNIA-KTEP--PKIFRYKPV 133  
Db 392 SYQLFQMLPQOEL---YNFTLNHNPLG--RSQSTI--LVNITEKYVPHPTSEKVDI 444  
OY 134 LGIKRMIOIEWKPELAPVSSDLKTYLRFRTVNSTSMEV---NFAKNRKD-----KNQ 184  
Db 445 --NSTAVVLSMHLG-----NFAINFLCELEIKNSVQOQRVNTIKGVENS 490  
OY 185 TY--NLGLQPTFEYVIALRCVAKESKFWSDMSQEKMGTEBEAPC-GLEIMRYLKPAEA 241  
Db 491 SYLVALDKLNTYTLTETFRICSTETEFMKWSKMSKQHLTTEASPSKPDTPWR---EWS 547  
OY 242 DGRVRVRLMKKAGAPVLE---KTLGYNIMYIPESNTN-LLETMTTNOOLELHIGGSF 298  
Db 548 DGNKLI-LYMKP---LPINEANGKILSYNSCSDSEPTQSLSETPDQHKAEIRLDKNDY 603  
OY 299 WWSMISYNSLGSKSP---VATLRIPAIOEKSFQCLIEVMQCYAEDQLVYKMOSSALDVNTM 355  
Db 604 IISVAKNSVGSPPSKRIASMEIRPDDLIKIQVOMGKG-----ILTMHYDPRMTCDY 657  
OY 356 MIEWFPVDSEPTTILSWESV--SQATMTTQOQKLPFCWYNISV-----YPMLDKVG 407  
Db 658 VIKMWNSSRSPCLMDMKRVPSNSTETVIESDEFPRGIRYNEFLYGCRCNQGOLLRSMIG 717  
OY 408 EPTISQAARAKGVSEGEPTVENIGVATVITIMKEIKSERKGIICNTIIFYOAGCGKG 467  
Db 718 -----YIEELAPVAPNFTVEDTSADSLVKKWEDIVEELRGFLRGYLYF---GKG 766  
OY 468 FSKTVNSILOYG-----LESILKRTSYIVOMASTAGTNGTSIN 509  
Db 767 ERDTSKMNVLSSGRDIDKVNITDSQKTLNADQGTSTVHLVIRATITDGGVGEKEM 826  
OY 510 FKTSFSVFELIILITSLIGGLIILITVAAGL-----KPNKLTNLCWPTVP 558  
Db 827 VVTKENSV-----GLIATILIPVAVVAVGVVTSILCYRKREMIKETFYPDIP 874  
OY 559 NPAESSITWHDGDKDLINKESDSDSVNTEPRILKPCSTPSDKLIDLVVAFGVNLQEIFDEART 626  
Db 875 NPENCKALOQ-----QKSYCEGSSALKTLE--MNPQ--TNNNEVLELTRSAFPIEDTE 924  
OY 607 -----KLIVNF-----GNVLQEIFTD----- 622

Db 925 IISPAEREDRSDAEPENHVVSYCPPIIEEIPNPADEAGTAQVYIDVQSMYOPQ 984  
 QY 623 -EARTGOENN-LGSGKNGVYTCFPRPD--CPLGKSFEEELPVSPKPSQYLRMRMEG 678  
 Db 965 AKPEEQENDPVGGA--GY-----KPMHLPLNSTVEDIAEEDLD-----KTAG 1027  
 QY 679 TRPEAKEQLFSGQSLVDP-----HLCBEGAPNPYLKNSVTAREFLVSEK 723  
 Db 1028 YRPQAN---VNTWNLVSPDSPRSDSNSEIVSFGSP-----CSINSRQFLIPPK 1073

## RESULT 9

JX0312  
 differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor - mou  
 C:Species: Mus musculus (house mouse)  
 C:Date: 28-Aug-1985 #sequence-revision 07-Oct-1994 #text-change 01-Dec-2000  
 C:Accession: JX0312; J02181; S38942  
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.  
 J. Biochem. 115, 557-562, 1994  
 A:Title: Three different cDNAs encoding mouse D-factor/LIF receptor.  
 A:Reference number: JX0312; MUID:94334302; PMID:8056772  
 A:Accession: JX0312  
 A:Molecule type: mRNA  
 A:Residues: 1-1092 <TOM>  
 A:Cross-references: DDBJ:D26177; NID:9473718; PIDN:BA05165.1; PID:d1005707; PID:g825506  
 A:Accession: J02181  
 A:Molecule type: mRNA  
 A:Residues: 1-717, 'EA' <TOM1>  
 A:Cross-references: DDBJ:D17444; NID:9441493; PIDN:BA04258.1; PID:d1004778; PID:g441494  
 A:Experimental source: Liver  
 R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.  
 FEBS Lett. 334, 193-197, 1993  
 A:Title: Pregnancy associated increase in mRNA for soluble D-factor/LIF receptor in mous  
 A:Reference number: S38942; MUID:94039833; PMID:7901054  
 A:Accession: S38942  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-717, 'EA' <TOM2>  
 A:Cross-references: GB:D17444; NID:9441493; PIDN:BA04258.1; PID:d1004778; PID:g441494  
 C:Keywords: differentiation; receptor; transmembrane protein  
 F:1-43/Domain: signal sequence #status predicted <SIG>  
 F:44-1092/Product: differentiation-stimulating factor/leukemia inhibitory factor recepto  
 F:828-854/Domain: transmembrane #status predicted <TM>

Query Match 10.4%; Score 405.5; DB 2; Length 1092;  
 Best Local Similarity 21.7%; Pred. 5.6e-21;  
 Matches 180; Conservative 131; Mismatches 304; Indels 213; Gaps 36;

QY 22 PAKPENISCVYYRRKRLCTWSPGKESY-----TOYTV-----KRT 58  
 Db 328 PDVPQKLCEETHDLKEIICSNWPGRTGLVGRNTEYTLFESIGKSAVFRIEGLTNET 387  
 QY 59 YAFG-EKHDNCTNSTSENRAISCFILPRITIPNTIYEAEAGDGVISHMITYMLE 117  
 Db 368 YRLGVOMHPGGEIHFFLTGR-----NPLGQAOASAVINYTE 424  
 QY 118 NIAKTEPKIRFVKVPLGKIRMIQIEWIKPELAPVSSDLKYLRLRYTNSMMEVNPFAK 177  
 Db 425 RVAHPDPTSL-KVNDI--NSTVYTFESWYLPG-----NFKTNLNLQIETICAN 469  
 QY 178 NRKD-----KNQYNTLT--GIQPTFEVIALRCVAKSKESKSWDSOEKMGMTTEEA 226  
 Db 470 SKKEVRNATIRGAEDSTYHAVADKLNPYATYFRVRCSSKTFMKWSRMSDEKRHLTTEAT 529  
 QY 227 PC-GELMRVLKPAEADRRVRLMKARCAPVE---KLGVIWITYPESNTNLTETM 282  
 Db 530 PSKGGDTR---EMSSDKNLI-YWKP---LPINANGKILSYVSCSLNEETOSVLEI 582  
 QY 283 NTKNOELHLHGESEFWMSISYSLGSP---VATLRIPALIOEKSFQCIEMQCAVAD 339  
 Db 583 FDPQHRARIQLSKNDYIISVYARNAGSSPSKIASMEIPN-----DITVEQAVGLGN 636

QY 340 QLVAKMOSSALDVTNMTIEMFPDVSDEPTLLSMESV-SQATNMITQODKLPKFWCYNISV 398  
 Db 637 RIFLTHRDPMNMTTCVYIKMKNSSRSPECLDMRVRVPSNSTETVIESQFQGVYRNYFL 696  
 QY 399 YPMLHDKGEPISDIAYAKEGVSPETKVENICVYTTWKETIPSEKGIICNTI 458  
 Db 697 YGCTNOGYQLNRSIIIGVEELAPVAPNPTVEDTSADSLVYMDIDIPVEELGFLRGY-L 755  
 QY 459 FYQAEAGKGESKT-----VSSILQYGLSELSKRTSYIQVMASTAG 501  
 Db 756 FYQKGERDPTKTRBLEPHHSDIKLNITDISOQLR--IADLQKTSIHLVLRVYTHGG 813  
 QY 502 GTNGTSINEKTLFSVFELLITLSLGGCLLILITVAYGL-----KKRNKLT 550  
 Db 814 LGPEKSMFVYRKNSEV-----GLIAILIPVAVAYGVYSILCYRRKRENIK 861  
 QY 551 HLCWPTVVRPAESSIATWHGDDFKRLNLKESDSDVNTEDRLKCSIPSKVLVD--KL 608  
 Db 862 ETEYEDIPNPENCKALQF-----QKSVCEGSNALKTLE--MNPCLPNNVEVLESRSI 911  
 QY 609 VVNFQNVLOEIPPTDEA-RTGOENNLGEGKNGVYTCP-----PRPC----- 648  
 Db 912 VPKIDT--EITSPAERGERSEVDPENHVVSYCPPIIEEIPNPADEAGTAQVYIDVQSMYOPQ 969  
 QY 649 -----PLGKSFEE-----LPVSPETIPPKSQYLRMRMEGTRPEAK 684  
 Db 970 IDVQSMYOPQAKAEEDQVDVYVAGYKPMQLPISPVEDTAAADEGK-TAGYRQAN 1028  
 QY 665 EQLFSGQSLVDP-----HLCBEGAPNPYLKNSVTAREFLVSEK 723  
 Db 1029 --VNTWNLVSPDSPRSDSNSEIVSFGSP-----CSINSRQFLIPPK 1068

## RESULT 10

PC4184  
 leptin receptor, Ob-Rb - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 15-Aug-1996 #sequence-revision 13-Mar-1997 #text-change 01-Dec-2000  
 C:Accession: J04895; J04896; J04897; PC4184; J04797  
 R:Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Ta  
 Biochem. Biophys. Res. Commun. 225, 75-83, 1996  
 A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi  
 A:Reference number: J04895; MUID:96332408; PMID:8769097  
 A:Accession: J04895  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1162 <TAK>  
 A:Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BA12831.1; PID:d1013515; PID:g15  
 A:Accession: J04896  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-889, 'RADTL' <TA2>  
 A:Cross-references: DDBJ:D85557  
 A:Accession: J04897  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-796, 'G', '1157-1158', 'TVLLN' <TA3>  
 A:Cross-references: DDBJ:D85559  
 R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.  
 Biochem. Biophys. Res. Commun. 224, 597-604, 1996  
 A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)  
 A:Reference number: PC4184; MUID:96295531; PMID:8702432  
 A:Accession: PC4184  
 A:Molecule type: mRNA  
 A:Residues: 840-1162 <IID>  
 A:Cross-references: DDBJ:D84550  
 R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.  
 Biochem. Biophys. Res. Commun. 222, 19-26, 1996  
 A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker f  
 A:Reference number: J04797; MUID:96212906; PMID:8630068  
 A:Accession: J04797  
 A:Molecule type: mRNA  
 A:Residues: 1-889, 'RADTL' <I12>



A:Cross-references: DDBJ:D84125; NID:91374707; PIDN:BAAL2230.1; PID:91374708  
 A:Experimental source: adipose cell  
 C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa) rat  
 C:Genetics:  
 A:Gene: fa  
 C:Keywords: appetite; transmembrane protein  
 F:840-860/Domain: transmembrane #status predicted <TM>  
 F:861-1162/Domain: intracellular #status predicted <INT>

Query Match 6.2%; Score 242.5; DB 2; Length 1162;  
 Best Local Similarity 22.0%; Pred. No. 4.2e-09;  
 Matches 170; Conservative 99; Mismatches 305; Indels 199; Gaps 42;

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27 NISC-VYYRKNLCTWSPCKETSYQYTKRYAFGEKHDCNTNS--TSENRAK- 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
431 NISCETGYLTKMKCRKSPSTIOSLVSTVOLRI--HRSILYCPDNPSIRFTESEK-NCV 487
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
82 -----SFLPRITTPDNTTIEVANGDGVKSHMTYRLNENIAKTEPPKIFRYKPV 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
488 LQDGFYECVQRP-IFLSGYTMIIRINHSLSGLSDPTCYLPDSYVYKPLPPS--NYKAE 544
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
134 LGIR-MIQEWIRPELAIVSSDLKYLRFRTVNSTSMVEYNFAKNRKNQTYNLGLQ 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
545 ITITGLIKVSEKPPVP--ENNLOFOIRYGLNGKEIQMKTHEVFDAKSKASLPVSD- 601
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193 PFEYVIALRCVAKES-KFMSDMQSEKMGW-ESEAPC-GLELWRLKPAADGRPPVRL 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
602 -CANYVQVRKRLDGLGIVSNMSSPAYTLMDYKVPGRGPEFRIMDGIITKERNTL 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
250 LMK-----KARGAPVLEKTLGVNIWYIPESN-TNL--ETMNTTNOOLEHLG 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
661 LMKRLMKNDLSVYRVRVYKHTAHNGTWSQDVGNQNLFLMAESAHTVIV-----LAI 715
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
296 ESFVSMISYSLKSPVATIRIPAIQKSFQCIEMQACVAEQOLVYKQSSALDVT- 354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
716 NSIGASLVNENLTFSPMS--KVNAVQ--SLSAVPLSSCV-----ILSWLSPENDYSL 766
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
355 -WMIEW--FPDVSEPTLLSWESVSQATNMTIQQDKLPFCWCYNISYVPMJHDVGEYS 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
767 YLVEMKNLNDG--MKWLRIPSNVKNKYIHDFPIKYOFSLYPVMEGVGKRI 822
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
412 IQAYAKGVPSGE--TKVENIGVKTVT-----ITWKEIPKSEKGI 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
823 INGTCKDIKQONDAGLYVPIIISCVLLGLTLLSHQRMKLFMDVDPNPKN--- 878
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
454 CNRTIFFOABEGKRFKTVNSIIQYGLSKRTSYIVQMASTSAGTNGTSINFKTL 513
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
879 CSWA-----QGLNFQKPEP----- 892
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
514 SFSVEEILL--ITSLIGGLI-----LIILTVANGKK--PNKLTILCMTVPNP 560
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
893 -----FEHLFTKHAASVIFGLLPPEYSEISYDTAKKNDEWPAVMSLL-TPDS 947
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
561 AESSIAFWHGDGDKLNLKESDVSNTEDRIKPC-STPSDKLVTDKLVVNFQNVLOEI 619
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
948 TRGSIC-----ISDQCSANFSGAOSTGCEDECOSQSVKVA--TLVSN---YKT 995
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
620 FTDEARIGQENNLGKNGVYTCFPRPCPLKSFELPVSELPVPRKSOILRSMRPGT 679
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
996 ETDEEQ-----SAIHSSVOCIAKHSPLRQSFSS--NSWEIEAQAFLLSDHPNVI 1046
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
680 RPEAKEQILFSGSLVDPDLCE-EGAPNPYLKNSVTAREFLVSEKLEPHETKGE 731
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1047 SP-----QLSFSGL-----DELLELG-----NFPENHGE 1072
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 11  
 137892  
 IL12 receptor component - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: 137892  
 R:Chua, A.O.; Chizomile, R.; Desai, B.B.; Tuit, T.P.; Nunes, P.; Minetti, L.J.; Warr

J. Immunol. 153, 128-136, 1994  
 A:Title: Expression cloning of a human IL-12 receptor component. A new member of the  
 A:Reference number: 137892; MUID:9426217; PMID:7911493  
 A:Accession: 137892  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-662 <RES>  
 A:Cross-references: EMBL:U03187; NID:9507150; PIDN:AA21340.1; PID:9507151

Query Match 5.9%; Score 231.5; DB 2; Length 662;  
 Best Local Similarity 21.7%; Pred. No. 1.1e-08;  
 Matches 149; Conservative 96; Mismatches 253; Indels 189; Gaps 34;

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8 WMLPSLCKFSLALAPK-----PENISCYIYKKNLCTWSP 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7 WVPPLFLFLSLRGCACRTSECCFQDPYPADSGASGRDLCYRISSDRYECSMQY 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
45 GKETSQYQYTKRYAFGEKHDCNTNSSTENRASCSEFLPRITPDNTTIE--VBAEN 102
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 EGPTAGVSHFLRCLSSG-----RCQYFAGSATPLQ--PSDQGVSVLYITVLWESMA 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
103 GDGVKSHMTYRLNENIAKTEPP-KIFRVKPVGLIKRMIDQEWIKPELAIVSSDLKYL 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 RNQTEKSPREVTLQLYNSVKEPPLGDIKSKLAGQLRM--EMETPD-NQVGAEVQF--R 173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 FRTYNSTSW-----MEVFAKNRDKNOTYLTGLQPTFVIALRC 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
174 HRT-PSSFWKLGDCPODDDTESCLCLEMNAQ-----EFQLRRQ 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
204 AVKSEKFWSDSQ-----EKNG-----MTEEARPCGELWRLKPA 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
215 LGSQSSSKSKSSPVCPENPPQPVRFVSQDGLGGRRLTLKEQTOLEL-----PE 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 EADGRPVRLMKARGAPVLEKTLGVNIWYIPESNLTLETMTTNOOLEHLG----- 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
270 GCOGL-----APGTEVT--YRLQLMHLSCPCKAKART-----LHIGKMPYL 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
295 -GESFVSMISYSLKSPVATIRIPAIQKSFQCIEMQACVAEQOLVYKQSSALDVTN 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
310 SGAATNVAIVSNQFGLNOTWHIPADTHTEPALNI---SVGNGTMTWPAKQSM- 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
354 TWMIETWP-----DVDSEPTLLSWESVSQATNMTIQQDKLPFCWCYN 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
366 TYCIEMQPVGDGLATCSLAPDPPDAGMATWSMESGA-----WQEK-----CYI 416
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
397 SVYPLMDKGEPS--IQAY-----AKGVPSGEPTKVENIGVKTVTITWKEIPKSE 448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
417 TIFASAPHEKLLMTSTVLTSTYHFGMASAAGTPH---HVSYKNHSLDSVSVDMAPSLST 473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
449 RKGITCNTIYQABEGGKFSK-TVNSIILQYGLSKRTSYIVQMASTSAGTNGT 506
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
474 CPGLVKEIVYACRQEDSKQVSEHPQPTETVITSLGACVAYVQVADTAMLRGWSQ 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
507 SINKTILSFSVEEILLITSLIGGLIILITLVAY-GLKRNKLTILCMTVPNPRESSI 565
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
534 PQRF-SIEVQSDMLIFPASFSGFLSILVGLVGLINRARR--HLC-PLLPFPCASSA 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
566 ATWHD-----DFKDKLNKES 582
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
590 IEPFGKETWQINPVDFOEASIOEA 616
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12  
 S74225  
 leptin receptor, isoform Ob-Rf - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 29-Jan-1998 #sequence\_revision 13-Feb-1998 #text\_change 05-Nov-1999  
 C:Accession: S74225  
 R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.  
 FEBS Lett. 392, 87-90, 1996  
 A:Title: A novel leptin receptor isoform in rat.  
 A:Reference number: S74225; MUID:96368027; PMID:8772180  
 A:Accession: S74225



A: Molecule type: mRNA  
A: Residues: 1-738 <RES>  
A: Cross-references: EMBL:U23922; NID:q1046233; PIDN:AAA87457.1; PID:q1046234

Query Match 5.8%; Score 226; DB 2; Length 738;  
Best Local Similarity 20.1%; Pred. No. 3.3e-08;  
Matches 163; Conservative 113; Mismatches 309; Indels 224; Gaps 37;

```
QY 22 PAKENISCVYYKKNLCTW---SPGKETSIVQYVARTAFGKHNC---TINSSTS 75
DB 45 PLGPNNLSGVNKSRTDYCSWQYDQPEDNVSHVLMC-----CVPNNHTTG 91
QY 76 ENRASCSEFF-----LPRTIPDNTTIEEAENGCVIKSHMTYRLNIAKTE 123
DB 92 QER--CRYFSSGPDRTQYFQWEDGIPVLSKYNFVWESLGRNFKSKISQYLYNMTT 149
QY 124 PPKIFRYPVGLIKRMIOIENIKPELAVSSDLKTYLRFRTVNSTSMMEVNFARKN 183
DB 150 PP-LGHK-KVSQSHQQLRMDV-----NVSEBAGAEOVFRMRMPTTN 188
QY 184 QTYNLTGQPT- EYVIALRC-AVKESEF-----WSQWS 215
DB 189 WTLGDCGQVNVSGSLGIDIGCSMSQCLCPSENMAOEIQRRLSSGAPGQWSDMS 248
QY 216 QEKMGMTDEEAPCGLELRLVLPADGR-----PVRLMKKARGAP-----V 259
DB 249 M-PCVPEVLP-QAKIKELVEPLNQGRRRLTMGOSPOLAVPEGCGRGAQYKRLV 306
QY 260 LEKTLGIWYIPESNTNLTMTNTNOOLELHGESFWSMISYNSLGSVPATLRIP 319
DB 307 LVRLM-----SCRCQOTSKTVPPLGKLNLSGATYDLNVLAKTRFGSTIQKMLP 357
QY 320 AIOESFOCIEMQACVADOLVYKWSALDVNTMTTEP-----D 362
DB 368 AOELTETALNV---SVGNNMTSMQWAAQA-PGTYCLEQWQFQHRNHTTCLIVPEE 413
QY 363 VDSEPTLWSVESVQATNMTIQODKIKPFWCYNISVY-----PMLHDKVGEPSIOAY 415
DB 414 DPAKAVTWSWSKP-----TLEQEE---CYRIVFAKSNPKNMALATVLSYFFGN 463
QY 416 A-KEVSESEGPETKVENIGVTYITTKKEIPKSEKGIICNTIYQAEQKGSK-TYN 473
DB 464 ASRAQTPR---HVSVRNQTGDSVSVEWTASQSLCTCPGLQYVVRCEADGEMSEMLVP 520
QY 474 SSIIQGLSESLKRTSYIVQWASTSAGTNGTSINFKTLSPSY--FELLITSLIGGL 531
DB 521 PTKIOVTLIDGLRSRMYKVOYRADTAR--LPEAMSHPRFSFEVOISRSITIFASLGSPA 578
QY 532 LILILIVAY-GLKKPNKLTLCMPTVPNPASSIATWHDGDFKDLNKESSDVSNTED 590
DB 579 SVLLVGSIGYIGLNK-AAAMHLC-PRLPTPGSTAVEFPQSG-----KQAMQMCNED 629
QY 591 RLKACSTPDSKLVLDKLVNFGVNLQELFTDEARTGOENNLGKNGVTCPPRPDCL 650
DB 630 --FPEVLYPRDALVE-----MPGDR----- 648
QY 651 KGSFELVSPETIPRKSOYLRSRMEGTRPEAKRQLLFSQSLVPRDLCEGAPN---- 706
DB 649 GDGTSTPOAAPPCA-----LDTRRPLETOROVOLSEARL--GLAREDCPRGDLA 699
QY 707 ---PYLKNSTVAREFLVSEKLPENTKGE 731
DB 700 HTVLPILLGVTGAGASVLDLMDRTHTKTA 728
```

RESULT 15

S68440  
leptin receptor, splice form Ob-Rd - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 31-Dec-2000  
C:Accession: S68440  
R:Lee, G.H.; Piroenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fu  
Nature 379, 632-635, 1996

A:Title: Abnormal splicing of the leptin receptor in diabetic mice.  
A:Reference number: S68437; MUID:96231997; PMID:8628397

A:Accession: S68440  
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA  
A:Residues: 1-900 <LEE>

A:Cross-references: EMBL:U49109; NID:q1195490; PIDN:ACS2423.1; PID:q1195491

A:Experimental source: tissue hypothalamus  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

C:Keywords: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:  
A:Gene: Ob-Rd  
A:Keywords: alternative splicing; appetite; transmembrane protein

F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 5.7%; Score 221; DB 2; Length 900;  
Best Local Similarity 20.0%; Pred. No. 1e-07;  
Matches 119; Conservative 86; Mismatches 219; Indels 172; Gaps 26;

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QY 27 NISC-VYYRRNLTQTSFGKETSIVQYVARTAFGKHNCNTNS--TSENKASC- 81
DB 431 NISCETDGYLTRKTCRMSPTTQSLVSTVOLRY--HRSLYCPDPSIHPTSEPK-NCV 487
QY 82 -----SFLPRTIPDNTTIEEAENGCVIKSHMTYRLNIAKTEPKIFRVPV 133
DB 488 LQROGFYCVQOP-IFLLSGYTMIRINHSLSGSDSPPTCVLPDSVVKPLPSS--NVKAE 544
QY 134 LGIRK-MIQIEMIKPELAVSSDLKTYLRFRTVNSTSMMEVNFARKNKOYVNLGLQ 192
DB 545 ITVNTGLLKVSEKVFEP--ENNLQFOIRYGLSCKEIQMKTHEVADAKSASLIVSDL- 601
QY 193 PTEVYIALRCVAKES-KFWSQWSQEKMGMT-EEAPC-GLELMLVLPADGRGRRVRL 249
DB 602 -CAVTVQVRCRRDLGLGICVSNWSSPAYTLVMDVAVPMRGPEFMKMGDYTKERNVTL 660
QY 250 LMK-----KARGAVLEKTLGYNIMYPPESN-TNL---TETMTNTNOOLELHGG 295
DB 661 LMKPLTKNDLSQSVRRYVVKHRTAHNGWSEDEVGRNTLTFLMTEPAHT----- 709
QY 296 ESFWYSMTSYNSLGSPPV-----ATLRIPALQEKSFQCIEMQACVADOLVYKWS 347
DB 710 ---VTVALVNSISGLSVNFMNLFSPMPSKVASVE--SLSAVPLSSSCV-----ILSWTL 758
QY 348 SALDVNT--WMTEWPDVDEPTLWSVESVQATNMTIQODKIKPFWCYNISVYPLMDK 405
DB 759 SPDDISLLYLVLEM--KILNEDGKKMLRIPSNAKKFIYIHDFPIEKYQSLYFVMEG 816
QY 406 VGEPSIOAYAKEGVSEGPETKVENIGVTYITTKKEIPKSEKGIICNTIYQAEQK 465
DB 817 VGRPKIINGFTDAIDKO-----QNDAG 839
QY 466 KGFSTVNSIIQYGLSESLKRTSYIVQWASTSAGTNGTSINFKTLSPSYFELLITLS 525
DB 840 L-----YVIPI 846
QY 526 LIGGGLLILITVAYGLKKPNKLTLCMPTVPNPASSIATWHDGDFKDLNKE 581
DB 847 IISCVLLGLTLLISH-----QRMKKLFWDDVPMKNCSSWA--QGLNFQKDISLHE 895
```

Search completed: August 4, 2003, 11:26:06  
Job time : 51 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:17:11 ; Search time 26 Seconds  
(without alignments)  
1323.983 Million cell updates/sec

Title: US-09-892-949-2  
Perfect score: 3908  
Sequence: 1 MMTWALMMLPSLCKFSLAA.....VTAREFLVSEKLPHTKGEV 732

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Swissprot.41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688.5	17.6	917	116B_MOUSE	Q00560 mus musculus
2	682.5	17.5	918	116B_RAT	P40190 rattus norv
3	679.5	17.4	918	116B_HUMAN	P40189 homo sapien
4	517.5	13.2	836	116B_HUMAN	Q09062 homo sapien
5	471.5	12.1	837	116B_MOUSE	P40223 mus musculus
6	408.5	10.5	1097	116B_HUMAN	P42702 homo sapien
7	405.5	10.4	1092	116B_MOUSE	P42703 mus musculus
8	385	9.9	874	112S_MOUSE	P97378 mus musculus
9	383	9.8	862	112S_HUMAN	Q09665 homo sapien
10	242.5	6.2	1162	112R_MOUSE	Q62959 rattus norv
11	231.5	5.9	662	112R_HUMAN	P43701 homo sapien
12	227	5.8	1162	112R_MOUSE	P43356 mus musculus
13	226	5.8	738	112R_MOUSE	Q06837 mus musculus
14	224	5.7	3119	112R_MOUSE	Q06847 mus musculus
15	221	5.7	1165	116B_HUMAN	P40357 homo sapien
16	219.5	5.6	830	116B_HUMAN	Q09374 columba liv
17	208.5	5.3	831	116B_HUMAN	Q02835 cervus elap
18	205	5.2	831	116B_HUMAN	Q04594 gallus gall
19	204	5.2	1165	116B_HUMAN	Q02671 sus scrofa
20	201	5.1	831	116B_HUMAN	Q09104 macaca mla
21	200	5.1	1163	116B_HUMAN	Q09104 macaca mla
22	198.5	5.1	610	116B_HUMAN	P05710 rattus norv
23	191	4.9	608	116B_HUMAN	Q08501 mus musculus
24	189	4.8	581	116B_HUMAN	Q04561 ovis aries
25	188	4.8	639	116B_HUMAN	Q02992 oryctolagus
26	187.5	4.8	581	116B_HUMAN	Q02172 bos taurus
27	185	4.7	3063	116B_HUMAN	Q099715 homo sapien
28	182.5	4.7	1897	116B_HUMAN	P10588 homo sapien
29	176.5	4.5	1912	116B_HUMAN	P23468 homo sapien
30	175.5	4.5	2481	116B_HUMAN	P091740 xenopus lae
31	171	4.4	1447	116B_HUMAN	P43146 homo sapien
32	169.5	4.3	2386	116B_HUMAN	P07551 homo sapien
33	169	4.3	616	116B_HUMAN	P14787 oryctolagus

34	169	4.3	929	1	CA1C_NOTVI	Q01145 notophthalm
35	168	4.3	1238	1	PRPJ_MOUSE	Q04455 mus musculus
36	168	4.3	2029	1	LAR_DROME	P16621 drosophila
37	166	4.2	1447	1	DCC_MOUSE	P70211 mus musculus
38	163.5	4.2	1461	1	NEOL_HUMAN	Q02859 homo sapien
39	162.5	4.2	1377	1	NEOL_RAT	P97603 rattus norv
40	161.5	4.1	2012	1	DECA_HUMAN	Q04469 homo sapien
41	160.5	4.1	2201	1	TENA_HUMAN	P24821 homo sapien
42	159	4.1	2200	1	LAR_CAEEL	Q09008 caenorhabdi
43	158.5	4.1	1328	1	FINC_PLEMA	Q01289 pleurodeles
44	158.5	4.1	2265	1	FINC_BOVIN	P07589 bos taurus
45	158	4.0	424	1	1131_MOUSE	Q09030 mus musculus

## ALIGNMENTS

RESULT 1  
ID IL6B\_MOUSE  
AC Q00560;  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin  
DE 6 signal transducer) (Membrane glycoprotein 130) (GP130).  
GN IL6ST.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ICR, TISSUE=Macrophage;  
RX MEDLINE=92291532; PubMed=1602143;  
RA Saito M., Yoshida K., Hibi M., Tega T., Kishimoto T.;  
RT "Molecular cloning of a murine IL-6 receptor-associated signal  
RT transducer, gp130, and its regulated expression in vivo.";  
RT J. Immunol. 148:4066-4071(1992).  
RL J. Immunol. 148:4066-4071(1992).  
CC - FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR  
CC IL-6, IL-6, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING  
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,  
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,  
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN  
CC EMBRYONIC DEVELOPMENT.  
CC - SUBUNIT: Heterodimer of an alpha and a beta chain.  
CC - TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,  
CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED  
CC EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE  
CC CELLS.  
CC - DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY  
CC 6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES  
CC DURING THE REST OF EMBRYOGENESIS.  
CC - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC - SIMILARITY: Contains 5 fibronectin type III domains.  
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL: X62646; AAA44515.1; -  
CC EMBL: M83336; AAA37723.1; -  
CC PIR: I49699; I49699.  
CC HSSP: P40189; 1B0U.  
CC MGD: MGI:96560; 116st.  
CC GO: GO:0007165; P:signal transduction; IDA.  
CC InterPro: IPR002996; CRIA.

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DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hemtopoptn_L_F2.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 5.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
Repeat.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 917 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 617 EXTRACELLULAR (POTENTIAL).
FT TRASMEM 618 639 POTENTIAL.
FT DOMAIN 640 917 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE.
FT DOMAIN 124 220 FIBRONECTIN TYPE-III 1.
FT DOMAIN 221 322 FIBRONECTIN TYPE-III 2.
FT DOMAIN 323 420 FIBRONECTIN TYPE-III 3.
FT DOMAIN 422 515 FIBRONECTIN TYPE-III 4.
FT DOMAIN 516 611 FIBRONECTIN TYPE-III 5.
FT DOMAIN 723 741 SER-RICH.
FT DISULFID 28 54 By similarity.
FT DISULFID 48 103 By similarity.
FT DISULFID 134 144 By similarity.
FT DISULFID 172 180 By similarity.
FT DISULFID 426 464 By similarity.
FT CARBOHYD 43 43 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAc. . .) (POTENTIAL).
SQ SEQUENCE 917 AA; 102452 MW; FCEFD20BC2466f4 CMC64;

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Query Match 17.6%; Score 688.5; DB 1; Length 917;
Best Local Similarity 26.5%; Pred. No. 1.6e-44;
Matches 204; Conservative 130; Mismatches 317; Indels 119; Gaps 24;

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22 PAKPNISGVYVYRNLCITMSPGKETSF-TOYTVKRYVAGEGKIDNCTNSTSENAS 80
126 PDKPNTLNCIVNEGKMLCQMDPGRETYLETWTYTKSEMA-TEKPPDOCKSGT-----S 179
81 CSF-FLPRITPDNTYIEVEANGDGVKSHMTYRLNIAKTEPKIFRYKPVLGIRKM 139
180 CMVSTMPYTYV--NIEVWVEAENALGKVSSEINPDVKYPTPPYNLSTVNSELSI 237
140 IQEIKPELAPVSSDLKTYLFRVNSTSMVEVFAKNRKDKNTYNLGTQPTTEYVI 199
238 LKLSWSSGLGL-LDLKSDIOYRKDASTWIQVL-EDTMSPTSTFVODLKPTTEYVF 295
200 ALKCAVKES--KFNWSDMSQEKMGMTSEAPC-GLELMVRLKPAEADGRPVLLKKARG 256
296 RIR-SIKSGKGYWDSDEASGTYEDRPSRPFWKTNPSHQEKRVRLLIKALPL 354
257 APVLEKTLGVNIWYIPESNTNLTTMTNTNOQLHLHGCESEFWMSISYLSGKSPVATL 316
355 SEANGLIDYEV--ILTQSKSVSQTYTYGTGLVNLNDRVYLAARNKVKSAAVL 412
317 RIPAQEKSFQCIEMQACVAEDOLVVKWSSALDVNTWMLMEFPDVUSEPTITLSEVVS 376
413 TTPSPHTAAVSYNLKAFPKDNLLMWTMPPPKVSAFYIIEWCYLSNACVDEMOED 472
377 QATWNTIQODKLKPPMCYNISVYPLHDKVGEPSYIQAYAKGVSEPEKVENIGYKT 436
473 ATVNTHTLRGRLEBKCYQITVTFATGPGSESLAKYLQOAPARPTVTKTKVGVNE 532
437 VTIWKEIPKSGERKGIICNYTIFYQAEKGKFSKTVNSIIQYGLSLKRTSYIVQYA 496
533 AVLAMDQIPVDONQFINRYSISYTSYKEMVAVHDSHREYTLSSLSPTLVVMAA 592
497 STSAGCTGTSTNFTILSFVFEIILTLISLGGGLIILITLVAYGLKKPKLHLCPPT 556

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DB 593 YTDEGKDGPFEFTTPPKFAQGEIAYVPCIAFLITLLGLVLCFCKNRDLKHKHWP 652
QY 557 VNPAPSSIAIYW-----HGDFPKDKLNKESDSS-----VNTEDILKPCSTPSOKL 603
DB 653 VPDPSKSHIAQWSPHTPPRHNFNSKDM---YSDGNFTDVSVETEANNKPC--PDOLK 707
QY 604 VIDKLIVNFGNVLQEIFTDE--ARTGOENLGC----- 634
DB 708 SVD-----LFFKEKYSTEGSHSGGSCSSCMSSSRPSISSNEENASOSTASTV 755
QY 635 EKNGVTCPPRPDPLGKSF-----EELPV-----SPEIPRKSOYLK 672
DB 756 EYSTVHSHGGRQVPSVQVFSRSESTOPLDSEEPEDLQIVDSYDGDDELIPROPYKQ 815
QY 673 S-----RMPEGRPREAKCOLLEFGS-----GSLVDDHICEBAPPY 708
DB 816 MCSQEPACPEISHFRSMQVL-SGNEEDPVRLKQOOVSDHLSQ-----PY 859

RESULT 2
IL6B_RAT STANDARD: PRT: 918 AA.
ID IL6B_RAT
AC P40190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130."
RL Genomics 14:666-672(1992).
CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M92340; -; NOT_ANNOTATED_CDS.
CC PIR: A44257; A44257.
CC HSSP: P40189; 1B0U.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hemtopoptn_L_F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 4.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;

```

```

KW Repeat. 1 22 POTENTIAL.
FT SIGNAL 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT CHAIN 23 618 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 619 640 POTENTIAL.
FT TRANSMEM 641 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE.
FT DOMAIN 124 221 FIBRONECTIN TYPE-III 1.
FT DOMAIN 222 323 FIBRONECTIN TYPE-III 2.
FT DOMAIN 324 422 FIBRONECTIN TYPE-III 3.
FT DOMAIN 423 516 FIBRONECTIN TYPE-III 4.
FT DOMAIN 517 612 FIBRONECTIN TYPE-III 5.
FT DOMAIN 724 754 SER-RICH.
FT DISULFID 28 54 By similarity.
FT DISULFID 48 103 By similarity.
FT DISULFID 134 144 By similarity.
FT DISULFID 172 181 By similarity.
FT DISULFID 457 465 By similarity.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FEFCF087E7 CRC64;

```

```

Query Match 17.5% Score 682.5; DB 1; Length 918;
Best Local Similarity 27.0%; Pred. No. 4.5e-44;
Matches 214; Conservative 125; Mismatches 339; Indels 115; Gaps 25;

```

```

OY 22 PAKENISCVYVYRNKLTCTWSPEKETS-TOYVRYTAGEKHNDCTNSSTSENKAS 80
DB 126 PDIPNTSCIVNEGNMQLQDPRGRETLETNYTLKSSMA-TEKPPDCRTKHGTS----S 180
OY 81 CSF-FLPRITIPDNTTIVEAENGDDGVKSHMTYRLNLEAKTEPKLFRKPVLCIRM 139
DB 181 CMGCTPIYFV--NLEVVVEAEMALGNVSSSEPIINDPVKPKPSPHNLSTVNSELSI 238
OY 140 IOIEWIKPELAPVSSDLKYTLRFTVNSTSMWVEFAKNRKDKNOTYMLTGLOPTEVYI 199
DB 239 LKLANVNSGLDSILR-LKSDTQYRKDASTNIQVPL-EDYSPKTSFVQDLKPTTEYF 296
OY 200 ALRCAYKES--KFSWDSQOEKMGMTDEEAPC-GELMRYLKPAAEDGRRPVALLKKARG 256
DB 297 RIR-SIKENKGGYMSDEEASGTYEDRPSKAPSFYKVVANHPQEVRSARLIMKTLPL 355
OY 257 APVLEKTYGNIWYPPESNTNITEFMTNTNOOLEHLOGESVWWSMISYLSGKSPVATL 316
DB 356 SEANKKILDEYVLTQSKSVSQTYYVNGT--ELVLTNNRNVASLAAARNVYKSPAYVL 413
OY 317 RIPAIQESFOCIEWQACVAEDOLVVKMOSSALDVNTMIEMFADVSEPTTLESMSVS 376
DB 414 TTPGHFKASHPYVDLKAFPKDNLLWEMTPSPKVNKYLIEMCVLSSENSFCIPWQOED 473
OY 377 QATMTTIOQDKLKPEWKNISVYPMILHDVGEPPYSIOAYAKEGVSEGEPTVENIGYKT 436
DB 474 GTVNRTHLRGSLLESKCYLITVYFPGPGSPBEMKAYLQAAAPSKGPTVATKVGKNE 533
OY 437 VTITKELPKSERKCIITNYTIFYOAGKGFSTVNSIIQGLSLKRTSYIYOVA 496
DB 534 AVLEMDHLPIVYVQNFIRNYSYRTSVGKEVNVVDSHREYTLSSSDTLVYVHMA 593
OY 497 STSAGTGTSTINERTLSFSVEEILITSLGGGLILITLVAAGLKKPKNLTHLCMPT 556
DB 594 YTEBGKRGKPEFTTTLKFAQGEIATVYPCVLAFLITLLGLVLCFCKNRDLIKHINPN 653
OY 557 VNPFAESSIATW-----HGDDFKDKL--NLKESDGS-VNTEDRILKCPSTPSDKLYD 606

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DB 654 VPDPKSHIAQWSPHTPRHNFSKQWYSDANFTDVSVEIEANKKPC--PDDLKSLD 711
OY 607 KLVNFGVNDIEITFDE--ARTGOENNLGG-----EKN----- 637
DB 712 -----LFEKKEISTEGHSGIGGSSCMSSNRPSISSSEBNSAOSTASTVOYS 759
OY 638 GYVTCPPRPDPCPLGKSF-----EELP-----VSEIIPPKSOYLRSRM 675
DB 760 TVHSGYRHOQVPSVOVESRSESTOPLDSEERPEDLQVDSGDELLPPOQYTFKQSCS 819
OY 676 PEGTRPE-----AKEDLLFSGQSLVPDHLCEGAPNPYLKNSVYAREF---L 719
DB 820 QPASPVDVSHRGRSSQVPSGSEDEPVRLLKQOQVSDHISE-----PY--GSGQRLYFCQGS 872
OY 720 VSEKIPHTKGEV 732
DB 873 VADALGTGTGDOI 885

RESULT 3
ID IL6B_HUMAN STANDARD; PRT; 918 AA.
AC P40189; G90Q41;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein I30) (GPI30) (Oncostatin M
DE receptor) (CDW130) (CD130 antigen).
GN IL6ST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Myeloma, and Placenta;
RX MEDLINE=91084844; PubMed=2261637;
RA Hihi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130."
RL Cell 63:1149-1157(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Synovium;
RX MEDLINE=20341529; PubMed=10880057;
RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RT "Cloning of novel soluble gp130 and detection of its neutralizing
RT autoantibodies in rheumatoid arthritis."
RL J. Clin. Invest. 106:137-144(2000).
RN [3]
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=21269388; PubMed=11098061;
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
RT "Determination of the disulfide structure and N-glycosylation sites of
RT the extracellular domain of the human signal transducer gp130."
RL J. Biol. Chem. 276:8244-8253(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
RX MEDLINE=98169383; PubMed=9501088;
RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130."
RL EMBO J. 17:1665-1674(1998).
CC -I- FUNCTION: Signal-transducing molecule. The receptor systems for
CC IL-6, LIF, OSM, CNTF, IL-11 and CT-1 can utilize gp130 for
CC initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)
CC complex, resulting in the formation of high-affinity IL-6 binding
CC sites, and transduces the signal. Does not bind IL-6. May have a
CC role in embryonic development (By similarity).
CC -I- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).

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CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1:
CC IsoId=P40189-1; Sequence=Displayed;
CC Name=2: Synonyms=GPI30-RAPS;
CC IsoId=P40189-2; Sequence=VSP_001684, VSP_001685;
CC -1- TISSUE SPECIFICITY: Found in all the tissues and cell lines
CC examined. Expression not restricted to IL-6 responsive cells.
CC -1- DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
CC (RA) but it is not specific to patients with RA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD130 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M57230; AA59155.1; -
DR EMBL: AB015706; BAA78112.1; -
DR PIR: A36337; A36337.
DR PDB: 1B0U; 26-AUG-98.
DR PDB: 1HJ8; 13-JAN-99.
DR PDB: 1IIR; 28-MAR-01.
DR GeneW: HGNC:6021; IL6ST.
DR MIM: 600694; -
DR GO: GO:0005887; C:Integral to plasma membrane; TAS.
DR GO: GO:0004988; F:gpi30; TAS.
DR GO: GO:0004924; F:oncostatin-M receptor activity; TAS.
DR GO: GO:0004872; F:receptor activity; TAS.
DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
DR GO: GO:0006955; P:immune response; TAS.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hemtopopt_L_F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 4.
DR PROSITE: PS01533; HEMATOPO_REC_L_F2; 1.
DR KMW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
DR Repeat; 3d-structure; Alternative splicing.
KW SIGNAL
FT 1 22
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 620 641 POTENTIAL.
FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE.
FT DOMAIN 124 222 FIBRONECTIN TYPE-III 1.
FT DOMAIN 223 324 FIBRONECTIN TYPE-III 2.
FT DOMAIN 325 423 FIBRONECTIN TYPE-III 3.
FT DOMAIN 424 517 FIBRONECTIN TYPE-III 4.
FT DOMAIN 518 613 FIBRONECTIN TYPE-III 5.
FT DOMAIN 725 755 SER-RICH.
FT DISULFID 28 54
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 182
FT DISULFID 458 466
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .).
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .).
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .).
FT VARSPLIC 325 329 RPSKA -> NIASF (in isoform 2).

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FT VARSPLIC 330 918 /FTID=VSP_001684.
FT STRAND 130 137 Missing (in isoform 2).
FT TURN 138 139 /FTID=VSP_001685.
FT STRAND 143 147
FT STRAND 157 164
FT TURN 165 166
FT STRAND 167 168
FT STRAND 172 173
FT TURN 179 180
FT STRAND 181 183
FT TURN 190 191
FT STRAND 194 202
FT TURN 203 204
FT STRAND 205 208
FT STRAND 212 214
FT HELIX 216 218
FT STRAND 220 221
FT STRAND 226 231
FT STRAND 240 245
FT HELIX 248 251
FT TURN 252 252
FT STRAND 255 263
FT TURN 264 265
FT STRAND 270 271
FT HELIX 274 277
FT STRAND 283 286
FT STRAND 293 303
FT TURN 304 305
FT STRAND 317 321
FT HELIX 325 331
SQ SEQUENCE 918 AA; 103522 MW; D813F3672D010D53 CRC64;

Query Match 17.4%; Score 679.5; DB 1; Length 918;
Best Local Similarity 28.4%; Pred. No. 7.7e-44;
Matches 175; Conservative 113; Mismatches 261; Indels 67; Gaps 16;

22 PAKPENISCVYYRRNLCTNSPGKETS-TOYTVK---RYYAFGE---KHD---NCTTN 71
126 PEKPNLSCIVNEGKKMKCEMDGGRHLEHNFILTKSEKAIHKFPADCAKRDTPISCTVD 185
72 SSTSERNRSCSEFLRPIITPDNYTIEVEANGDVYKS-HMTYRLNIARTTEPKIRFY 130
186 YST-----YEFV-----NIEVVAEAMALGKVTSDHINFDVYKV-KPNPNHLSV 230
131 KPVLGIRKMIQIEMIKPELAPVSSDLKTYLFRFVYNSISMEAEVNAKRRKKNQYINLTG 190
231 INSEELSSILKLTWTNPISIKSVII-LKYNIQYRTYDASTWSQIP-PEDTASTRSSFFYQD 288
191 LQPFEEVIALRCAYKESK-FWSDMSQKMGMTTEEAFC-GLELWRVLKPAEADGRPRVR 248
289 LKPFIEVYFRIRKMEDEKGYMSDEASGITTYDRSKAPSFYKIDPSHTQGYRIVQ 348
249 LLMKRCAPVLEKTLGYINWYYPESNTLTETMNTTNOOLELHLCGESFVWSMISYSL 308
349 LVMKTLPEFEANGKILIDYEVTLTRKSHLQNTVNAI--KLTVNLTDNRVYLATLVRLMV 406
309 GKSPATIRIPALIOKSKOCIEVMQACVAEDQLVYKMSALDVNTWMIEMFPPVDSEPT 368
407 GKSDAAVLTIPACDFQAAHPVMDLKAFPKDKMLVEMWTTPRESVKKYILLECVLSDKAPC 466
369 TLSMESVSQATNMTTIOQOKLKPFMCYNISVYPMILDKVGEPSIOAVAKEGVSPSGPETK 428
467 ITDMQDEGTYHRTILRGNLASEKCYLITVPVYADGSGSPESIKAYIKQAPSGPVR 526
429 VENIGVKTVTITWKEIPKSEKGIICNTIFYOAGGSGFKYVNSITLQGLSKRKRT 488
527 TKVQKNDAVLEMDQLPDVQNGFIRNYYIFRTIIGNETAVNVDSSHTETLSLSDT 586
489 SYIVQVMASTAGGNGISINFKTLSESVFELLITLSLGGGLLILITLYAVYGLKRNK 548
587 LYWRMAAYVTDEGGKDGDEFTTTPPKFAQGEIAEIVAVCLAFLLTLLGLVLCFENKRD 646

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OY 549 LTHLCMPVNPAPSAESSIATW-----HGDFKDKL----- 577
DB 647 IKKHMPVNPDPKSHIOWMSPHPRHNFNSKDMYSDGNNTDVSVEIENDKKPPPE 706
OY 578 NIKESD---DSVNT 589
DB 707 DLKSIDLFRKKEKINTE 722

RESULT 4
GCSR_HUMAN STANDARD: PRT: 836 AA.
AC 099062;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Granulocyte colony stimulating factor precursor (G-CSF-R)
DE (CD114 antigen).
DE CSF3R OR GCSR.
GN CSF3R (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91079757; PubMed=2147944;
RA Larsen A., Davis T., Curtis B.M., Sims J.E., Cosman D.,
RA Park L., Sorensen E., March C.J., Smith C.A.;
RT "Expression cloning of a human granulocyte colony-stimulating factor
RT receptor: a structural mosaic of hematopoietin receptor,
RT immunoglobulin, and fibronectin domains.";
RL J. Exp. Med. 172:1558-1570(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91062348; PubMed=1701053;
RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;
RT "Three different mRNAs encoding human granulocyte colony-stimulating
RT factor receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92091782; PubMed=1530796;
RA Seto Y., Fukunaga R., Nagata S.;
RT "Chromosomal gene organization of the human granulocyte colony-
RT stimulating factor receptor.";
RL J. Immunol. 148:259-266(1992).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS THR-231; ASN-320; ARG-346; LYS-405;
RX GLN-440; HIS-510; HIS-562 AND CYS-583.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS STRUCTURE.
RX MEDLINE=92007729; PubMed=1717255;
RA Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;
RT "Functional domains of the granulocyte colony-stimulating factor
RT receptor.";
RL EMBO J. 10:2855-2865(1991).
RN [6]
RP DISEASE.
RX MEDLINE=94240159; PubMed=7514305;
RA Dong F., Heefstoot L.H., Schelen A.M., Broeders C.A., Meijer Y.,
RA Veerman A.J., Touw I.P., Lowenberg B.;
RT "Identification of a nonsense mutation in the granulocyte-colony-
RT stimulating factor receptor in severe congenital neutropenia.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4480-4484(1994).
RN [7]
RP STRUCTURE BY NMR OF 227-334
RX MEDLINE=97331377; PubMed=9187659;

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RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
RT "Solution structure of an extracellular domain containing the Wxxxs
RT motif of the granulocyte colony-stimulating factor receptor and its
RT interaction with ligand.";
RL Nat. Struct. Biol. 4:498-503(1997).
RN [8]
RP 3D-STRUCTURE MODELING OF 125-331.
RX MEDLINE=98037802; PubMed=9368043;
RA Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;
RT "Identification of a ligand-binding site on the granulocyte colony-
RT stimulating factor receptor by molecular modelling and mutagenesis.";
RL J. Biol. Chem. 272:29735-29741(1997).
CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
CC EVENTS AT THE CELL SURFACE.
CC -1- SUBUNIT: DIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
CC OF THE RECEPTOR.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Comment-Additional isoforms seem to exist. Experimental
CC confirmation may be lacking for some isoforms;
CC Name=1; Synonyms=GCSFR-1;
CC IsoId=Q99062-1; Sequence=Displayed;
CC Name=2; Synonyms=GCSFR-2;
CC IsoId=Q99062-2; Sequence=VSP_001674;
CC Name=3; Synonyms=GCSFR-3;
CC IsoId=Q99062-3; Sequence=VSP_001673;
CC Name=4; Synonyms=GCSFR-4, D7;
CC IsoId=Q99062-4; Sequence=VSP_001671, VSP_001672;
CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
CC MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES. THE
CC GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
CC DISEASE: Defects in CSF3R might be a cause of severe congenital
CC neutropenia (SCN) in some patients.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD114 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
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CC -----
DR EMBL; X55721; CAA39253.1; -
DR EMBL; X55720; CAA39252.1; -
DR EMBL; S71484; AAB20660.1; -
DR EMBL; M59818; AAB31766.1; -
DR EMBL; M59819; AAB31777.1; -
DR EMBL; M59820; AAB31781.1; -
DR EMBL; A1146100; AAN05790.1; -
DR PIR; B38252; B38252.
DR PIR; C38252; C38252.
DR PIR; JH0329; JH0329.
DR PDB; 1A27; 28-JAN-98.
DR Genew; HGNC:2439; CSF3R.
DR MIM; 138971; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; E:receptor activity; TAS.
DR GO; GO:0006952; P:defense response; TAS.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hemtopoptn_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 2.

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RX MEDLINE-97331327; PubMed-9187659;  
RA Yamaeaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;  
RT "solution structure of an extracellular domain containing the MSXMS  
RT motif of the granulocyte colony-stimulating factor receptor and its  
RT interaction with ligand";  
RL Struct. Biol. 4:498-504(1997).  
CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN  
CC ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT  
CC THE CELL SURFACE.  
CC -1- SUBUNIT: DIMER (PROBABLE).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: FOUND IN BONE MARROW.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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CC -----  
DR EMBL: M58288; AAA37673.1; -  
DR PIR: A34898; A34898.  
DR PDB: 1GCF; 22-OCT-97.  
DR PDB: 1CNO; 22-OCT-97.  
DR PDB: 1CD9; 08-MAR-00.  
DR PDB: 1PGR; 08-MAR-00.  
DR MGD: MGI:1339755; Csf3r.  
DR GO: GO:0030593; P:neutrophil chemotaxis; IMP.  
DR InterPro: IPR002996; CRIA.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
DR Pfam: PF00041; fn3; 3.  
DR SMART: SM00060; FN3; 2.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
DR Cell adhesion: Receptor; Repeat; Signal; Transmembrane;  
KM Immunoglobulin domain; Glycoprotein; 3D-structure.  
FT SIGNAL 1 25  
FT CHAIN 26 837  
FT DOMAIN 26 626  
FT TRANSSEM 627 650  
FT DOMAIN 651 837  
FT DOMAIN 118 118  
FT DOMAIN 122 228  
FT DOMAIN 229 333  
FT DOMAIN 334 431  
FT DOMAIN 432 528  
FT DOMAIN 529 624  
FT DISULFID 132 143  
FT DISULFID 249 296  
FT DISULFID 267 310  
FT CARBOHYD 51 94  
FT CARBOHYD 129 129  
FT CARBOHYD 186 186  
FT CARBOHYD 279 279  
FT CARBOHYD 392 392  
FT CARBOHYD 408 408  
FT CARBOHYD 474 474  
FT CARBOHYD 487 487  
FT CARBOHYD 582 582  
FT CARBOHYD 613 613  
FT CARBOHYD 232 235  
FT STRAND 249 255  
FT STRAND 266 274  
FT STRAND 281 286  
FT STRAND 290 296  
FT STRAND 303 311  
FT STRAND 323 328

SQ SEQUENCE 837 AA; 93406 MW; 42295989E2C8531 CRC64;  
Query Match 12.1%; Score 471.5; DB 1; Length 837;  
Best Local Similarity 25.3%; Pred. No. 5.3e-28;  
Matches 185; Conservative 105; Mismatches 293; Indels 147; Gaps 33;  
QY 22 PAKPENISCVYYRRKN-LTCTMSPGKETS-TQYTVRYTAFGEKHNDCTNST-----74  
DB 124 PAPSRLNLSCLMHLTNSLVCOWBERGPEITHLPTEFIK-----SFSRAD-CQYGDITPDVC 179  
QY 75 -SENRAISCFELPRITIPDNYTIEVENAGDGYIKSHMYRLLENIAKTEPKI--FRVK 131  
DB 180 AKRKONNSIPRKRLLYQYMAIWOAENMLGSESPKCLDPMADYKLEPPMIALDIDG 239  
QY 132 PVL-----GIKRMQIEMIRPELAPVSSDKYLIRFTVSTSMMEVFKKNDKQTY 166  
DB 240 PDVAVSHQPGCLMWSMKRKPSEYMEDECELRYPOLKGAN--WTLVFHLPSKDD--F 293  
QY 187 NLNGLOPFTEYVIALRCAYKES--KFWSDMSQEMKMTTEEAR-CGLELRVLRKPAEADG 243  
DB 294 ELGGLHAPRYTTLQMRG-IRSSLPGEFSPSPGLQLRPTKAPRIILDTWCOKOLD-PG 351  
QY 244 RRPVRLMKRKARCAPVLE--KTLGYNI-WYPESSNTLETMTTNOQLHLGGESFW 299  
DB 352 TVSVOLFMRP---TPLOEDSGOIGYLLSNWSPDHQODIHLCTNTQLSCIFLLPSEAGN 408  
QY 300 VSMSTYNSLSKSPATIRIRAIQESFQCIEVWQACVAEQOLVYKQSSALDVNTMIEM 359  
DB 409 VTLVAVYKAGTSPTTY--VFLEN-----EGPAVTGLIAMAQDINTJTWMDV 452  
QY 360 -FPVDSEPTTLISVESVQATN-----WTIQ-----ODKLKPFMCYNISVYPMH 403  
DB 453 EAPSLRPOGLIEMKSPSYNNYSKSMLEPNONITGILLKONINFOLYRITVAPL 512  
QY 404 DKVGEPISTAYAKEGVSGEPETKENIGVKTIVTWKIEPSEKGIIT--CNVITFYQ 461  
DB 513 GIYGPVNVYTFGERAPRPHAPALHLKHTVGTWAOLEW--VPEAPRLGMIPLHYITFWA 570  
QY 462 AEGGKSGSKVNSILIOYGLSKRTSYIOWWASISAGTNGTSINFTLSFVPEIT 521  
DB 571 DAGHSSVTLNLSLHDFVTLKLEPASYLVHVAIYMAISRASTNGTGLTFLPDSLNIF 630  
QY 522 LITSILIGGLIILITVAAGLKKPKNLTHLC-----WPIVPAARSSTIATGDD 572  
DB 631 L-----GLTCLVLTSTC-----VTMLCCRRKRTSFMSPVPPAISLSSWL--- 674  
QY 573 FKDKLNKESDVSNTEDRIKPCSTPSDKLVYDKLVVNGVNLQELFTDEARTGOENL 632  
DB 675 -----PTIMTETPQLPSFMDSSVPSITKIN-----ELEEDKKPTHMDSSES 715  
QY 633 GGEKNGVYTC-----PFRP-DCPLKSPFELPVSEIIPPKSQYL 671  
DB 716 SG--NGSLPALVQAYVLQGDPREISNOSOPPSRTGQVLYGQVLESPTSPGV---MOYI 769  
QY 672 RSSRMECTRP 681  
DB 770 RS---DSTOP 776  
RESULT 6  
LIFR\_HUMAN STANDARD; PRT; 1097 AA.  
ID LIFR\_HUMAN  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leukemia inhibitory factor receptor precursor (LIF-R).  
GN LIFR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]

[illegible]

Query Match	10.5%	Score 408.5	DB 1:	Length 1097
Best Local Similarity	21.3%	Pred. No.5,2e-23:		
Matches 178:	Conservative 139:	Mismatches 292:	Indels 225:	Gaps 40:
QY	22	PAKPNINISGVVYVYRRNLCTMSPCRETSY----	TOYVAKRYVAGEKHDNCTWNSPS	76
Db	333	PTPQOLNETHDNLKEIICSNMGRVTLVYGRRAISYTLVSEFS-GKIVRLKRAAPAPNE		391
QY	77	NRASCSFFLPRTITPDNTTIEVEANGDGVIKSHMTYRLLENIA-KTEP--PKIFRVKPV		133
Db	392	SYOLLFOMLPNOEI---YNFTLNHNPLG--RSOSTI--LVNITEKVVPHPTSEKVKADI		444
QY	134	LGIKRMIOEWIKPELAPVSSDKLTTLFRYVNSTSMWEV--NFAKKRKD-----KNO		184
Db	445	---NSTAVKISMHLPG-----NFAKINFLCEIIEIKKSNVQDQRNNTIKGVENS		490
QY	185	TV--NLTGLOPTEEVYALRCVAKESKFMDSMOEKMGMTTEEARC-GLELMRYLKPAEA		241
Db	491	SYLVADLKNLPYTLTFTRICSTETEFMKSKMSNKKHULTTEASPSSKPDIMR---EWS		547
QY	242	DGRVRVRLMKAKRQAPVLE--KTLGINIMYTPSPSNLTETMMTTMOOLEHLHGGSF		298
Db	548	DGKNLI-ITYMKP--LPINEANGKILSYNSVCSDEELQSELPDPQHKKEIRLDKNDY		603
QY	299	WVSMISYNSIGLSP--VATLIRPILQEKSPFCIEVMQACVADQLYVQWSSALDVTM		355
Db	604	IISVYAKNSVSGSPSPKISKASMEIPDDLIKIEOVVMGKG-----ILLTMHYDPMTCDY		657
QY	356	MIEMEPDVDSBPTLTSMSV--SOATNMWTIOODKLKPFMCYNISV-----YPMILHDVKG		407
Db	658	VTKMCSRSSEPCCLMDMRKRPVNSTETVIESDEFPRGIRIYNFLYCGRNOGYQLRSMIG		717
QY	408	EPYSIQAAKEVSEBGPETKVENIGVTVITTMKEIPKSKRGKIGLCITNTTIFYOAEGRKG		467
Db	718	-----YIEELAPIVAPNFTVEDTSADSLVWKMEDIVHEELRGFLRGYLFY---GKG		766
QY	468	FSKTYNSSLIQYG-----LESLEKRTSYIVQVMASTAGTNGTSIN		509
Db	767	ERDTSEKMAVLESGRSDIKVKNITDLSQKTLRIADLGSTSHLVYRAATYDDGVEPEKMY		826
QY	510	EKTLSEVFEIILITSLIGGLILIIILTVAYGL-----KPKNLTLHCWTPVP		558
Db	827	VYTKENSV-----GLTILIPVAVAVIVGVVTSILCYRKREWKIETFEYDIP		874
QY	559	NPAESIAFTWGGDDFKDLINKESDSDSVNTDRILKPCSTSDKLYID-----		606
Db	875	NPENCKALOQ-----OKSVCEGSSALKTLE--MNPc-TYNNNEVLTETSAFPKIEDTE		924
QY	607	-----KLNVN-----GNVLOEITFD-----		622
Db	925	IISPAERPEDRSDAEPENHVYVSCPIIEEETPNPADEAGGTAQVYIYIDVQSMYPOQ		984
QY	623	-EARTGQENN-LGGEKNGVYTCPPRPD--CPUGSFEELPVSPETIPPKSOTYLSRMDEG		678
Db	985	AKPEBEDQENDVPGA--GY-----KPKMHLPIINSTVEDIAAEDLD-----KTAG		1027
QY	679	TRPEAKEDLLTSSGSLVPD-----HCEEGAPNRYLANSYAREFLVSEK		723
Db	1028	YRPOAN-----VMTWNLVSPDSPRSIDNSSEIVSFGSP-----CSINSRQFLIIPK		1073
RESULT 7				
LIFR_MOUSE				
AC	LIFR_MOUSE	STANDARD:	PRT:	1092 AA.
AD	P42703:			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Leukemia inhibitory factor receptor precursor (LIF-R) (D-factor/LIF			
GN	receptor).			
GN	LIFR_MOUSE			
OS	Mus musculus (Mouse).			

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=92007727; PubMed=1915266;  
 RA Gearling D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,  
 King J., Price V., Cosman D., Beckmann M.P.;  
 RT "Leukemia inhibitory factor receptor is structurally related to the  
 IL-6 signal transducer, gp130.";  
 RL EMO J. 10:2839-2848(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=ICR; TISSUE=Liver;  
 RX MEDLINE=94039833; PubMed=7901054;  
 RA Tomida M., Yamamoto-Yamaguchi Y., Hozumi M.;  
 RT "Pregnancy associated increase in mRNA for soluble D-factor/LIF  
 receptor in mouse liver.";  
 RL FEBS Lett. 334:193-197(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=9434302; PubMed=8056772;  
 RA Tomida M., Yamamoto-Yamaguchi Y., Hozumi M.;  
 RT "Three different cDNAs encoding mouse D-factor/LIF receptor.";  
 RL J. Biochem. 115:557-562(1994).  
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY  
 WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF  
 LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.  
 CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A  
 MEMBRANE-BOUND AND A SECRETED FORM.  
 CC -1- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named Isoforms=2;  
 Name=1; Synonyms=Membrane;  
 IsoId=p42703-1; Sequence=Displayed;  
 Name=2; Synonyms=Secreted;  
 IsoId=p42703-2; Sequence=VSP\_001686, VSP\_001687;  
 Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN,  
 AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF THE  
 SECRETED FORM.  
 CC -1- SIMILARITY: Contains 4 fibronectin type III domains.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: S73496; AAC60698.1; -;  
 DR EMBL: S73495; AAC60697.1; -;  
 DR EMBL: D26177; BA005165.1; -;  
 DR EMBL: D17444; BA004258.1; -;  
 DR PIR: JX0312; JX0312.  
 DR MGI: MGI:96788; Lftr.  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003961; FN.III.  
 DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
 DR Pfam: PF00041; fn3; 4.  
 DR SMART: SM00060; FN3; 4.  
 DR PROSITE: PS01353; HEMATOPO. REC. L\_F2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;  
 Repeat.  
 KW Repeat.  
 FT SIGNAL 1 43  
 FT CHAIN 44 1092  
 FT DOMAIN 44 828  
 FT TRANSMEM 829 853  
 FT DOMAIN 854 1092  
 FT DISULFD 53 63  
 FT CARBOHYD 164 164  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 LEUKEMIA INHIBITORY FACTOR RECEPTOR.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 BY SIMILARITY.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 647 647 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 658 658 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 724 724 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 782 782 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 718 719 AP -> EA (in isoform 2).  
 FT VARSPLIC 720 1092 /FTId=VSP\_001687.  
 FT Missing (in isoform 2).  
 SQ SEQUENCE 1092 AA; 122573 MW; 6F02B8CE15ADE70 CRC64;  
 Query Match 10.4%; Score 405.5; DB: 1; Length 1092;  
 Best Local Similarity 21.7%; Pred. No. 8.8e-23;  
 Matches 180; Conservative 131; Mismatches 304; Indels 213; Gaps 36;  
 22 PAKPENISCVYVYRKNICTWSPKETSYSY-----TOYTV-----KRT 58  
 328 PDVQOKLSCEHDLKEIICSNPRITGLVCPRTETTLPESTIGSKSAVFRIGLNET 387  
 59 YAFG-EKHDNCTNNTSSENRASCSFLLPRITIPDNTYIEAENGGVAKSHMTYRLE 117  
 388 YRLGVOMHPGOEIHNFLLTGR-----NPLGAQASAVINWTE 424  
 118 NIATPEPKIRRVVPLVIGIKRMIDEMIKPELAVSSDLKTLAFRVYNSNMHEVPAK 177  
 425 RVAPHDPISL-KVXDI-NSTVTFVSWLPG-----NFTKINILCOIEICKAN 469  
 178 NRKD-----KNQTYNLT--GLOPTEVIALRCVAKSKRWSDMSQMKMTEEEA 226  
 470 SKREVRNNTINGADSTYHVAVDKLNPTATYTPRVKRSCKTFPMKMSKRSDEKRLITTEAT 529  
 227 PC-GLEIMRVLKPADGRRPRLLLMKARGAVLE---KTLGVYINWYPPESNTNLTETM 282  
 530 PSKGPDTWR---EMSSDCKNLI-VYMKP---LPINEANGKILTSVAVSCSLNEFTQSVLEI 582  
 283 NTTMOGLELHGGSEFWMSMSTVSLGSP---VATLRIRAIQKRSQCIEVMACVAED 339  
 583 FDPQHRAEIQSKNDYIISVAVRNASGSSPSKIASMEIPN-----DQITVEQAVGIGN 636  
 340 QLVVVKMOSSALDVNTWMIEMFPDVSDEPTTLMSESV--SOATNMTIQDRLKPFVCYNISV 398  
 637 RIFLWRHRDPMWTCDDYVIAKMCNSSRSRECLDMKKVYNSNTEYVIESQPGVGRVNYFL 696  
 399 YPMCHDKVGEPEYSIOAVAKGCVPESEGPETKVENIGKVTITTYKKEIPKSKKGIICNVTI 458  
 697 YGCTNOGYQLRSLIIGVEELAPIVAPNFTVEDTSADSIIVKMPDIDPEELGRGLRGY-L 755  
 459 FYQAEAGKGFSTK-----VNSSLIQGLSELSLRKTSYIVQWNASVSAG 501  
 756 FYFQGERDPKPTKSLPEPHSDIKLKNITDISQKTLR--LADLOGKTSYHVLVLAAYTHGG 813  
 502 CTNGTSINFKTLSEFVEEIIITSLIGGLLIIILVYAYGL-----KKPNKIT 550  
 814 LGPKSMFVTVKENS-----GLIATILIPAVAVIYGVVTSILCYKRRKREIK 861  
 551 HLCMPYVNPRESSIATWGDDEKDKLNLKASDSQVNTEDRIILPCSTPSSKLVLD--KL 608  
 862 ETFPDPIDFNPENCKALQF-----QKSVCGSGLNAKTLLE--MPNC-TPNNVEVLESRSI 911  
 609 VVNGVNLQELFTDEA-RTGOENNLGEGKNGYV-CP-----FRPDC-----648  
 912 VPKIEDT--ELISPAERPERSEVDPENHVAVSYCPPIIEETITNPADEVGASOVVY 969



AC Q99665; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2) (IL-12R-beta2).  
 GN IL12RB2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97098510; PubMed=8943050;  
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y., Gately M.K., Gubler U.;  
 RA "A functional Interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).  
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY.  
 CC -1- SUBUNIT: DIMER/OLIGOMER: DISULFIDE-LINKED. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 3 fibronectin type III domains.  
 CC -----  
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 CC -----  
 DR EMBL; U64198; AAB3675.1; ...  
 DR HSSP; P40189; IBOU.  
 DR Genew; HGNC:5972; IL12RB2.  
 DR MIM; 601642; ...  
 DR GO; GO:0005887; C:Integral to plasma membrane; TAS.  
 DR GO; GO:0004907; P:Interleukin receptor activity; TAS.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. ; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR InterPro; IPR002966; CRI1.  
 DR InterPro; IPR003529; Hemtopoptn\_L\_F2.  
 DR Pfam; PF00041; FN3; 3.  
 DR SMART; SM00060; FN3; 4.  
 DR PROSITE; PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; Polymorphism.  
 FT SIGNAL 1 21  
 FT CHAIN 22 862  
 FT DOMAIN 22 624  
 FT TRANSMEM 625 641  
 FT DOMAIN 642 862  
 FT DOMAIN 224 306  
 FT DOMAIN 421 508  
 FT DOMAIN 519 607  
 FT CARBOHD 48 48  
 FT CARBOHD 129 129  
 FT CARBOHD 166 166  
 FT CARBOHD 195 195  
 FT CARBOHD 271 271  
 FT CARBOHD 347 347  
 FT CARBOHD 376 376  
 FT CARBOHD 480 480  
 FT CARBOHD 485 485  
 FT VARIANT 420 420  
 FT VARIANT 426 426  
 FT VARIANT 426 426

FT VARIANT 465 465 G -> D (IN dbSNP:2307153).  
 FT /FTid=VAR\_014808.  
 SQ SEQUENCE 862 AA; 97134 MW; 67C0E0DD468BD58 CRC64;  
 Query Match 9.88; Score 383; DB 1; Length 862;  
 Best Local Similarity 22.88; Pred. No. 3.2e-21;  
 Matches 184; Conservative 116; Mismatches 322; Indels 184; Gaps 38;  
 QY 22 PAKENISCIYYVYRK-NLTCWSPGKETS-VYQTVRYRTAFGKHNCNTNSTSNNRA 79  
 DB 124 PEQPOLNLSCTQKGEQGVACTWGERGDTLHYETTLQLS--GPK-NLWQKCKO--I 176  
 QY 80 SCSEF-----LPRTIPDNVTIEVEAENCDGVKSHMTYRLNIAKTEPKIFRYAPVL 134  
 DB 177 YCVDLDGDMNLTPEPSNSNTAKTAVANSIGSSSLSTFTFLDIAPRLPMDIRIKFOK 236  
 QY 135 GIKRMIOEIMIKPELAPVSDLYTLFRFVNSTSMVEVNF-AKNRDKNQYNTLTGLQ 192  
 DB 237 ASVSRCTLYWRDEGLV-----LNLRLRYRPSNSRLMMVYTKAKGRHD-----LIDLK 285  
 QY 193 PFEYVIALGCAVRESK-FWSDMSQEKMGMTREEAPCG-LEIMRVLKPAEADGRPRVRL 250  
 DB 286 PFEYERQISKLLHYGSDMSSESLRAQTPPEEPGLMDVWYMKRHID-SKQQLSLF 344  
 QY 251 WKARGAPVLEKTLGVNINWYPPESNTNLTEMTNTNOQLBHLGSEFVWSMI----- 303  
 DB 345 WKNLVSDEARKILHYQV-----TLQEL--TGKAMQNITGHSMTTIVIRGNWA 394  
 QY 304 ----SYNSLGRSPATLRIPAIQESFQCEVWQACVA-----EDQLVYKW 345  
 DB 395 VAWSAANSKGS-----LPT-----RLNIMLCAGLAPROVSANSEGMNIIWTW 441  
 QY 346 QSSALD---VNTWMIEW---FPDYDSPTLTSMVSQATWMTIQDQKRFQVNYNSVY 399  
 DB 442 QPPKDSVAQOEYVENREHLPGDQV-PLNMLRSRPYNVSAIISENINICYETIRVY 500  
 QY 400 PMLHDVGEPPYSIOAVAKEGVSEGPETKVENIGVKTVTITWKEIPKSERGIICNYTF 459  
 DB 501 ALSGDQ-GGCSILGNKHKAPLGPHINATEKSGILSMNSIPVOEQMCLLHYRIY 559  
 QY 460 YQAEKGK-----FSKYVNSSTLOYGLESLKRTSYIYOVAASISAG-GTNGSTINF 510  
 DB 560 WKERDSNSOPOLCIPRYVSONS---HPINSLQPRVTVYLVMTALTAAGSSHGNREF 615  
 QY 511 -----KTLSPVSEIILLISLIGGLILLILVAAGKKPKNL-----THLCMPVNP 559  
 DB 616 CLOGKAMMAFVAPASICAIITWV-----TESTHYFOQVYVLLAALRPQWCSRELPD 668  
 QY 560 PAESSIATWHDDEKDKLNLKESDSVNTEDRIKPCSTPSDKLVIDKLVVFNGLQEI 619  
 DB 669 PANSTCA-----KKYPIAEKTOQLPL-DRLLIDMPTPEDP--EPLVIS--EVLHY 714  
 QY 620 FT-----DEARIGQENNLGCEKN-----G 638  
 DB 715 TPVERHPPCSNMPREKQIOGHOASEKDMHSAASPPPRALQAESQVLDVLYKVESRG 774  
 QY 639 YVTPRPFDPCDLGKSFEEPLVSPETIPPKSQYLSRRBDEGRPAKEQLJFSGSLVPH 698  
 DB 775 SDPPENPACP---WVYLPAQD--LPHDGYLPSNIDD--LPSEHAPLADSLTELEPOH 826  
 QY 699 LCEGAPNPYLKNSVTAREFLVSEKL 724  
 DB 827 ISLSVPS-----SSLHLPLTFSCGKLL 848  
 RESULT 10  
 LEPR\_RAT STANDARD; PRT; 1162 AA.  
 AC Q62959; Q5772; Q54805; P70493; P70494; P70495; P7589;  
 AC Q62960; Q63007; Q63385; Q63386; Q9ENR4;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).  
GN LEPR OR OBR OR FA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OK NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.  
RC STRAIN-Sprague-Dawley; TISSUE-Hypothalamus;  
RX MEDLINE=96241565; PubMed=8673096;  
RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,  
RA Hess J.F.,  
RT "Leptin receptor missense mutation in the fatty Zucker rat.";  
RL Nat. Genet. 13:18-19(1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.  
RC STRAIN-Sprague-Dawley, and Zucker fatty; TISSUE-Brain;  
RX MEDLINE=96295531; PubMed=8702432;  
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.,  
RT "Substitution at codon 269 (glutamine --> proline) of the leptin  
RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty  
RT (fa/fa) rat.";  
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND E), AND VARIANT FA PRO-269.  
RC STRAIN-Sprague-Dawley, and Zucker fatty;  
RX MEDLINE=96332408; PubMed=8769097;  
RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,  
RA Mori K., Tamura N., Hosoda K., Nakao K.,  
RT "Molecular cloning of rat leptin receptor isoform complementary  
RT DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)  
RT rats.";  
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RA Carlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,  
RT "Cloning of the rat leptin receptor.";  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM A), AND VARIANT FA PRO-269.  
RC STRAIN-Sprague-Dawley, and Zucker fatty;  
RX MEDLINE=96212906; PubMed=8630068;  
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.,  
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from  
RT Zucker fatty (fa/fa) rat.";  
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC STRAIN-Sprague-Dawley; TISSUE-Spleen;  
RA Park J.H., Ju S.K., Na S.Y., You K.H., Kim K.L.,  
RT "Molecular cloning, sequencing, and recombinant expression of the long  
RT form of the rat leptin receptor isolated from whole spleen RNA.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM F).  
RC STRAIN-Sprague-Dawley; TISSUE-Brain;  
RX MEDLINE=96368027; PubMed=8772180;  
RA Wang M.-Y., Zhou Y.T., Newgard C.B., Unger R.H.,  
RT "A novel leptin receptor isoform in rat.";  
RL FEBS Lett. 392:87-90(1996).  
RN [8]  
RP SEQUENCE OF 1-123 FROM N.A.  
RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.,  
RT "Analysis of rat leptin receptor gene.";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE OF 557-802 AND 843-892 FROM N.A. (ISOFORMS C AND E).  
RC STRAIN-Sprague-Dawley;  
RX MEDLINE=97415825; PubMed=9268737;  
RA Chien E.K., Hara M., Rouard M., Yano H., Philippe M., Polonsky K.S.,  
RA Bell G.I.,  
RT "Increase in serum leptin and uterine leptin receptor messenger RNA

RT levels during pregnancy in rats.";  
RN Biochem. Biophys. Res. Commun. 237:476-480(1997).  
RL [10]  
RP SEQUENCE OF 694-878 FROM N.A.  
RC STRAIN-Sprague-Dawley; TISSUE-Pancreas;  
RA Ma Z.,  
RT "Identification of a leptin receptor in islet.";  
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE OF 821-894 FROM N.A. (ISOFORM A).  
RC STRAIN-Mistar Munich; TISSUE-Kidney;  
RA Totsune K., Takahashi K., Mackenzie H.S., Murakami O., Arihara Z.,  
RA Some M., Satoh F., Mouri T., Brenner B.M., Ito S.,  
RT "Leptin receptor gene expression in rat kidney.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP VARIANT FA PRO-269.  
RX MEDLINE=96314329; PubMed=8690163;  
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,  
RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,  
RA Leibel R.L.,  
RT "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor  
RT (lepr).";  
RL Diabetes 45:1141-1143(1996).  
CC -I- FUNCTION: Receptor for obesity factor (leptin). Involved in the  
CC regulation of fat metabolism and in a hematopoietic pathway  
CC required for normal lymphopoiesis. May play a role in  
CC reproduction.  
CC -I- FUNCTION: The short form (isoform A) may act to transport leptin  
CC to the cerebrospinal fluid. The putative soluble receptor (isoform  
CC E) could function as a transport protein.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E  
CC which could be secreted.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing. Named isoforms-6;  
CC Name-B;  
CC Isoform-O62959-1; Sequence-Displayed;  
CC Name-A;  
CC Isoform-O62959-2; Sequence=VSP\_001705, VSP\_001706;  
CC Name-C;  
CC Isoform-O62959-3; Sequence=VSP\_001707, VSP\_001708;  
CC Name-D;  
CC Isoform-O62959-6; Sequence=Not described;  
CC Name-E;  
CC Isoform-O62959-4; Sequence=VSP\_001709, VSP\_001710;  
CC Name-F;  
CC Isoform-O62959-5; Sequence=VSP\_001711, VSP\_001712;  
CC -I- TISSUE SPECIFICITY: Isoform B is expressed in kidney, liver, lung,  
CC ovary, spleen and uterus. Increased level in uterus during  
CC gestation. Isoform F is expressed at high levels in liver and  
CC spleen and less in brain, stomach, kidney, thymus, heart, lung and  
CC hypothalamus.  
CC -I- PTM: Phosphorylated on two tyrosine residues. Tyr-965 may be the  
CC major site of phosphorylation. Phosphorylation on both sites is  
CC required for full activity (by similarity).  
CC -I- DISEASE: The fatty (FA) mutation produces profound obesity of  
CC early onset caused by hyperphagia, defective nonshivering  
CC thermogenesis, and preferential deposition of energy into adipose  
CC tissue.  
CC -I- SIMILARITY: Contains 3 fibronectin type III domains.  
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -----  
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CC -----  
DR EMBL: U52966; AAC52587.1; -;  
DR EMBL: D84550; BAA12697.1; -;  
DR EMBL: D84551; BAA12698.1; -;





RA Fischer A., Emile J.-F., Gaillard J.-L., Meinel E., Casanova J.-L.,  
 RT "Interleukin-12 receptor beta-1 deficiency in a patient with abdominal  
 RL tuberculosis." ;  
 CC J. Infect. Dis. 184:231-236(2001).  
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A  
 CC LOW AFFINITY.  
 CC -1- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH  
 CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND  
 CC IL12RB2.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms-2;  
 CC Name-Long;  
 CC IsoId-P42701-1; Sequence-Displayed;  
 CC Name-Short;  
 CC IsoId-P42701-2; Sequence-VSP\_001715;  
 CC -1- DISEASE: Defects in IL12RB1 are a cause of susceptibility to  
 CC severe mycobacterial and Salmonella infections in otherwise  
 CC healthy individuals.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
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 CC -----  
 DR EMBL: U03187; AAA21340.1; .  
 DR EMBL: AJ297688; CAC10446.1; .  
 DR EMBL: AJ297689; CAC10446.1; JOINED.  
 DR EMBL: AJ297690; CAC10446.1; JOINED.  
 DR EMBL: AJ297691; CAC10446.1; JOINED.  
 DR EMBL: AJ297692; CAC10446.1; JOINED.  
 DR EMBL: AJ297693; CAC10446.1; JOINED.  
 DR EMBL: AJ297694; CAC10446.1; JOINED.  
 DR EMBL: AJ297695; CAC10446.1; JOINED.  
 DR EMBL: AJ297696; CAC10446.1; JOINED.  
 DR EMBL: AJ297697; CAC10446.1; JOINED.  
 DR EMBL: AJ297698; CAC10446.1; JOINED.  
 DR EMBL: AJ297699; CAC10446.1; JOINED.  
 DR EMBL: AJ297700; CAC10446.1; JOINED.  
 DR EMBL: AJ297701; CAC10446.1; JOINED.  
 DR PIR: I37892; I37892.  
 DR GeneW: HGNC:5971; IL12RB1.  
 DR MIM: 601604; .  
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO: GO:0016517; F: interleukin-12 receptor activity; TAS.  
 DR GO: GO:0004888; F: transmembrane receptor activity; TAS.  
 DR GO: GO:0006960; P: antimicrobial humoral response (sensu Inver. . .); TAS.  
 DR GO: GO:0007166; P: cell surface receptor linked signal transdu. . .; TAS.  
 DR GO: GO:0008284; P: positive regulation of cell proliferation; NAS.  
 DR InterPro: IPR003361; FN-III.  
 DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
 DR Pfam: PF00041; fn3; 1.  
 DR SMART: SMD0060; FN3; 1.  
 DR PROSITE: PS01353; HEMATOPO. REC. L\_F2; 1.  
 KV Receptor: Transmembrane; Glycoprotein; Signal; Alternative splicing;  
 KV Repeat; Polymorphism.  
 FT SIGNAL 1 23  
 FT CHAIN 24 662  
 FT DOMAIN 24 545  
 FT TRANSMEM 546 570  
 FT DOMAIN 571 662  
 FT DOMAIN 43 133  
 FT DOMAIN 143 236  
 FT DOMAIN 237 337  
 FT DOMAIN 338 444  
 FT DOMAIN 445 540  
 FT DISULFID 52 62  
 BY SIMILARITY.

FT	CARBOHYD	121	121	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	329	329	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	346	346	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	352	352	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	456	456	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPIC	659	662	KAKM -> DR (in isoform short).
FT	VARIANT	213	213	R -> W (confers susceptibility to mycobacterial and salmonella infections).
FT	VARIANT	365	365	/FTid-VAR_015577
FT	VARIANT	378	378	M -> T (in dBSNP:373947).
FT	VARIANT	378	378	/FTid-VAR_011986
FT	VARIANT	378	378	G -> R (in dBSNP:401502).
FT	VARIANT	378	378	/FTid-VAR_011987
SO	SEQUENCE	662 AA; 73108 MM; 541ADA60F62DAA1EF CRC64;		
QY	Query Match	5.9%; Score 231.5; DB 1; Length 662;		
QY	Best Local Similarity	21.7%; Pred. No. 8.4e-10;		
QY	Matches 149; Conservative 96; Mismatches 253; Indels 189; Gaps 34;			
QY	8 MWLPSLCKFSLAALPAK-----PENISCVYYRKULTCWSP 44			
QY	7 MWVPLFLFLLSRQGAACRTSECCQDPPIPDADSGASGPRDLRCYRISDRYECSSWOY 66			
QY	45 GKSTSTQYTVKRTYAFGEKHNCTNSSTSENASCFFLPRTIPDNYTIE--VEAEN 102			
QY	67 ECPYAGVSHRLRCLSLSG-----RCYFAAGASATRLQ---FSDAGSVLTVTLVWESNA 119			
QY	103 GDGVKSHMTWMLNENAKTERP-KIFRKPVGLTRMIDIEIKELAPVSSDLKYTLR 161			
QY	120 RNOETKSPREYTDLYNSVKYEPGLDGIKSKLGLRLM--EWETPD-NQVGAEOVF--R 173			
QY	162 ERTVNSTSW-----MEVFAKNKKKKNQYNYLGLDPFTGYVALNC 203			
QY	174 HRT-PSSPMKLGDCGQDDTESCLCPLENNAAQ-----EFQLRRO 214			
QY	204 AYKESKFNQDWSQ-----EKMG-----MTEEPAGLEIMRLKPA 239			
QY	215 LSGSGSSWSKSSPVCVPPENPPQPVQRFSEVQLGDDGRRLTLKQPTQLEL-----PE 269			
QY	240 EADGRPRVRLMKKAGAVLEKTLGYNLWYRPESNTNLTEMTNTNOLEHLG----- 294			
QY	270 GCGGL-----AGTEVT--YRLQHLMLSCPCAKAKTRT-----LHLGMPYL 309			
QY	295 -GESFWMSISYNSLKSFPATLRIPALOEKSFQCEVQACVACEDQLVKKMOSSALDVN 353			
QY	310 SCAAYVAVIISNQGPGNLQNTWHLIPADHTHPVALNT---SVGTNGTMYPARAOSH- 365			
QY	354 TMMIEMFP-----DVSEPR---TTLMSVSOATMTWTIOQDLKPFWCYNI 396			
QY	366 TYCISWOPVGGDGLATCSLTAPODBPAGMATYSMSRSGA-----MGEK-----CYII 416			
QY	397 SVYPMHLKVGEPYS--IOAY-----AKEGVSPSGEPKEKVENICVYTTWTAKETPRSE 448			
QY	417 TIFSAHNEPKLTLMTSTVSTYHEGNAASAGPRH--HVSQKNHSLDSVDMAPSLST 473			
QY	449 RGIICNTTYFYQAGGKGFSK-TVNSSILOGLSLKRTSYIQVMASTS-ACGTNGT 506			
QY	474 CPGLVKEVYVVCGRDSDNSQVSEHPQPEYVTLTSLGAGVAYTVQVADTAMLRGWSQ 533			
QY	507 SINRTLSFVFEIILLTSLIGGLLIILTVAV-GLKRNKLTNLCMPVNPFAESSI 565			
QY	534 PQRF-SIEVQVSDWLIFFASGLSFLILVGLVGLNRAAR--HLC-PLPPTPCASSA 589			
QY	566 ATWHD-----DPKDKLNKES 582			
QY	590 IEPFGKETQWIMNPVDQEBASLQEA 616			
RESULT 12				
LEPR_MOUSE	STANDARD:	PRT: 1162 AA.		
ID	LEPR_MOUSE			

AC P48356: 035686; 054986; 061215; 064309; 090WC3; 090WV5;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219).  
GN LEP-R OR OB-R OR DB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI-TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RC TISSUE=Choroid plexus;  
RX MEDLINE=96128129; PubMed=8548812;  
RA Tartaglia L.A., Dembski M., Meng X., Deng N., Culpepper J.,  
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,  
RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,  
RA Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;  
RT "Identification and expression cloning of a leptin receptor, OB-R";  
RL Cell 83:1263-1271(1995).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC STRAIN=C57BL/KsJ; TISSUE=Hypothalamus;  
RX MEDLINE=96190816; PubMed=8608603;  
RA Chen H., Charlat O., Tartaglia L.A., Wolf E.A., Meng X.,  
RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,  
RA Duyk G.M., Tepper R.I., Morgenstern J.P.;  
RT "Evidence that the diabetes gene encodes the leptin receptor:  
RT Identification of a mutation in the leptin receptor gene in db/db  
RT mice";  
RL Cell 84:491-495(1996).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).  
RC STRAIN=C57BL/KsJ; TISSUE=Hypothalamus;  
RX MEDLINE=96231997; PubMed=8628397;  
RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,  
RA Lee J.I., Friedman J.M.;  
RT "Abnormal splicing of the leptin receptor in diabetic mice";  
RL Nature 379:632-635(1996).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM C).  
RC STRAIN=BA1B/C; TISSUE=Liver;  
RX MEDLINE=96206286; PubMed=8616721;  
RA Clouff J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,  
RA Mikhal B.I., Plarika D., Snodgrass H.R.;  
RT "Novel B219/OB receptor isoforms: possible role of leptin in  
RT hematopoiesis and reproduction";  
RL Natl. Med. 2:585-589(1996).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RC STRAIN=NZO; TISSUE=Hypothalamus;  
RX MEDLINE=97462708; PubMed=9322835;  
RA Igel M., Becker W., Herberg L., Joost H.G.;  
RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor  
RT in the New Zealand obese mouse";  
RL Endocrinology 138:4234-4239(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
RC STRAIN=FVB/N; TISSUE=Spleen;  
RX MEDLINE=96270520; PubMed=8692797;  
RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,  
RA Skoda R.C.;  
RT "Defective STAT signaling by the leptin receptor in diabetic mice";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND E).  
RC STRAIN=129/J;  
RX MEDLINE=96008913; PubMed=9344648;  
RA Chua S.C., Koutas T.K., Han L., Liu S.M., Kay J., Young S.J.,  
RA Chung W.K., Leibel R.L.;  
RT "Fine structure of the murine leptin receptor gene: splice site  
RT suppression is required to form two alternatively spliced  
RT transcripts";

RL Genomics 45:264-270(1997).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT ASN-600.  
RC STRAIN=KK Obese; TISSUE=Hypothalamus;  
RX MEDLINE=99061814; PubMed=9845674;  
RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,  
RA Joost H.G.;  
RT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,  
RT hyperinsulinemic KK mouse strain";  
RL J. Endocrinol. 21:337-345(1998).  
RN [9]  
RP SEQUENCE OF 890-1162 FROM N.A. (ISOFORM B).  
RC STRAIN=129;  
RA Banks A.S., Myers M.G. Jr.;  
RT "Murine leptin receptor genomic exon 1b and surrounding sequence";  
RN Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.  
RN [10]  
RP PHOSPHORYLATION OF TYR-985 AND TYR-1138, AND MUTAGENESIS OF TYR-985;  
RP TYR-1077 AND TYR-1138.  
RX MEDLINE=20261588; PubMed=10799542;  
RA Banks A.S., Davis S.M., Bates S.H., Myers M.G. Jr.;  
RT "Activation of downstream signals by the long form of the leptin  
RT receptor";  
RL J. Biol. Chem. 275:14563-14572(2000).  
CC -I- FUNCTION: Receptor for obesity factor (leptin). Involved in the  
CC regulation of fat metabolism and in a hematopoietic pathway  
CC regulated for normal lymphopoiesis. May play a role in  
CC reproduction.  
CC -I- FUNCTION: The short form (isoform A) may act to transport leptin  
CC to the cerebrospinal fluid. The putative soluble receptor (isoform  
CC E) could function as a transport protein.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E  
CC which could be secreted.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=5;  
CC Name=B;  
CC IsoId=P48356-1; Sequence=Displayed;  
CC Name=A;  
CC IsoId=P48356-2; Sequence=VSP\_001697, VSP\_001698;  
CC Name=C;  
CC IsoId=P48356-3; Sequence=VSP\_001699, VSP\_001700;  
CC Name=D;  
CC IsoId=P48356-4; Sequence=VSP\_001701, VSP\_001702;  
CC Name=E;  
CC IsoId=P48356-5; Sequence=VSP\_001703, VSP\_001704;  
CC -I- TISSUE SPECIFICITY: Isoform A: highest level of expression in lung  
CC and kidney, also present in kidney, heart, brain, spleen, liver,  
CC muscle, choroid plexus and hypothalamus. Isoform B: highest level  
CC of expression in hypothalamus and lower level in brain, testes and  
CC adipose tissue. Isoform E: expressed in adipose tissue,  
CC hypothalamus, heart, and testes.  
CC -I- PTM: Phosphorylated on two tyrosine residues. Tyr-985 may be the  
CC major site of phosphorylation. Phosphorylation on both sites is  
CC required for full activity.  
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC -I- SIMILARITY: Contains 3 fibronectin type III domains.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
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CC -----  
DR EMBL: U42467; AAA93014.1; -  
DR EMBL: U46135; AAC52408.1; -  
DR EMBL: U49106; AAC52420.1; -  
DR EMBL: U49107; AAC52421.1; -  
DR EMBL: U49108; AAC52422.1; -  
DR EMBL: U49109; AAC52423.1; -  
DR EMBL: U49110; AAC52424.1; -



CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.  
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 CC  
 DR EMBL: U23922; AA87457.1; -  
 DR PIR: I49295; I49295.  
 DR MGD: MGI:104579; I112r1.  
 DR InterPro: IPR003963; FN\_III.  
 DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
 DR Pfam: PF00041; fn3; 1.  
 DR SMART: SMO0060; FN3; 1.  
 DR ProSITE: PS01353; HEMATOPO\_REC\_L\_F2; FALSE NEG.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 738 INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.  
 FT DOMAIN 20 565 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 566 591 POTENTIAL.  
 FT TRANSMEM 592 738 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 44 142 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 152 258 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 259 359 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 360 465 FIBRONECTIN TYPE-III 4.  
 FT DOMAIN 467 553 FIBRONECTIN TYPE-III 5.  
 FT DISULFID 53 63 BY SIMILARITY.  
 FT CARBOHYD 50 73 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 130 130 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 330 330 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 374 374 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 463 463 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 477 477 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 738 AA; 81661 MW; 05D7AC306F1059CE CRC64;

Query Match 5.8%; Score 226; DB 1; Length 738;  
 Best Local Similarity 20.1%; Pred. No. 2.6e-09;  
 Matches 163; Conservative 113; Mismatches 309; Indels 224; Gaps 37;

OY 22 PAKENINSCVYYIKNLCTM---SPGKESITYOTYKRTYAFGEKHDNC---TTNSSTS 75  
 DB 45 PLGRNINSCVYKSVSTDECSWQYDGPEDNVSHVLMC-----CVPRPHHTGTG 91  
 OY 76 ENRASCSPF-----LPRITPDNTIEVANGDGVKSHMTYRLLENIAETE 123  
 DB 92 QER--CRFTSSGPDRTVOFPEODGIPVLSKYNFWESRLGNRYMSQKISOLYLYMTT 149  
 OY 124 PKRIEYKPVILGIRMIQIEMIKPELAVSSDLKYTLFRFVNSTSWMEVFAKRNKDKN 183  
 DB 150 PP-LGHK-VQSQHQQLMDW-----NVSEAGAEVQFRRMPTTN 188  
 OY 184 QTYNLGTQPTT-EYVIALRC-AVKESEF-----WSDWS 215  
 DB 189 WTLDDCGQVNVSSGVADIDGCSMSSECLPSENMAQEIQIRRRRLSSGAPGFWSDWS 248  
 OY 216 QEKGMTEEPAPCGLELRLVLPAPADGR-----PVRLMKKARGAP-----V 259  
 DB 249 M-PCVPEVLP-QAKIFELVEPLNQGRRRLTMOGOSPOLAVPGCGRGRAOYKKLIV 306  
 OY 260 LEKTLGVNIWYPPSNTNLFTMTNTNOQLHLGSEFWWSMISYNSIGKSPVATLRIP 319

DB 307 LVRL-----SCRQAOQTSKTVPLGKKLINSGATYDNLVLAKTRFGRSTIOKHL 357  
 OY 320 AIOEKSPCIEVMACVAEDLVYKMOSSALDVNTMIEWP-----D 362  
 DB 358 AOELTETALNV---SVGGNMTSMQMAQA-PGITYCLEWQPMFOHRNHTCLIVPEE 413  
 OY 363 VDSEPTTLTMSVSQATWITQODKLKPFMCYNISVY-----PMLDKGEPYSIQAY 415  
 DB 414 DPAKMTVHSMWSKP-----TLEQEE-----CYRITVFAKRPKPMMLATVLSYRGN 463  
 OY 416 A-KGVPSGEPETKVENIGKVTITTWKEIPKSERKGIICVYITFYQAGGKFSK-TVN 473  
 DB 464 ASRAGTPR---HVASRNOQDGSVEMTASQSLTSCPGVLTQYVVRCEADGAMSEMLVP 520  
 OY 474 SSIIQGLSELSKRTSYIVQYMASTAGTGTSTINFTLSFSV--FEIILITSLIGGL 531  
 DB 521 PTKQVTLTDLGRSRMKVQVRAPTAR--LPGAMSHPORFSEVOISRLSTIFASLSFA 578  
 OY 532 LILITFYAY-GLKKPNKLTLCWPTVNPAPSSIATWHGDDPDKLNLKESDSVNTED 590  
 DB 579 SYLVGSLGTYGLNR--AAHLC-PPLPTPCGSTAVEPFGSOG-----KAMQMCNPD 629  
 OY 591 RILKPCSTPSDKLYIDKLNVNFGVLOEIFTDEARTGOENMLGGERKNGYVTCPPRPDCL 650  
 DB 630 --PEVLVPRDALVE-----MPGDR----- 648  
 OY 651 GKSEELPVSEIPEPKSQYRSRMPSTREAKEQLFSQSLVPHLCEGAPN--- 706  
 DB 649 GDGTESPQAAECA-----LDTRPLETORORQOALSEARL---GLAREDCPRGDLA 699  
 OY 707 ---PYLKNSTAREFLVSEKLPETHKE 731  
 DB 700 HTVLPILGLGVYTGAGSALVDLMLRHKTRAE 728

RESULT 14  
 ID CALIC MOUSE STANDARD: PRF: 3119 AA.  
 AC 060847; P70332;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Collagen alpha 1(XII) chain precursor.  
 GN COL12A1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-1 AND XIIA-2).  
 RP STRAIN=Swiss Webster, and C57BL/6J; TISSUE=Skin;  
 RC MEDLINE=961170761; PubMed=8601036;  
 RA Boehme K., Li Y., Oh P.S., Olsen B.R.;  
 RA "Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic development.";  
 RL dev. Dyn. 204:432-445(1995).  
 RN [2]  
 RP PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS XIIA-2 AND XIIA-2).  
 RP STRAIN=C57BL/6J; TISSUE=Skin fibroblast;  
 RC MEDLINE=99348349; PubMed=10419532;  
 RA Kanla A.M., Reichenderger E., Baur S.T., Karimub N.Y., Taylor R.W.,  
 RA Olsen B.R., Nishimura I.;  
 RT "Structural variation of type XII collagen at its carboxyl-terminal NCI domain generated by tissue-specific alternative splicing.";  
 RT J. Biol. Chem. 274:22053-22059(1999)  
 CC -1- FUNCTION: TYPE XII COLLAGEN INTERACTS WITH TYPE I COLLAGEN-CONTAINING FIBRILS, THE COL1 DOMAIN COULD BE ASSOCIATED WITH THE SURFACE OF THE FIBRILS, AND THE COL2 AND NC3 DOMAINS MAY BE LOCALIZED IN THE PERIFIBRILLAR MATRIX (BY SIMILARITY).  
 CC -1- SUBUNIT: TRIMER OF IDENTICAL CHAINS EACH CONTAINING 190 KDA OF



QY 125 PKIFRKPVLGIKIMIQIEMIKPELAPVSSD-----LKYLRFRTVNST 168  
 DB 713 ---FSV-PIEGEETIAEVKGV-PRNLKYTDDETDSFKLWSQAPGRVLRIRRYRPSVSG 767  
 QY 169 SMVEYNFAKNRKNQYTNLTGLOPTEYVIALRCVAKESKFWSDWSEKMGMEDEAPC 228  
 DB 768 ESKEVSTPANORR-----TLENLPDPTKYEISV-----IAEYPSGSPGLTGNATEEVR 818  
 QY 229 GLELMRVLPKPAEADRRVRLLMKKARAPVLEKTLGNINMYPPSNNTLPTM---NTT 285  
 DB 819 GNP--RDLRVSDAT--TSTLKLWSRAPG-----KVKQYLVTYTPAGGETQGVTRGDTT 870  
 QY 286 NQOLELHGSEFWWSMISYNSIGKSPATLIRPIAIOESFOCIEMVACVAD-----QL 341  
 DB 871 TTMKLAKKEGTQYDLSVRLALASGGEALSGSGSLERGSP-----QNLVTKDITDTSI 925  
 QY 342 VVKMOSSALDVNTMNIEM---PPVDSEPTLISWESVSQATNMTIQDKLKEPWCYNISV 398  
 DB 926 GAYWTSADQWNGYVSWKSLYDDIEAGETTLNGDAIHTMI-----ENLQPEYKIKISV 979  
 QY 399 YPMILDKYGEPSYIAVAKEGVPSPEETKVENIGKVITVTKELPKSEKGIICNTI 458  
 DB 960 FATVSSGGEPE--VYGDATTELISQSKILRDEEHEHTMRVTKAP-----GKVVNRYV 1032  
 QY 459 FYOABGG-----KGFSTVNSIIOYGLSKRKTSYIVQVASTSAGTNGTSINFYTL 513  
 DB 1033 YVRPGGGRQWAKVPTVTSV-----LKRLQPTTIDTIVLPM-----YKT- 1075  
 QY 514 SFSVEIILLISLIGGCLILITVAVGLKPKNKLT-----HLCWPTVPNPAESS 564  
 DB 1076 -----GEGKLRQSGTJASFRKSPRLKTSDPMTSSFRVYWEPAPEVKGY 1121  
 QY 565 IATWH--GGDFK-DKLNKESDPSVNTEDRIILKPCSTPSDKLVIKLVNFEVNOIEFT 621  
 DB 1122 KTFEPTGDDRLGLVLPDNTV-----VLEEL-- 1151  
 QY 622 DEARTGOENLGEKNGVYTCFPRDCPLKGSFEELPYSPETIPKRSOYLRSMEGTERP 681  
 DB 1152 -RAGTTRYVNVFGMFDGGSPL-----VCGEMTILSDTTPV-----FLSSGMCLTRFA 1200  
 QY 682 EAKEQLFSG 691  
 DB 1201 EADIVLVDG 1210

RESULT 15  
 LEPR\_HUMAN  
 ID LEPR\_HUMAN STANDARD; PRT; 1165 AA.  
 AC P48357; Q13592; Q13593; Q13594; Q92919; Q92920; Q92921;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (HuB219).  
 GN LEP-R OR OB-R DB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORMS B AND E).  
 RC TISSUE=Brain;  
 RX MEDLINE=96128129; PubMed=8548812;  
 RA Tartaglia L.A., Dembski M., Wang X., Deng N., Culpepper J.,  
 RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,  
 RA Muir G., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,  
 RA Mays G.G., Woolf E.A., Montore C.A., Tepper R.I.;  
 RT "Identification and expression cloning of a leptin receptor, OB-R.";  
 RL Cell 83:1263-1274(1995).  
 RN (2)  
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).  
 RC TISSUE=retal liver;  
 RX MEDLINE=96398968; PubMed=8805376;  
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,

RA Mathews W.;  
 RT "A role for leptin and its cognate receptor in hematopoiesis.";  
 RL Curr. Biol. 6:1170-1180(1996).  
 RN (3)  
 RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS ARG-109 AND ARG-223.  
 RX MEDLINE=97301763; PubMed=9158141;  
 RA Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;  
 RT "Structure and sequence variation at the human leptin receptor gene in  
 RT lean and obese Pima Indians.";  
 RL Hum. Mol. Genet. 6:675-679(1997).  
 RN (4)  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RX MEDLINE=97215244; PubMed=9061609;  
 RA Luch S.-M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,  
 RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;  
 RT "Cloning and characterization of a human leptin receptor using a  
 RT biologically active leptin immunoadhesin.";  
 RL J. Mol. Endocrinol. 18:77-85(1997).  
 RN (5)  
 RP SEQUENCE FROM N.A. (ISOFORMS A; C AND D).  
 RC TISSUE=retal liver;  
 RX MEDLINE=96206286; PubMed=8616721;  
 RA Cioffi J.A., Shaler A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,  
 RA Platika D., Snodgrass H.R.;  
 RT "Novel B219/OB receptor isoforms: possible role of leptin in  
 RT hematopoiesis and reproduction.";  
 RL Nat. Med. 2:585-589(1996).  
 RN (6)  
 RP ALTERNATIVE SPLICING DUE TO AN ENDOGENOUS RETROVIRUS.  
 RX MEDLINE=99128223; PubMed=9929394;  
 RA Kapitonov V.V., Jurka J.;  
 RT "The long terminal repeat of an endogenous retrovirus induces  
 RT alternative splicing and encodes an additional carboxy-terminal  
 RT sequence in the human leptin receptor.";  
 RL J. Mol. Evol. 48:248-251(1999).  
 RN (7)  
 RP CARBOHYDRATE-LINKAGE SITES, DISULFIDE BONDS, AND PARTIAL SEQUENCE.  
 RX MEDLINE=99003211; PubMed=9786864;  
 RA Hanlu M., Arakawa T., Bures E.J., Young Y., Hui J.O., Rohde M.F.,  
 RA Welcher A.A., Horan T.;  
 RT "Human leptin receptor. Determination of disulfide structure and  
 RT N-glycosylation sites of the extracellular domain.";  
 RL J. Biol. Chem. 273:28691-28699(1998).  
 RN (8)  
 RP VARIANT ARG-223.  
 RX MEDLINE=96270489; PubMed=8666155;  
 RA Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;  
 RT "The hypothalamic leptin receptor in humans: identification of  
 RT identical sequence polymorphisms and absence of the db/db mouse and  
 RT fa/fa rat mutations.";  
 RL Diabetes 45:992-994(1996).  
 RN (9)  
 RP VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.  
 RX MEDLINE=97289527; PubMed=9144432;  
 RA Ewald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,  
 RA Andersen T., Chung W.K., Leibel R.L., Pedersen O.;  
 RT "Amino acid variants in the human leptin receptor: lack of association  
 RT to juvenile onset obesity.";  
 RL Biochem. Biophys. Res. Commun. 233:248-252(1997).  
 RN (10)  
 RP VARIANTS ARG-109; ARG-223 AND ASN-656.  
 RX MEDLINE=97431549; PubMed=9287054;  
 RA Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,  
 RA Southern M., Udaï J.N., Kahle B., Leibel R.L.;  
 RT "Exonic and intronic sequence variation in the human leptin receptor  
 RT gene (LEPR).";  
 RL Diabetes 46:1509-1511(1997).  
 RN (11)  
 RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.  
 RX MEDLINE=99075638; PubMed=9860295;  
 RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,  
 RA Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;  
 RT "Transmission disequilibrium and sequence variants at the leptin

RT receptor gene in extremely obese German children and adolescents.";  
 RL Hum. Genet. 103:540-546(1998).  
 RN [12]  
 RP VARIANTS ARG-109; ARG-223 AND ASN-656.  
 RX MEDLINE=97318795; PubMed=9175732;  
 RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,  
 RA Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;  
 RT "Leptin receptor gene variation and obesity: lack of association in a  
 RT white British male population."  
 RL Hum. Mol. Genet. 6:869-876(1997).  
 CC -1- FUNCTION: Receptor for obesity factor (leptin). Involved in the  
 CC regulation of fat metabolism and in a hematopoietic pathway  
 CC required for normal lymphopoiesis. May play a role in  
 CC reproduction.  
 CC -1- FUNCTION: The short form (isoform A) may act to transport leptin  
 CC to the cerebrospinal fluid (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E  
 CC which could be soluble.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=5;  
 CC Name=A; Synonyms=13.2, OBRD;  
 CC IsoId=P48357-1; Sequence=Displayed;  
 CC Name=B; Synonyms=6.4, HUB219.3;  
 CC IsoId=P48357-2; Sequence=VSP\_001689, VSP\_001690;  
 CC Name=C; Synonyms=12.1, OBRa;  
 CC IsoId=P48357-3; Sequence=VSP\_001691, VSP\_001692;  
 CC Name=D; Synonyms=HUB219.2;  
 CC IsoId=P48357-4; Sequence=VSP\_001693, VSP\_001694;  
 CC Name=E;  
 CC IsoId=P48357-5; Sequence=VSP\_001688;  
 CC -1- TISSUE SPECIFICITY: Isoform A expressed in fetal liver and in  
 CC hematopoietic tissues and choroid plexus. In adults highest  
 CC expression in heart, liver, small intestine, prostate and ovary.  
 CC Low level in lung and kidney. Isoform B is highly expressed in  
 CC hypothalamus.  
 CC -1- DOMAIN: The cytoplasmic domain may be essential for intracellular  
 CC signal transduction by activation of JAK tyrosine kinase and  
 CC STATs.  
 CC -1- PTM: Phosphorylated on two tyrosine residues. Tyr-986 may be the  
 CC major site of phosphorylation. Phosphorylation on both sites is  
 CC required for full activity (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: Contains 3 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 CC -----  
 DR EMBL: U43168; AAA93015.1; -;  
 DR EMBL: U66495; AAB07495.1; -;  
 DR EMBL: U66496; AAB07496.1; -;  
 DR EMBL: U66497; AAB07497.1; -;  
 DR EMBL: U59263; AAB09673.1; -;  
 DR EMBL: U59248; AAB09673.1; JOINED.  
 DR EMBL: U59249; AAB09673.1; JOINED.  
 DR EMBL: U59250; AAB09673.1; JOINED.  
 DR EMBL: U59252; AAB09673.1; JOINED.  
 DR EMBL: U59253; AAB09673.1; JOINED.  
 DR EMBL: U59254; AAB09673.1; JOINED.  
 DR EMBL: U59255; AAB09673.1; JOINED.  
 DR EMBL: U59256; AAB09673.1; JOINED.  
 DR EMBL: U59257; AAB09673.1; JOINED.  
 DR EMBL: U59258; AAB09673.1; JOINED.  
 DR EMBL: U59259; AAB09673.1; JOINED.  
 DR EMBL: U59260; AAB09673.1; JOINED.  
 DR EMBL: U59261; AAB09673.1; JOINED.  
 DR EMBL: U59262; AAB09673.1; JOINED.  
 DR EMBL: U50748; AAC23650.1; -;

DR EMBL: U52912; AAC50509.1; -;  
 DR EMBL: U52913; AAC50510.1; -;  
 DR EMBL: U52914; AAC50511.1; -;  
 DR HSSP: P16471; 1BP3.  
 DR Gene; HGNC:6554; LEPR.  
 DR MIM: 601007; -;  
 DR GO: GO:0004888; F:transmembrane receptor activity; TAS.  
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 DR GO: GO:0007275; P:development; TAS.  
 DR GO: GO:0006112; P:energy reserve metabolism; TAS.  
 DR InterPro: IPR002966; CR1A.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
 DR InterPro: IPR007110; Ig-like.  
 DR Pfam: PF00041; fn3; 2.  
 DR SMART: SM00060; FN3; 4.  
 DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 DR PROSITE: PS00835; Ig-LIKE; 1.  
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat; Alternative splicing; Phosphorylation;  
 KW Polymorphism.  
 FT SIGNAL 1 21  
 FT CHAIN 22 1165 LEPTIN RECEPTOR  
 FT DOMAIN 22 839 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 840 862 POTENTIAL.  
 FT DOMAIN 863 1165 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 237 320 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 325 429 IG-LIKE.  
 Query Match 5.7%; Score 221; DB 1; Length 1165;  
 Best Local Similarity 19.2%; Pred. No. 1.2e-08;  
 Matches 142; Conservative 121; Mismatches 296; Indels 180; Gaps 34;  
 27 NISC-VYYRKNLCTWSPGKSTSYQYTVKRTAFGEHNDCTNSS----- 73  
 433 NISCETDGLTKMTKRWSTTQSLAESTLQRYRSSLY--CSDIPSTHPISEPKCYL 490  
 74 TSENRA SCSEFLPRITPIDNTIEVEAENGDCVIRKSHMTYMRLENIAKTEPKIRVAPV 133  
 491 QSDGEYECF--QPIFLSGYTMWRIRHNSLGSLSDPCTVLPDVSVPVLPSSVKAELT 548  
 134 LGIKRMIOETWKPELPAYSSDLKTLRP-RVNVSTW--MEVNAKRNKDKNOTYNLTG 190  
 549 INI-GLIKISWEKPEP--ENNLOFQIRXGSGKEVQMKVEVYDAKSSVSLPVPDCA 605  
 191 LQPFREYIALRCAYKES-KFMSDWSQEMGMTTE-EPK-CLEDMRLKPAEADGRPV 247  
 606 V-----YAVQYRCKRLDGLGYSNMNSNPAITYVMDIKYPMKRPFRRIINDTKKKNV 660  
 248 RLWKRKAGAPYLEKTLGYNINWYYPESNTNLTEMTNTNOOLEHLGSEFW-----VS 301  
 661 TLMKRLPKKNDSLGSGVRVIVNHNSCN-----GTMSDEVGNHTKFTFLWTEQAHVYT 713  
 302 MISTVSLGK-----PVATLRIPAIQKESQCLIEWQACVADQLVYKKQSSALD 351  
 714 VLAINSIGASVANFNLTSPMSKVN-----VQSLSAVPLNNSCV-----IYSWILSPSD 764  
 352 VNT--WMIEMPDDVSEPTTLTSMESVSQATNWTIQDGLKPKWCNISVYPLLHKVGP 409  
 765 YKLMFIIEW--KNINDEGEIKWLRISSVKKYIYHDFIPEKIOFSLYFLPMEGVGRP 822  
 410 YSIQAYAKEGVSEPE-----TVENIGVKTVT-----ITKKEIPKSERGG 451  
 823 KIINSFTQDDIEKHQSDAGLYVIYVLISSILLGLTLLISHQKAKKLFWEVDYPRPKN-- 880  
 452 IICNTTIYYQAGGKGFSK-----TVNSIIQYGL--ESLKRKTSY----- 490  
 881 --CSWA-----OGINFORPETFEHLFKHTASVYCGPLLEPETISDIDSVTSMKNKD 932  
 491 -----IYQVMASTS-ACGTNGTSTINEKTLSPSVFEIILLISLIGGILLIILLVANGL 543  
 933 EMPTTVVSLSTDLDEKGSVCISDQFNVSNSSEAGTEVTEYEAESQROPFVKYATLLSN 992



```

OY 544 KKP-----NKLTPLCPVTPNPAESSI--ATWHDDEKDKLNLKESDDSYNTEDR 591
Db 993 SKPSETGEQGLINSSVTKCFSSKNSPLKDSFNSNSW---ETBAQAFILSDQHFN---- 1045
OY 592 ILKPCSTPSDKLVIDKLVNFGNVLOE-----IFTDEARTGOE 629
Db 1046 IISPHLTFSEGL--DELKLEGNPEENNDRKSIYILGVTSIKKRESGVLLTDKSR---- 1099
OY 630 NNLGGEKNGYVTCPPRPDC 648
Db 1100 -----VSCPPRPAC 1108

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Search completed: August 4, 2003, 11:23:16  
 Job time : 31 secs

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OM protein - protein search, using sw model

Run on: August 4, 2003, 11:20:22 ; Search time 111 seconds  
(without alignments)  
1701.752 Million cell updates/sec

Title: US-09-892-949-2  
Perfect score: 3908  
Sequence: 1 MMWTWALMLPCLCKFSLAA.....VTAREFLVSEKLPENKGEV 732

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3908	100.0	732	4	08N117
2	2635.5	67.4	509	4	08WY10
3	2132.5	54.6	716	11	08K5B1
4	2128.5	54.5	716	11	08R501
5	707.5	18.1	918	13	09M609
6	664.5	17.0	235	11	08BSU3
7	620.5	15.9	881	13	057519
8	606	15.5	710	13	057520
9	430.5	11.0	848	6	08WN24
10	425.5	10.9	861	6	08MJ51
11	412.5	10.6	861	6	09BEG2
12	395.5	10.1	1093	11	070535
13	375	9.6	979	4	099650
14	361	9.2	1083	13	080F07
15	343	8.8	970	11	088821
16	342.5	8.8	971	11	070458

17	247	6.3	623	11	070394	070394 mus musculu
18	233.5	6.0	1147	13	09DDK1	09ddk1 melagris g
19	233	6.0	422	4	09UHH5	09uhh5 homo sapien
20	233	6.0	422	4	075452	075452 homo sapien
21	232	5.9	1148	13	091BA7	091ba7 homo sapien
22	231	5.9	425	11	09JW58	09jw58 mus musculu
23	216	5.5	2222	5	097394	097394 drosophila
24	213	5.5	1146	13	091RV6	091rv6 gallus gall
25	207	5.3	636	4	060624	060624 homo sapien
26	207	5.3	1212	5	095TG0	095tg0 drosophila
27	207	5.3	2016	5	08MKM7	08mkm7 drosophila
28	207	5.3	2016	5	08MKM6	08mkm6 drosophila
29	207	5.3	2016	5	09NBA1	09nba1 drosophila
30	207	5.3	2019	5	08MKM8	08mkm8 drosophila
31	204	5.2	2221	5	09UIM1	09uim1 drosophila
32	197	5.0	152	6	09N148	09n148 mecaea mula
33	196.5	5.0	608	11	099J21	099j21 mus musculu
34	194.5	5.0	1723	11	08CHB2	08chb2 mus musculu
35	194	5.0	292	11	08C7G1	08c7g1 mus musculu
36	193.5	5.0	629	4	08NFG9	08nfg9 homo sapien
37	193.5	5.0	1842	4	081ZY3	081zy3 homo sapien
38	193.5	5.0	2053	4	08WY17	08wy17 homo sapien
39	193.5	5.0	2053	4	081ZY4	081zy4 homo sapien
40	193.5	5.0	2113	4	08TDB4	08tdb4 homo sapien
41	193	4.9	26926	4	08WZB3	08wzb3 homo sapien
42	193	4.9	34350	4	08WZ42	08wz42 homo sapien
43	192.5	4.9	1232	13	090284	090284 carassius a
44	190.5	4.9	1898	11	09ED17	09ed17 mus musculu
45	190	4.9	4280	5	09UB29	09ub29 caenorhabdi

## ALIGNMENTS

RESULT 1	
08N117	PRELIMINARY: PRT; 732 AA.
AC 08N117:	
DT 01-OCT-2002 (TREMBLrel. 22. Created)	
DT 01-OCT-2002 (TREMBLrel. 22. Last sequence update)	
DT 01-MAR-2003 (TREMBLrel. 23. Last annotation update)	
DE Gpi30-like monocyte receptor.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_Taxid=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=21988187; PubMed=11877449;	
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;	
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals Proliferation, and Activates STAT-3 and STAT-5.";	
RL J. Biol. Chem. 277:16831-16836 (2002).	
DR EMBL: AF466620; AAM27958.1; -	
DR InterPro: IPR002996; CRIA.	
DR InterPro: IPR003961; FN_III.	
DR Pfam: PF00041; fn3; 1.	
DR SMART: SM00060; FN3; 3.	
RK Receptor.	
RW SEQUENCE 732 AA; 82953 MW; 30F84BD3DD99A20E CRC64;	
SO	
Query Match 100.0%; Score 3908; DB 4; Length 732;	
Best Local Similarity 100.0%; Pred. No. 6.5e-304;	
Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY 1 MMWTWALMLPCLCKFSLAAPAKPENISCVYYRKNLTCTWSPGKETSYYQTVVKRYA 60	
DB 1 MMWTWALMLPCLCKFSLAAPAKPENISCVYYRKNLTCTWSPGKETSYYQTVVKRYA 60	
OY 61 FGEKHDNCTTSSSENASCSPFLPRITTDNTTIEVEANGGVKISHMTYRLLENIA 120	
DB 61 FGEKHDNCTTSSSENASCSPFLPRITTDNTTIEVEANGGVKISHMTYRLLENIA 120	

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OY 121 KTEPKIFRVKPVLCIKRMIOEWIKPELAPVSSDLKYYTLRFRVNSTSMMEVNEAKNRK 180
DB 121 KTEPKIFRVKPVLCIKRMIOEWIKPELAPVSSDLKYYTLRFRVNSTSMMEVNEAKNRK 180
OY 181 DKNQYNTLTGLOPFTEYIYALRCAYKESKFSMSQEMKMGTEEPAPCGLELMRYLPAE 240
DB 181 DKNQYNTLTGLOPFTEYIYALRCAYKESKFSMSQEMKMGTEEPAPCGLELMRYLPAE 240
OY 241 ADGRRPVRLMKKAGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLEHLGGESEFW 300
DB 241 ADGRRPVRLMKKAGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLEHLGGESEFW 300
OY 301 SMISYNSLGKSPVATLRIPALQKSFQCIYEWQACVADQLVVKQSSALDVNTWIMEF 360
DB 301 SMISYNSLGKSPVATLRIPALQKSFQCIYEWQACVADQLVVKQSSALDVNTWIMEF 360
OY 361 PDVDEPTLTLSWESYSQATNMNTIOODKLPKPCYNISYVPMHDKVGPYSIOAYAKRGV 420
DB 361 PDVDEPTLTLSWESYSQATNMNTIOODKLPKPCYNISYVPMHDKVGPYSIOAYAKRGV 420
OY 421 PSEGETVENIGVKTVTITWKEIPKSERKGIICNYTTFYQAEKGKFSKTVNSSILOYG 480
DB 421 PSEGETVENIGVKTVTITWKEIPKSERKGIICNYTTFYQAEKGKFSKTVNSSILOYG 480
OY 481 LESLKRKTSYIVQVMASTAGTNGTSINFKTLSPFVEIILITSLIGGLILILITVA 540
DB 481 LESLKRKTSYIVQVMASTAGTNGTSINFKTLSPFVEIILITSLIGGLILILITVA 540
OY 541 YGLKPKNLTLHCWPTVNPAPASSIATWHDGDFKRLKMLKESDSDSVNTEDLKPCSTPS 600
DB 541 YGLKPKNLTLHCWPTVNPAPASSIATWHDGDFKRLKMLKESDSDSVNTEDLKPCSTPS 600
OY 601 DKLVIDKLIVNFGNVLQEIFTDEARTGOENNLGCKNGVYTCFPRDCPLKGFPELPS 660
DB 601 DKLVIDKLIVNFGNVLQEIFTDEARTGOENNLGCKNGVYTCFPRDCPLKGFPELPS 660
OY 661 PEIPPRKSOYLRSRMEPTREPAKQQLFSGOSLVPDHLCEGAPNPLKNSVTAREFLV 720
DB 661 PEIPPRKSOYLRSRMEPTREPAKQQLFSGOSLVPDHLCEGAPNPLKNSVTAREFLV 720
OY 721 SEKLPEHTKGEV 732
DB 721 SEKLPEHTKGEV 732

```

## RESULT 2

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O8WYJ0 PRELIMINARY: PRT: 509 AA.
AC O8WYJ0:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CRJ3 protein.
CN CRJ3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., He L., Yuan Z., Cao X.;
RT "A novel soluble type I cytokine receptor."
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF106913; AAL36452.1;
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 2.
DR SMART: SMO0060; FN3; 3.
SQ SEQUENCE 509 AA; 58390 MW; 5DC85C59E170D44B CRC64;

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Query Match 67.4%; Score 2635.5; DB 4; Length 509;  
 Best Local Similarity 98.4%; Pred. No. 2.7e-202;  
 Matches 493; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

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OY 1 MMTWALMLPSLCKFSLAALPAKPENISCVYYRRKNTCTWSPCKETSYQTYVKRYA 60
DB 14 MMTWALMLPSLCKFSLAALPAKPENISCVYYRRKNTCTWSPCKETSYQTYVKRYA 73
OY 61 FGEKHDCNTSSSTSENBAKSFLLPRTITPDNTTIEVAENGQGVKSHMTYRLENIA 120
DB 74 FGEKHDCNTSSSTSENBAKSFLLPRTITPDNTTIEVAENGQGVKSHMTYRLENIA 133
OY 121 KTEPKIFRVKPVLCIKRMIOEWIKPELAPVSSDLKYYTLRFRVNSTSMMEVNEAKNRK 180
DB 121 KTEPKIFRVKPVLCIKRMIOEWIKPELAPVSSDLKYYTLRFRVNSTSMMEVNEAKNRK 180
OY 181 DKNQYNTLTGLOPFTEYIYALRCAYKESKFSMSQEMKMGTEEPAPCGLELMRYLPAE 240
DB 181 DKNQYNTLTGLOPFTEYIYALRCAYKESKFSMSQEMKMGTEEPAPCGLELMRYLPAE 240
OY 241 ADGRRPVRLMKKAGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLEHLGGESEFW 300
DB 241 ADGRRPVRLMKKAGAVLEKTLGYNIWYYPESNTNLTETMNTTNOOLEHLGGESEFW 300
OY 301 SMISYNSLGKSPVATLRIPALQKSFQCIYEWQACVADQLVVKQSSALDVNTWIMEF 360
DB 301 SMISYNSLGKSPVATLRIPALQKSFQCIYEWQACVADQLVVKQSSALDVNTWIMEF 360
OY 361 PDVDEPTLTLSWESYSQATNMNTIOODKLPKPCYNISYVPMHDKVGPYSIOAYAKRGV 420
DB 361 PDVDEPTLTLSWESYSQATNMNTIOODKLPKPCYNISYVPMHDKVGPYSIOAYAKRGV 420
OY 421 PSEGETVENIGVKTVTITWKEIPKSERKGIICNYTTFYQAEKGKFSKTVNSSILOYG 480
DB 421 PSEGETVENIGVKTVTITWKEIPKSERKGIICNYTTFYQAEKGKFSKTVNSSILOYG 480
OY 481 LESLKRKTSYIVQVMASTAG 501
DB 481 LESLKRKTSYIVQVMASTAG 509

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## RESULT 3

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O8K5B1 PRELIMINARY: PRT: 716 AA.
AC O8K5B1:
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE GP130-like monocyte receptor.
CN GLMR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21986187; PubMed-11877449;
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals
RT Proliferation, and Activates STAT-3 and STAT-5."
RL J. Biol. Chem. 277:16831-16836(2002).
DR EMBL: AF486621; AAM27959.1;
DR MGI: 2180511; Glmr.
DR InterPro: IPR002996; CRIA.
DR Pfam: PF00041; fn3; 1.
DR SMART: SMO0060; FN3; 3.
SQ SEQUENCE 716 AA; 80641 MW; 39E6B0B2537C7E5 CRC64;

```

Query Match 54.6%; Score 2132.5; DB 11; Length 716;  
 Best Local Similarity 59.4%; Pred. No. 8.3e-162;  
 Matches 437; Conservative 85; Mismatches 189; Indels 25; Gaps 10;  
 2 MMTWALMLPSLCKFSLAALPAKPENISCVYYRRKNTCTWSPCKETSYQTYVKRYA 61  
 ||| ||| ||||||||| ||||||||| ||| ||| |||

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Db 1 MMTLALWAFSLCKFSLAALPDKRENISCVYFEDRLCTWRPEKENTDSYIVTLTYSY 60
QY 62 GEKHDNCTSSSTSENASCSPFLPRITL--PDNYTTEVEANGDVYKSHMTWRLNT 119
Db 61 GK-----SNVSDNATEASYSPFRSCAMPDICSVEQAQNDGKVKSDITWHLISI 112
QY 120 AKTEPKIFRYKPVLGIRMIQIEMIKPELAPVSSDKYTLRFRTVNSTSMVEYNFAKNR 179
Db 113 AKTEPPIILISVNP1--CNRMFQIOW-KPREKTRGFPLVCMILRFRTVNSKRTVEYNF---- 165
QY 180 KDKNQTYNLGLOPFTYVIALRCVAKESKFWSDMSQKMGMEEARPCGLEMLRVLPKA 239
Db 166 ENCKOVNLTGLQAFTEYVIALRFRFNDSRYSKWSKEETRVTEEVPHVLDLWRLLEPA 225
QY 240 EADRRVRLMLKARAPVLEKTLGYINMYPPESNTNLTETMTTNOOLELHGGSEFW 299
Db 226 DMNDKRVRLMLKARAPVLEKTLGYHIOYFAENSNTLNTINNITTOVELLMSQASH 285
QY 300 VSMISYNSLGSPPATLRIPALIOESKFOCIEVMQACVAEDOLVYKMOSSALDVTWMIEM 359
Db 286 VSVTSFNSLGSQOETLIRIPDVHEKTFQYIKSMQAYIAEPLLVYNNQSSIPAVDTWIVEM 345
QY 360 FPDVD--SEPTTLESVESQATNWTIOQDKLPFCYINISYVPMILHDKVGEPSIOAYAKE 418
Db 346 LPEAMSKFPALSWESQVYNTMTIEODKLPFCYINISYVPLGHRVGEPSIOAYAKE 405
QY 419 GVPSEGETRYENIGVTVITITWKEIKPSERKGIICVYTFYQAEKGKSGSKTYNSSILO 478
Db 406 GTPKGEPTREYENIGLRTATITWKEIKPSANGFINNTVYFQAEKGKSKTYNSSILO 465
QY 479 YGLESLRKTSYIVQVNASTAGTNGTSINFKTLSPVEEILITSLIGGLLILITL 538
Db 466 CDLESILRRTSYTYVWMASTAGTNGVRINFKTLISVEFIVLTLISVGGGLLSIKT 525
QY 539 VAYGLKRPKNLTLHCWPTVPNPASSIATWHGDFKDKLNLKESDSDSVNTEDRILKPCST 598
Db 526 VTFGLRKPNNLTLPLCCPDVPNPASSLATWLGDFK-KSNMKETGNSGNTEDVYLKPCPV 584
QY 599 PSDKLVIDKLIVNGVNLQELFTDEARTGOENNLGEGKNGVYTCPPRPDCPLGKSFELL 658
Db 585 PAD--LIDKLIVNENLELVLTLEAGKQASILGEGANEVYTPSRPDGPGKSFEPSS 642
QY 659 VSPETPRKSOYLRSMEPEGRPEAKQLLFSGSS--LVPDHLCEEGAPNPYLKNSVTAR 716
Db 643 ILTEVASDSDSHSTCSRADEAYSELARQPSSCSPGLSPRR--EDQAQNPYLKNSVTAR 700
QY 717 EFLVSEKLPEHTKGEV 732
Db 701 EFLVHENIPEHSKGEV 716

RESULT 4
Q8RS01 PRELIMINARY; PRT; 716 AA.
AC Q8RS01;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Cytokine receptor NR10.
GN GLMR OR NR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
RT "Polymorphism between C57BL/6 and Balb/c in the novel cytokine
receptor NR10."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083111; BAB88745.1; -.
MGD; MGI:2180511; GImr.
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DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_LIII.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 3.
DR KEGG; K01101; IL13.
SQ SEQUENCE 716 AA; 80598 MW; CBF8718DCD40FC7 CRC64;

Query Match 54.5%; Score 2128.5; DA 11; Length 716;
Best Local Similarity 59.4%; Pred. No. 1,7e-161;
Matches 437; Conservative 86; Mismatches 188; Indels 25; Gaps 10;

QY 2 MMTLWALMPSLCKFSLAALPAKRENISCVYKRNLTCTWSPKERTSYQYTVKRYAF 61
Db 1 MMTLALWAFSLCKFSLAALPDKRENISCVYFEDRLCTWRPEKENTDSYIVTLTYSY 60
QY 62 GEKHDNCTSSSTSENASCSPFLPRITL--PDNYTTEVEANGDVYKSHMTWRLNT 119
Db 61 GK-----SNVSDNATEASYSPFRSCAMPDICSVEQAQNDGKVKSDITWHLISI 112
QY 120 AKTEPKIFRYKPVLGIRMIQIEMIKPELAPVSSDKYTLRFRTVNSTSMVEYNFAKNR 179
Db 113 AKTEPPIILISVNP1--CNRMFQIOW-KPREKTRGFPLVCMILRFRTVNSKRTVEYNF---- 165
QY 180 KDKNQTYNLGLOPFTYVIALRCVAKESKFWSDMSQKMGMEEARPCGLEMLRVLPKA 239
Db 166 ENCKOVNLTGLQAFTEYVIALRFRFNDSRYSKWSKEETRVTEEVPHVLDLWRLLEPA 225
QY 240 EADRRVRLMLKARAPVLEKTLGYINMYPPESNTNLTETMTTNOOLELHGGSEFW 299
Db 226 DMNDKRVRLMLKARAPVLEKTLGYHIOYFAENSNTLNTINNITTOVELLMSQASH 285
QY 300 VSMISYNSLGSPPATLRIPALIOESKFOCIEVMQACVAEDOLVYKMOSSALDVTWMIEM 359
Db 286 VSVTSFNSLGSQOETLIRIPDVHEKTFQYIKSMQAYIAEPLLVYNNQSSIPAVDTWIVEM 345
QY 360 FPDVD--SEPTTLESVESQATNWTIOQDKLPFCYINISYVPMILHDKVGEPSIOAYAKE 418
Db 346 LPEAMSKFPALSWESQVYNTMTIEODKLPFCYINISYVPLGHRVGEPSIOAYAKE 405
QY 419 GVPSEGETRYENIGVTVITITWKEIKPSERKGIICVYTFYQAEKGKSGSKTYNSSILO 478
Db 406 GTPKGEPTREYENIGLRTATITWKEIKPSANGFINNTVYFQAEKGKSKTYNSSILO 465
QY 479 YGLESLRKTSYIVQVNASTAGTNGTSINFKTLSPVEEILITSLIGGLLILITL 538
Db 466 CDLESILRRTSYTYVWMASTAGTNGVRINFKTLISVEFIVLTLISVGGGLLSIKT 525
QY 539 VAYGLKRPKNLTLHCWPTVPNPASSIATWHGDFKDKLNLKESDSDSVNTEDRILKPCST 598
Db 526 VTFGLRKPNNLTLPLCCPDVPNPASSLATWLGDFK-KSNMKETGNSGNTEDVYLKPCPV 584
QY 599 PSDKLVIDKLIVNGVNLQELFTDEARTGOENNLGEGKNGVYTCPPRPDCPLGKSFELL 658
Db 585 PAD--LIDKLIVNENLELVLTLEAGKQASILGEGANEVYTPSRPDGPGKSFEPSS 642
QY 659 VSPETPRKSOYLRSMEPEGRPEAKQLLFSGSS--LVPDHLCEEGAPNPYLKNSVTAR 716
Db 643 ILTEVASDSDSHSTCSRADEAYSELARQPSSCSPGLSPRR--EDQAQNPYLKNSVTAR 700
QY 717 EFLVSEKLPEHTKGEV 732
Db 701 EFLVHENIPEHSKGEV 716

RESULT 5
Q9W609 PRELIMINARY; PRT; 918 AA.
AC Q9W609;
ID Q9W609;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Glycoprotein 130 precursor.
GN GPI30.
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Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF041845; AAC03531.1; -  
DR HSSP: P40189; IBOU.  
DR InterPro: IPR002996; CR1A.  
DR InterPro: IPR003961; FN.III.  
DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
DR Pfam: PF00041; fn3; 4.  
DR SMART: SM00060; FN3; 3.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
SO SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 15.9%; Score 620.5; DB 13; Length 881;  
Best Local Similarity 25.5%; Pred. No. 1.2e-40;  
Matches 194; Conservative 123; Mismatches 344; Indels 101; Gaps 23;

16 PSALALAKPENISCVYYKRLNLCWSPGKETS-YIQYTKRYTA-FGEHMDCTINSS 73  
116 FTGLPDKPTNLCTIYNDNLCTWDPGPTMLPTNYTLISHMAHFGANYCGANN-- 173  
74 TSENKASCFELPRITTPDNTYIEAENGSGVYKSHMTYRLNIAKTEPKIFRYKPV 133  
174 -----SCTIHSPOFOYIOTTFVEATNELGIQKSELTITDPVNIYKPNPQLSELLS 227  
134 LGIKRMIOIEMIKELAPVSSDLKYTLRFVTNSTSMWENFAKRRDKNOTYMLTGLDP 193  
228 LELPNALIKIEWKN--ITNAFNLYKNIYRPVKQDW-EMVPEDTASHRDSFTLODLP 284  
194 FTEVIALRCVAKSK-FMSDMSOEKGMTEEAPC-GLEIMRYLKPAEADGRPRVLLW 251  
285 NTVEVYSIRCIHKHKGHFSWDSMLKQVPEAPSRDPDWKRIIDSDANGNDVMIMW 344  
252 KKANGAVLEKTLGYNIWYYPESNTNLETMTNNOLEHLGGESEFVMSISYSLGKS 311  
345 KNLSDVANGILLIYVTFQSGSQT--FENVITGTSYKTKLSLDIVSVATAANRRAS 401  
312 PVATLRIPALIOEKSFCIEV----MOACVAEDOLVYKMOSSALDVNTMTIEMEPDVSE 366  
402 PPSKLNIP---RSGNCQVLHPEFKLAFPKDOLWEMTPQNSKLDGYIEMCNKYAKE 457  
367 PTLTSMESVSQATWMTIIOOKLKPFMCYNISVYMLHDKVEPYSIAVAKEGVPSEBE 426  
458 GCVSMDQRESNNGVTELRGELPEHKCYWKIVQLYKDCESVSEEVYLDQGPPIVGPS 517  
427 TKVENIGVKTITWKEIPKSERKGIICNTYIFQAEGSGFKSTVNSILOYGLESILKR 486  
518 IHTNOVEKRAIPQMTYVPEPKNGFIRNTYILIKPHNGNTAVYINQTLNITVYGAWK 577  
487 KTSYIYOVMASTSAGTNGTISINFKTLSFSVFEIILITSLIGGLIILITVAYGLKRP 546  
578 HTVLCTHA-GIOERGGKDGPIFTFTTLKFANGEVEAIVSCVAFLLIVLAVILCFNNR 636  
547 NKLHLDMPTVPYNAESSIAW-----HGDDFKD-----KLNKES-DD 584  
637 DLKIKHMPNVPDPSKSNIAQWSPQTPNRHDFNAKGHPFDGSEFTDVSVAVEITKQKEQ 696  
585 SVNTEDELRIKCSPPSKLVLDKLVNFGNV-----LQEIFDEARTGQENNLGGEKN 637  
697 DIKMDPLKNTSP-----LSSGIGSSCLSSPRLASDCDEVEASQTTSTVOYS 748  
638 GYVTCPRPDCPLKSEELVPSPEIPPKSQYLRSRMEGTRP---EAKEQLFSQS 693  
749 TVIISGRDQD-----SAVIP-----HVFSR-SESTQPLDCEERPEEHAD- 791  
694 LVPHLCEGAP---NPLKNSVAREP-----LVSEKLPEH 727  
792 -----KEGEPQGANQYFKQNGREDFTNKLQALHOEPEH 826

RESULT 8  
057520 PRELIMINARY; PRT; 710 AA.  
AC 057520;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)

01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Gp130p3 (Fragment).  
CN Xp130.  
OC Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Chen J., Grace A., Chien K.R.;  
RT "Partial characterization of putative Xenopus gp130";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF041846; AAC03532.1; -  
DR HSSP: P40189; IBOU.  
DR InterPro: IPR003961; FN.III.  
DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
DR Pfam: PF00041; fn3; 4.  
DR SMART: SM00060; FN3; 3.  
DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 710 AA; 79849 MW; BFA7C7E32BCE6F CRC64;

Query Match 15.5%; Score 606; DB 13; Length 710;  
Best Local Similarity 25.5%; Pred. NO. 1.3e-39;  
Matches 178; Conservative 122; Mismatches 319; Indels 78; Gaps 18;

77 NRASCFELPRITTPDNTYIEAENGSGVYKSHMTYRLNIAKTEPKIFRYKPVYGI 136  
1 NSGCSIYPEFOGFVDITLQVEKNELGSGESPTLVDPVNIYKPNPQSDLSIAVEL 60  
137 KRMIOIEMIKELAPVSSDLKYTLRFVTNSTSMWENFAKRRDKNOTYMLTGLDPTE 196  
61 PNAIKIKRNLNLAFT--LKNIRYRPVKQDW-EMVPEDTASHRDSFTLODLPYTE 117  
197 VVIALRCVAKSK-FMSDMSOEKGMTEEAPC-GLEIMRYLKPAEADGRPRVLLWKA 254  
118 YEVSRCKEKEDRGFSWDSMEVKKQVPEAPSRDPDWKRIIESPDANGNEVIMWKNL 177  
255 RGAPVLEKTLGYNIWYYPESNTNLETMTNNOLEHLGGESEFVMSISYSLGSPA 314  
178 SDSVANGILLIYVTFQSGSQT--FENVITTSYKTKLSLDIVSVATANGRPASPS 234  
315 TLRIIP-----AIOEKSFCIEVMOACVAEDOLVYKMOSSALDVNTMTIEMEPDVSEPTT 369  
235 KLNIPRSGNCVLLDOEFR---VTFPEKEKLWEMTPPNKSLDGYIEMCNKYAOEGCI 290  
370 LSMESVSQATWMTIIOOKLKPFMCYNISVYMLHDKVEPYSIAVAKEGVPSEGETKV 429  
291 SDMOETRNNGVTELRGELPEKCYLKVLYKDCESVSEEVYLDQGPPIVGPNIHT 350  
430 ENIGVKTITWKEIPKSERKGIICNTYIFQAEGSGFKSTVNSILOYGLESILKRTS 489  
351 KOVEKRYALDMPTVPEPKRNGFIRNTYITKSSGNASTYVIDPTDTEYILSLLEGNTL 410  
490 YIVOVMASTSAGTNGTISINFKTLSFSVFEIILITSLIGGLIILITVAYGLKPKL 549  
411 YSVHVAATVEEGKDGPIFTFTTLKFANGEVEAIVSCVAFLLIVLIGVLMCFNKRDLI 470  
550 THLCMPYVNPNAESSIAW-----HGDDFKKLMKESDQSVNTEDELRIKCS 597  
471 KKHIMPVNPDPSPSKSNIAQWSPQTPNRHDFNTKGHFPDGSFTDVSVAVEITAEHO-----K 525  
598 TPSPDKLVLDKLVNFGNVLOEIFTDEARTGQENNLGGEKNQYVTCPRP-----DCPLGK 652  
526 SEQDIKSMPLKKN-----TSE---GSSSGIGS-----SCLSSPRLISDCDEVE 568  
653 SFEELPVSEIPPKRSQYLRSRMBGTRPEAKKQLLS-GSLVPHLICF----- 701  
569 SAQTTSTVQYSTVIISGYRDQPSAVAPH-----VFSRSESTQPLDCEERPEEPGPGD 623

OY 702 -BGAP---NPKNSVTAREFL--VSEKLEPHTKGEV 732  
 DB 624 KEGEPGQNOYFKONCLEDFTNKLQOEPSHTQEQ 660

## RESULT 9

O8BN24 PRELIMINARY: PRT: 848 AA.  
 ID O8WN24  
 AC O8WN24: 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Interleukin 12 receptor beta 2 chain (fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Solano-Aguilar G.I., Zarlanga D.S., Beshah E., Vengroski K.,  
 RA Gasbarré L.C., Junker D., Cochran M., Weston C., Valencia D.,  
 RA Chiang C., Lunney J.K.;  
 RT Limited effect of recombinant porcine interleukin-12 on porcine  
 lymphocytes due to a low expression of IL-12 Beta2 receptor.\*;  
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF48143; AAL60218.1;  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
 DR Pfam: PF00041; fn3; 4.  
 DR SMART: SM00060; FN3; 4.  
 DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 KW Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 848 AA; 94753 MW; AD66C885A27DA427 CRC64;

Query Match 11.0%; Score 430.5; DB 6; Length 848;  
 Best Local Similarity 23.8%; Pred. No. 1.8e-25;  
 Matches 193; Conservative 108; Mismatches 329; Indels 181; Gaps 37;

OY 15 KFSLAALPAKPNISCVY-YRKNLCTMSPKETS-YTOYVKTAFGEHNDCTNS 72  
 DB 106 EISVGVPEQPNQVNSCMKGEGYACSMDCRGDRHTLTATYLLQLN--GPK--NLTWOK 160  
 OY 73 STSE---NRASCSEFLPRITIPDNTYIEVEANGGVIKSHMTYRLNIATKTEPKIFR 129  
 DB 161 QCSVDYCCSLDGLINLPESPESSTYTAQTAINSLGTASSFCFTLLDVVRPLPMDIR 220  
 OY 130 VKPVIGIKRMIOIEIKPELAVSSDLKTYTLRFYVNSTSMVEVFAKNRKDKNOTYLT 189  
 DB 221 IKCVNASMSTCTLQWRDEGLV-----LNLRLRYRVPYSRSMNVN-ATNAKGR--HDLV 271  
 OY 190 GLOPTEVIALRCVAKESK-FWSDMSQKKMGTEEPAGC-LELMRVLKPAEADGRPV 247  
 DB 272 DLKPTTEFEFOISSRPHLOKGRMSWSLSLTQTPKEKPTGLMDVWYMKOHIDY-ROOI 330  
 OY 248 RLWK-----KARGAVLEKTLGYNIWYPPESNTNLTEMTNTNOQLHLGSEFWVSM 302  
 DB 331 SLFWKNLISLEARG-----KILHYQVTLQEVAGNATJONTIERSWMTIPTRTGIMAA 385  
 OY 303 ISYNSLGSVPATLIPALQESFOCIEVMAQVA-----EDOLVVKWOS- 347  
 DB 386 VSAANSKSSSLPTR-----INADLCGAGLAPQOVASANPEGSIDLIVKWTSP 433  
 OY 348 ---SALDVMTMMIEMFPDVDS-----PTTLMSWSVSQATMMTIOQOKIPFWCYNISV 398  
 DB 434 GEGATAVEIYVEM-----RELHLGGMQPLSLMSPRPYPNTSTLISINIKPIYCEYELR 488  
 OY 399 YPMLHDKVGEPYSIOAVAKGVPEGPEPKVENIGKVTITVTKELIPKSEKGIICNTYI 458  
 DB 489 HALSDQDGRS-SINGDLKHKAPLSGPHINAISEKKSILISMDIETPAQOEGCILHYRI 547

OY 459 FYQAEKGKFSK-----TVNSILQYGLSLKRRKSYIVQVMASTSAG-CTNGTSINF--- 510  
 DB 548 YMKERDSQDQPOLCELPYVSPKSHPINSLQGRVTVLMMTLTAAGSEPOGNERFCIQ 607  
 OY 511 KTLFSVFETIILITSLIGGGLILITLYAVGK-----KPKTLHLCPWTV 557  
 DB 608 GRANNSTF-----VAPSIQAVITVGVSFMRGFRQKVFALLALRP-----QWCSREI 655  
 OY 558 PPAESSIATWHGDPEKDKLNLKESDDSVNTDRILKPCSTPS--DKLVIDKLNVNF--- 612  
 DB 656 PDPANS--TW-----AKYPIVEEKQSLT-DRLADMPTPEEPPLVINEVLQVPTV 706  
 OY 613 -----GNVLOEIFTEARTQEN-----LGCEKNQY 639  
 DB 707 FRPRLHNPMPGKQGLQGHNASEEDPSSASSPPRRLATGTAVIDLYKVLGSR--- 762  
 OY 640 VTCPRPDCPLCKSFEELPVSP-ELPPKRSQYLRSR--MREGTRP--EAKDQLFSGOS 693  
 DB 763 -----RPSKPGNPVSHLVLPVDYLPTEGYLPSNIDYLPSEARITDSLEL----- 811  
 OY 694 LVPDHLCGEGAPNPKNSVTAREFLVSEKL 724  
 DB 812 --PQHISLVFSP-----NSLHPLTFSCGEKL 836

## RESULT 10

O8MJ51 PRELIMINARY: PRT: 861 AA.  
 ID O8MJ51  
 AC O8MJ51: 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Interleukin-12 receptor beta 2.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kohno T.;  
 RT Cloning of porcine interleukin-12 receptor beta 2 gene.\*;  
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF30213; AAM47543.1;  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003529; Hemtopoptn\_L\_F2.  
 DR Pfam: PF00041; fn3; 3.  
 DR SMART: SM00060; FN3; 4.  
 DR PROSITE: PS01353; HEMATOPO\_REC\_L\_F2; 1.  
 KW Receptor.  
 SQ SEQUENCE 861 AA; 96055 MW; 2AB663E3C5F42534 CRC64;

Query Match 10.9%; Score 425.5; DB 6; Length 861;  
 Best Local Similarity 24.3%; Pred. No. 4.8e-25;  
 Matches 194; Conservative 109; Mismatches 339; Indels 157; Gaps 37;

OY 15 KFSLAALPAKPNISCVY-YRKNLCTMSPKETS-YTOYVKTAFGEHNDCTNS 72  
 DB 117 EISVGVPEQPNQVNSCMKGEGYACSMDCRGDRHTLTATYLLQLN--GPK--NLTWOK 171  
 OY 73 STSE---NRASCSEFLPRITIPDNTYIEVEANGGVIKSHMTYRLNIATKTEPKIFR 129  
 DB 172 QCSVDYCCSLDGLINLPESPESSTYTAQTAINSLGTASSLPSTFTLLDVVRPLPMDIR 231  
 OY 130 VKPVIGIKRMIOIEIKPELAVSSDLKTYTLRFYVNSTSMVEVFAKNRKDKNOTYLT 189  
 DB 232 IKCVNASVSTCTLQWRDEGLV-----LNLRLRYRVPYSRSMNVN-ATNAKGR--HDLV 282  
 OY 190 GLOPTEVIALRCVAKESK-FWSDMSQKKMGTEEPAGC-LELMRVLKPAEADGRPV 247  
 DB 283 DLKPTTEFEFOISSRPHLOKGRMSWSLSLTQTPKEKPTGLMDVWYMKOHIDY-ROOI 341  
 OY 248 RLWK-----KARGAVLEKTLGYNIWYPPESNTNLTEMTNTNOQLHLGSEFWVSM 302



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Db      342 SLFWKNLSLSEARG-----KILHYOYTLQVEAEGNATLQNTERNSTWTPRTGIMAAA 396
Oy      303 IS-INSLSKSPVATLRIPALIOEKSPQCIEMQA-CVABDOLVVKMQS---SALDNTMMI 357
Db      397 VSANSSKSSLPTRINTADLCAGILAPQOVSANDEGSDNLLWTKTSGBEGATVAOEIVV 456
Oy      358 EMFPDVDS-----PTTSMESVSQATNMTIQODKLKPPWCYNISVYPMHLKVGEPY 410
Db      457 EM-----RELHRLRGMOPLSLMSPRYNTSTLISDNKPYICYEIRHALISGQ-GGCS 510
Oy      411 SIQAAKEGVSEGEPTKVENIGVTVITTKELPKSERKGIICNTYTFIOAEGGKFSK 470
Db      511 SIRDLKHKAPLSPHINAISEEKGSILISWDEIPAOQOMGCIHRYRYMKERDSOQ 570
Oy      471 ----TVNSSILOYGLESIKRKTSYIVQMASTAG-GINGNISINP---KITLSVFELL 522
Db      571 LCEIPRYVSPKSHPNLSQPRVTVLWMTALTLAGESPQGNRECECLOGKANWTF----- 626
Oy      523 ITSLIGGLILILITVAVGLK-----KPKKLTHLCWTPVNPAPAESIATWH 569
Db      627 ----VAPICIAVITVGVFSMKRCFRQKVFVLLALRP-----QMGREIIPDANS---TW- 674
Oy      570 GDDEKDKLNKESDSDVNTEDRIKPCSTPS--DKLVIDKLNVN----- 612
Db      675 ----AKKPYIEEKKOISL-DRLADMPTPEEPPELVINEVLPQVTPVFRPRHHNMPGK 729
Oy      613 GNVLOEIFTDEARQOENN-----IGGKNGVTCFRPRDCLG 651
Db      730 GORLOGRHASEDEGSSASPPPPRALTAETGPAVDLYKVLGSR-----RDSKPG 780
Oy      652 KSFEELPVSP-EIPPRKSQYLRSRW---PEGTRP--EAKEQLLFSGSLVDPHLCCEGAP 705
Db      781 NPVSLFLVLPVDYLPTHGTYLPSNMIDYLPSSHAPITDSLEEL-----PQHISLSVFP 832
Oy      706 NPYLKNSTVAREFLVSEKL 724
Db      833 S-----NSLHPLTFSCGEXL 847

RESULT 11
OyBEG2 ID 09BEG2 PRELIMINARY: PRT: 861 AA.
AC 09BEG2;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE IL-12 receptor beta2 precursor.
GN IL-12R BETA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node;
RA Waldevogel A.S., Zahner A., Heussler V.T.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ308426; CAC28320.1; -.
DR HSSP: P40189; IBCU.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hemtopophtn_L_F2.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 4.
DR PROSITE: PS0153; HEMATOPO_REC_L_F2; 1.
DR Receptor; Signal.
FT SIGNAL 1
FT CHAIN 24 861 POTENTIAL.
FT SEQUENCE 861 AA: 96208 MW: 487B1E5D1E358E5B CR664;
SQ
Query Match 10.6%; Score 412.5; DB 6; Length 861;

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Best Local Similarity 24.1%; Pred. No. 5.2e-24;
Matches 195; Conservative 117; Mismatches 321; Indels 175; Gaps 40;

Oy      15 KESLAALPAKPEINISCVYV-YRKNLCTWSPGKENS-YTOYTKRTVAFGKHONCTNS 72
Db      117 EISGVVPEQPRNSICIOGKRGVTCYWHGRDHLTAATYLLQ--GKR--NLTWOK 171
Oy      73 STSE---NRACSEFLPRTITPDNYTIEVEANGDVKISHMTYRLNIAKTEPPKIFR 129
Db      172 QCNBHYCHDLGINTLPRESLESYTVKTAINSLSGSSSPFSTLLDIYRPLRPMOIR 231
Oy      130 VKPVLGIRMTQIEMIKELAPVSSDKYTLRFPTVNSTWMEVNF-AKNEKDKQTYN 187
Db      232 IKFVNASVDRCTLLMRDEGLV-----LNLRLRYRINSRWMMVYTNAGRHD----- 280
Oy      188 LTGLOPTEFEYVIALRCVAKESK-FWSDMSQEKMTTEEAQCG-LELIRVLKPAADRR 245
Db      281 LLDLRPFTEYEFQISSKHLKGSWDSSESIRQTPEEPFGMLNVMYMQHIDYN-RQ 339
Oy      246 PVRLIMK-----KARGAVLEKTLGYNIMYYPESNTNLETMTNTNQLLEHLGSEFV 300
Db      340 QISLFWKNLSLSEARG-----KILHYOYTLQVAGGETTLQNTITHTSWTVIIPRTGMA 394
Oy      301 SMIS-YNSLSKSPVATLRIPALIOEKSPQCIEMQAQVAE-----DOLVVKW 345
Db      395 AAVSAANSKGS-----LPT-----RINTDLGAEALLAPQOVLAKSGMDKLWYTW 441
Oy      346 ---QSSALDVNTMIMEM---FPDVSEPTTSLMESVSQATWTF-----IQODKLKFPW 392
Db      442 TPPEKATAAVOEYVEMRELHPGAGMOP-PLGW-----LMSPYRLSALISENIKRYI 493
Oy      393 CYNISVYPMHLHDKVGEPYSIQAAKEGVSEGEPTKVENIGVTVITTKELPKSERKGI 452
Db      494 CYEINVAHLADGQ-GGCGSTNGNSQHKAPLSPHINAISEEKGSVLISMDLPAEQMG 552
Oy      453 ICNTYTFIOAEGKKG-----FSKYVNSSILOYGLESIKRKTSYIVQMASTAG-GT 503
Db      553 ILHYRIYMKERDSNSQPOLCEIPYRISPNs-----HPIDSLQPRVTVLWMTALTAAGESP 608
Oy      504 NOTSINFKLSFVFEIILITSLIGGLILILITVAAGLKKPKNLTHL---CWPTYPN 559
Db      609 QGNREPEFCLOGKANSTFVAPISMAVIMVGLSMRCFRQKVFVLLALRPWCSEKELPD 668
Oy      560 PAESSIATWGHGDFDKLNKESDSDVNTEDRIKPCSTPS--DKLVIDKLNVN----- 612
Db      669 PANS---TW-----AKKPYIEDEKQTL-ALDRLLTEWTPPEEPPELVINEVLCRTVPFR 719
Oy      613 -----GNVLOEIFTDE-----ARTGOENNLG---GKNGVYTC 642
Db      720 PPHHRSWSEKGGGQGHYTSSEDTGYSSASPPPPRAPTAETGQVDLYKVLGSKG----- 774
Oy      643 PPRPCCPLGKSFEELPVSP-EIPPRKSQYLRSRW---PEGTRP--EAKEQLLFSGSLVP 696
Db      775 ---PDSKGNPASPLTILPVDYLPTHDGYLPSNMIDYLPSSHAPITDPLEEL-----P 823
Oy      697 DHLCEGAPNPYLKNSVTAREFLVSEKL 724
Db      824 QHISLSTPS-----SLRPLTFSCGEXL 847

RESULT 12
Oy0535 ID 070535 PRELIMINARY: PRT: 1093 AA.
AC 070535;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Leukemia inhibitor factor receptor alpha-chain.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

```

RP SEQUENCE FROM N.A.  
 RP STRAIN-Mister-Imamichi, TISSUE-Liver;  
 RX MEDLINE-98007878; PubMed-9349722;  
 RA Alkwa J., Ikeda-Naito S., Ohgane J., Min K.S., Imamura T., Sasai K.,  
 RA Shioita K., Ogawa T.,  
 RT "Molecular cloning of rat leukemia inhibitory factor receptor alpha-  
 RT chain gene and its expression during pregnancy.";  
 RT Blochm. Biophys. Acta 1353:266-276(1997).  
 RL EMBL; D86345; BAA25907.1; -.  
 DR HSSP; P40189; 1BOU.  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003961; FN.III.  
 DR InterPro: IPR003529; Hemtopoptrn\_L.F2.  
 DR Pfam: PF00041; fn3; 4.  
 DR SMART: SM00060; FN3; 4.  
 DR PROSITE; PS01553; HEMATOPO\_REC\_L.F2; 1.  
 KW Receptor.  
 SO SEQUENCE 1093 AA; 122394 MW; 08DA3DEAF8F5E3F6 CRC64;

Query Match	10.1%	Score 395.5	DB 11	Length 1093
Best Local Similarity	23.2%	Pred. No. 1.7e+22		
Matches 151	Conservative 115	Mismatches 248	Indels 137	Gaps 28

QY	22	PAKPNISCVXYXRNLCNCTMSPGKETS- ----TQYUWKPRYABEKKDNCNTNST- --	74
Db	329	PDVQKJSCETHDLKEIICSNWPGITGLVGRNTEIYL- ----FESISGKAVFH	379
QY	75	-SENKASCFLLPRITIBD- ----NYTIEVEAENGGVIKSHMTYMLNIAKTEPPKIFR	129
Db	380	RFEELANETMYLTKMADPOEIHNFTL- --TANPLQOTESALIVNTEVALHVPISL- K	436
QY	130	VKPYLGIRKMQIEIKPELAVSSDKTYTLFRIYVNSTSMWENFAKRRKD- ----	181
Db	437	VKDY- NSTVYTLNMYLPG- ----NFTKINVLQOIEICKANKKKEVRNVTMKG	482
QY	182	-KNQYENLT- -GLQPFTEYVIALRCAYEKSKFWSMOSQKMOKMTBEEAPC- -GLETRVLK	237
Db	483	AEDSYHYAVADKLNLYITLTFPRVRCSSSEFFMKMKMSNKRLLTTEATYTSKGPDIYR- --	539
QY	238	PAEADGRPRVRLMKKARGAPVLE- --KTLGINIMYIPESNLTLETMTNTMOQLEHLIG	294
Db	540	EMSSDGKMLI- IYMP- --LPINENGKILSYNVSCSSSEETQSLEILDPOHKKEIKYN	595
QY	295	GESEFVSMISYNSLCKSP- --VATIRIPIQKSFQCIEMVOACVAEDOLVYKMOSSALD	351
Db	596	KNDYIIISVYANNSAGSSPPKTIASHEIR- ----DITVEAYGIGNRIFLPSMOHNPM	649
QY	352	VNTWMIWEPDVDEPPTLLSMESV- -SOATNMTIOODKILPWCYNISV- ----YPMIL	403
Db	650	TCDYVIKKNCSMSSEPCLLDMTKVPSNSTGVIESDQPOGVARNPYLIVGCGINOQOLLR	709
QY	404	DKWGEPSYQIAYAKEGVSEGEPEYVENIGKVTYITITKEIRPKSERKGIICNTTYQAE	463
Db	710	STIG- ----YIELAPIVAPNFVEJETSADSLVYKDDPIVEELRGLFRY- LFYPOK	761
QY	464	GGKGFSKT- ----VNSIILOYGLESILKRSYIYOVWASVAGTNGT	506
Db	762	GEROTPKRSLTSHSDIKLANIIDISOKTLR- -IADLOGKTYHLVLAATYHGLGCPK	819
QY	507	SINFKTUSFVEIILLITSLIGGGLLIIILTVAYGL- ----KKPKLTHLCP	555
Db	820	SMFVVTKENSV- ----GLIIMILPVAAVIVGVVTSILCYRKREKIMETFFP	867
QY	556	TVNPAEBSIATWIGDDPKDLNLKESDVSVTERIILKPCSTPBDKLYID	606
Db	868	DIPDENCKALQF- ----OKSVCEGSNAKLTLE- -NNPC- -TPNHVEVLE	908

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DT      01-MAY-1997 (TREMBlrel_03, last sequence update)
DE      01-MAR-2003 (TREMBlrel_23, last annotation update)
GN      Oncostatin-M specific receptor beta subunit.
OS      OSMR.
OC      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97115791; PubMed=8999038;
RA      Mosley B., De Imus C., Friend D., Boiani N., Thoma B., Park L.S.,
RT      Cosman D.;
RT      "Dnal oncostatin M (OSM) receptors. Cloning and characterization of an
RT      alternative signaling subunit conferring OSM-specific receptor
RT      activation.";
RL      J. Biol. Chem. 271:32635-32643(1996).
DR      EMBL; U60805; AAC50946.1; -.
DR      Genew; HGNC:8507; OSMR.
DR      InterPro: IPR002996; CR1A.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR003529; Hemtopoptn_L_F2.
DR      InterPro: IPR001005; Myb_DNA_Binding.
DR      Pfam; PF00041; fn3_4.
DR      SMART; SMO0060; FN3_4.
DR      PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
DR      PROSITE; PS00037; MYB_1; 1.
KM      Receptor.
SQ      SEQUENCE 979 AA: 110508 MW: 179852CA3D90DEFF CRC64;

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Query Match	9.68;	Score 375;	DB 4;	Length 979;
Best Local Similarity	23.28;	Pred. No. 6.3e-21;		
Matches 182;	Conservative 122;	Mismatches 292;	Indels 190;	Gaps 35;

QY	24	KPEKISCVYVYXRNLCITCSPKENS	YQYVAKRRYANGK	HONCITNS	72
Db	239	EPRKDFSEITDFLTLCITWDPGIDIALGMSKOPSOSITLFEBS	GEAKLCTHNMCMNQ		297
QY	73	STEENRASCSEFLRITIPDNYTIEVEANGDVAKSHMYTRLENIKTEPRKIFVKP			132
Db	298	ITQDSOETVNFLL	IADNYLRK	RSVNILFNLTHRVYLMNP	336
QY	133	VLGKRIKIQLEMIKPELAPVSSDKYTLRFKRVNST	SMEVNFPAKNR		179
Db	337		FSVNEFVNNTAINTM	KVHSIRNNFTYLCQEL	370
QY	180	-KDKNOTYN	LTGLOFEFTYVIALCAVKESENF	WSDMSQKMGTE	22
Db	371	HGECKMMQIVNISKVNGEYFLSELEPATEYMARVCA	DASHFMKMSWSGONTTLEAA		429
QY	224	-EAPAGCLELMRV	LKPAEADGRRPVRLMLMKAKGAVLEKTYLGYNIMY	PESNTMLTE	280
Db	430	PSEAP	DVMRIVSLER	GNHTVTLFMKPLSKLANOKLIFYN	473
QY	281	TMTYTNOOLELH			328
Db	474	NLDRPSSS	ELHSHIPAPANSTKLIDRCGYOICVIANNSVGASPA	SVIVISADENR	529
QY	329	IEMQAOCAV	-EDQVLVKKMOSSALDNYMTMIEMFDPVDS	ETPLSMESVS	QAINMT IQQ 365
Db	530	-EVEEERLAGEGFSLSMKPQPGDVI	IGYVDMCDHTODVLGDFQMKVACNTTSTVIST		568
QY	386	DKLKPWCNIAISYR	MLHDKGEPEYSIOAFAKEGVS	SEGEPTVENIGKTV	437
Db	589	DARPEVRDIFRILGISTRICKLEKTKG		YSOELASDNP	HYVDTLTSHF 641
QY	438	TITWKEIPSEKRGILCNYTIFYQAEKG	GFESKTV	NSSILQYGL	481
Db	642	TLSMKDYSTESQGFIOGYHYVLKSKARQCH	PREKAVLSDGSECKYKIDNPEKALIV		701
QY	482	ESLKRRTSYIVQVMASTSGNGTNGSINF	KLTSVSVEITLITSLIGGLILITLTV		540
Db	702	DNKRPSEFEFTTPTTSAG	EGCSAFETKVTTPDESSMLHILLPMVECVLHVMC		759

ID	Accession	Species	Gene	Protein	Length	Score	Similarity	Matches	Conservative	Indels	Gaps
QY	541	YGLKPKNLTFLHPTVLPNPPSSIAWGGDDFKDNL	---	KSDSDSVNVEDRLTKPCS	597						
Db	760	Y--LKSMQIKETCTIPDIPDPKSSILS--IKFENPHLLIMNVSDCIPDAIEVSKPEG	815								
QY	598	TPSDKLVIDKLV---VNEGVNLQEIFTEARTGO-----EN--NLGGERKNVYTCPF	644								
Db	816	TKIQFLGRKSLTETELTRKPNVYLLPTEKHNSGPGPICPENLITYNQASDSG--SCGH	873								
QY	645	RPDCPLKGSFEEELVSP--IPPKRSQYLKSRMPEGTRPEAKKEDLLFSGQSLVPDHLCF	702								
Db	874	VVPSPKAPSMGLMTSPENVLKALEKNMNSL--GEIPAGETSLNVYSQLASPWFQDKD	930								
QY	703	GAP--NP 707									
Db	931	SLPTNP 936									
RESULT 14											
080F07	080F07	PRELIMINARY;	PRF:	1083 AA.							
AC	080F07	01-JUN-2002 (TRENBLREL 21, Created)									
DT	01-JUN-2002 (TRENBLREL 21, Last sequence update)										
DT	01-MAR-2003 (TRENBLREL 23, Last annotation update)										
DE	Cyclokinine receptor-beta precursor.										
GN	LIFR.										
OS	Gallus gallus (chicken).										
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
CC	Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;										
OC	Gallus.										
OX	NCBI_TaxID=9031;										
RN	[1]										
RP	SEQUENCE FROM N.A.										
RA	MEDLINE=21870003; PubMed=11880348;										
RT	Duong C.V., Geissen M., Kohner H.;										
RT	"The developmental expression of vasopressin receptor (VPR)										
RT	in cholinergic sympathetic neurons depends on cytokines signaling										
RT	through LIFRbeta-containing receptors."										
RL	Development 129:1387-1396(2002).										
DR	EMBL, AJ416111, CAC94786.1; --										
DR	InterPro: IPR002926; CRIA.										
DR	InterPro: IPR003961; FN_III.										
DR	InterPro: IPR003529; Hemtopoptn_L_F2.										
DR	InterPro: IPR003531; Hemtopoptn_S_F1.										
DR	Pfam: PF00041; fn3; 4.										
DR	SMART, SM00060; FN3; 3.										
DR	PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.										
DR	PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.										
KW	Signal; Receptor.										
FT	SIGNAL 1 24	POTENTIAL.									
FT	CHAIN 25 1083	CYTOKINE RECEPTOR-BETA.									
SO	SEQUENCE 1083 AA; 120863 MW; 885862080068F5B7 CRC64;										
Query Match											
Best Local Similarity 22.2%; Pred. No. 9.7e-20;											
Matches 141; Conservative 106; Mismatches 282; Indels 106; Gaps 22											

[illegible]

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QY 112 TYWRLENIATKPEPKIFRVKPEVLGKRMIOIEMIKPELAPVSDLKYYT-----LRFRTV 165
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Db 349 T-MKVH-----SHGNNTLILQVVKLOQGEV 372
| : : |
QY 166 NSTSMMEYNFAKNKKDKNQITNLGLOPTEYVIALRCVAKESKF-WSDMSOEKMGMTPE 224
| : : |
Db 373 IHEHNSVHMSAN-----YLFSDLPDPTKYKAFVRCASANHFMKWSMDWTOKEFs--TPE 424
| : : |
QY 225 EAPC-GLELWRLVLPADAGRRPRLLMKKARGAPVLEKTLGYNIWYYPESNTLUTETMN 283
| : : |
Db 425 TAPQALDVMR--QVMSNGRRIVTLERKPLKQANGKIISYNI--VVENEAKPTSEH 480
| : : |
QY 284 -----TTNQOLELHGGSEFWVSMISYSLGSPVATLRIP-----AIQEKSPQIE 330
| : : |
Db 481 YCVWAPALSTNLSDL---QPYKIRITANNSMGASPESLAVLSNDGHEVKEKTIKGI- 535
| : : |
QY 331 VMQACVADOLVWQSSALDVNTWMIEMFPDVDEPTTLESSEVS-QATNWTIQDQKLK 389
| : : |
Db 536 -----KDAENISMEPVSGDTMGVYVDMCAHSODORDLOMKNLGPNITSTTTSDDFK 588
| : : |
QY 390 PFMCYNISVYP-MLHDVVGEPYYSIOAYAKEGVPESEGPETKVENIGVKTVTITWKEIPKE 448
| : : |
Db 589 PGVRYNFRIPERSVEHKAFLVEKQGYTOELAPLVNPKVELIPYSTPNSFVLKMPDYDSDF 648
| : : |
QY 449 RKGIICNVTITFYQA--EGKGFSKTY--NSSILOYGL-----ESLKRRTSYIV 492
| : : |
Db 649 QAGFIKGYLVYVKSKEQCNQPMWERTLLPDNSVLCCKYDINGSEKTLTVENLOPESLYEF 708
| : : |
QY 493 QVMASTSAG-GTNGTSINFKT---LSFSVEIILITSLIGGLILILIVAYGLKKPK 548
| : : |
Db 709 FVTPYTSAGRPQNETFTKVTTPDARSHMLQIILPMT---LCVLLSIIVCYW--KSOW 761
| : : |
QY 549 LTHLCMPVTPNPASISATWGHGDFKDK-----LNLEKE-----S 582
| : : |
Db 762 VKKCYRPDIPIPKYSSILSL---IKSKKNPHLIMNYKDCIPDYLEVINAKAEGSKTCQVG 817
| : : |
QY 583 DDSVNTEDRIKPCSTPSDK-----LVIDKLNVN----- 611
| : : |
Db 818 SGKLIHEDVPTKRPPIVPEKDSGPPVCIFEFENFTYDQSAFDSGSHGLIPGLKDTAHL 877
| : : |
QY 612 -----FGNVLOEIFTD---EARTQENNLGSEKNGYVTCPPRPDCPLKSFEEPLVS 660
| : : |
Db 878 GLAPPNKFOVNLKNDYMKPLVESPTETSLI-----YVSQLASPMC---GDKDTLATE 928
| : : |
QY 661 PEIPPRKSOYLRSRMPEGT--RPEAKE 685
| : : |
Db 929 PPVPVHGSEYKROMVVPGLASPSLKE 955
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Search completed: August 4, 2003, 11:25:15  
Job time : 117 secs